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OM nucleic - nucleic search, using sw model

Run on: February 20, 2003, 04:22:08 ; Search time 4768.86 Seconds

(without alignments)
10661.374 Million cell updates/sec

Title: US-09-804-014A-7

Perfect score: 1747

Sequence: 1 gaagcctgattctgacgaaa.....agttctgacgacctcacac 1747

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

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18: em_in:*

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21: em_or:*

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28: em_un:*

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32: em_htg_other:*

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35: em_htg_rtd:*

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41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1747	100.0	1747	6	AX268121
2	1606.4	92.0	4372	9	HSN310479
3	1408.2	80.6	1447	9	AE315818
4	1321.6	75.6	1341	6	AX352535
5	1069	61.2	1599	6	126643
6	1065.8	61.0	1599	10	AF032099
7	844.2	48.3	157633	9	AC008687
8	658.2	37.7	1551	4	OC038240
9	643.2	36.8	90458	2	AL513469
10	640.6	36.7	155343	9	AL365361
11	639	36.6	1836	9	HUMKCHN
12	637.4	36.5	3004	9	HUMKCHN
13	635.8	36.4	1820	9	HUMKCHN
14	632.2	36.2	208632	2	AC073711
15	632.2	36.2	2459	10	MMKCMC2
16	631.8	35.2	172671	2	AC128792
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ALIGNMENTS

RESULT 1

AX268121 1747 bp DNA linear PAT 26-OCT-2001

LOCUS Sequence 7 from Patent WO0168651.

DEFINITION AX268121

ACCESSION AX268121.1 GI:16516622

VERSION

KEYWORDS

SOURCE

ORGANISM human.

human sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 Padigar,M., Vernet,C.A., Fernandes,E., Shinkets,R.A., Spaderna,S.K., Majumder,K. and Li,L.

Polyptides and nucleic acids encoding same

TITLE

JOURNAL Patent: WO 0168851-A 7 20-SEP-2001;
 FEATURES Curagen Corporation (US)
 Location/Qualifiers
 source 1.1747
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 255 a 582 c 575 g 335 t
 ORIGIN

Query Match 100.0%; Score 1747; DB 6; Length 1747;
 Best Local Similarity 100.0%; Pred. No. 1.1e-230;
 Matches 1747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GAAGCCTGATTCTGACGAAACACACGACACGGAACATGAGAGACGACGAGATC 60
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DB 421 GCGGCGCGGACGCTGGGCGGCTCCGCGGACACGTCGTAGGGAGACCGCGCGCGCG 480
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DB 1621 GGGCAAGGCCAATGGGGGCTGTGGAGCGGGAAGTACTGAGCTACACCTCCACTCTG 1680
QY 1681 GGGACCCCGGCAAGACCTGTCACCGAAGTGTGGAAGACGTTGAGGTGTGCAAGAC 1740
DB 1681 GGGACCCCGGCAAGACCTGTCACCGAAGTGTGGAAGACGTTGAGGTGTGCAAGAC 1740
QY 1741 CTCACAC 1747
DB 1741 CTCACAC 1747

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RESULT 2
 HSA310479
 LOCUS
 DEFINITION
 Homo sapiens mRNA for potassium voltage-gated channel,
 Shaker-related subfamily, member 7 (KCNAT7 gene).
 ACCESSION
 AJ310479.1 GI:12830376
 VERSION
 KCNAT7 gene; KVL7 gene; potassium voltage-gated channel,
 Shaker-related subfamily, member*.
 KEYWORDS
 human.
 SOURCE
 Homo sapiens
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Qy	1486	TGCGGGCGGCGACTATTTCCTCCGACAGTGGCCGTCATTTGCTCCAAATTTCAGCTACTT	1545
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Db	1556	TTATACCGGGAGACAGAGGGCGAAGAGGCTGGATGTTCAACCATGTGGACATGCGAGCC	1615
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Qy	1666	ACCACCTCCACTCTTGGGACCCGCCAGGAAACCTGTGTACACGGAAGTGTGAGAAACAGT	1725
Db	1676	ACCACCTCCACTCTTGGGACCCGCCAGGAAACCTGTGTGTACACGGAAGTGTGAGAAACAGT	1735
Qy	1726	TGAGGTCTGCAGAGCACTCACAC	1747
Db	1736	TGAGGTCTGCAGAGCACTCACAC	1757

RESULT 3	
AF315818	
LOCUS	1447 bp mRNA linear PRI 19-JUN-2001
DEFINITION	Homo sapiens voltage-gated potassium channel KCNA7 mRNA, complete cds.
ACCESSION	AF315818
VERSION	AF315818.1 GI:1448554
KEYWORDS	.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens

REFERENCE	1 (bases 1 to 1447)
AUTHORS	Bardien-Kruger, S., Wulff, H., Arieff, Z., Brink, P., Chandý, K. G. and Corfield, V.
TITLE	Characterization of the human voltage-gated potassium channel gene, KCNV7, a candidate gene for inherited cardiac disorders, and its exclusion as cause of progressive familial heart block I (PFHBI)
JOURNAL	unpublished
REFERENCE	2 (bases 1 to 1447)
AUTHORS	Bardien-Kruger, S., Wulff, H., Arieff, Z., Brink, P., Chandý, K. G. and Corfield, V.
TITLE	Direct Submission
JOURNAL	Submitted (22-OCT-2000) SANBI, University of Western Cape, Woodderdam Road, Cape town 7535, South Africa
FEATURES	Location/Qualifiers
SOURCE	1..1447

CDS

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BASE COUNT
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RESULT 4
AX352535 1341 bp DNA linear PART 06-FEB-2002
LOCUS Sequence 7 from Patent WO0194390.
DEFINITION AX352535
ACCESSION AX352535
VERSION AX352535.1 GI:18617765
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Curtis, R.A.
52906, 33408, and 12189, potassium channel family members and uses
thereof
Patent: WO 0194390-A 7 13-DEC-2001.
JOURNAL Millennium Pharmaceuticals, Inc. (US)
FEATURES
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BASE COUNT 190 a 443 c 411 g 297 t
ORIGIN

Query Match 75.6% Score 1321.6; DB 6; Length 1341;
Best Local Similarity 99.5%; Pred. No. 2,7e-172;
Matches 1337; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

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QY 914 CTGATGCTCTCAAGCAATGCTGGAATTCACCCCGCTGCTCAATGACCGGTTTC 973
Db 538 CTGATGCTCTCAAGCAATGCTGGAATTCACCCCGCTGCTCAATGACCGGTTTC 597
QY 974 TTGCTGTGGAGAGCGCTGTATTTGTTGCTTGTGAGCGCTGCTGCTGCTGCTGCTG 1033
Db 598 TTGCTGTGGAGAGCGCTGTATTTGTTGCTTGTGAGCGCTGCTGCTGCTGCTGCTG 657
QY 1034 GTCTGTCAAGCAAGGCTATCTTCAAGAAAGATGATCAACTCATGATTTTGGGCT 1093
Db 658 GTCTGTCAAGCAAGGCTATCTTCAAGAAAGATGATCAACTCATGATTTTGGGCT 717
QY 1094 ATCTCTCTCTACTTGTGCACTGGGCGGCGGAGCTGGCGGCGGAGGCGGCGGCGG 1153
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QY 1154 CAGGCGATGTCATGGGCGATCTGAGAGATTCATCCGATTTGGTGGTCTTCCGATCTTC 1213
Db 778 CAGGCGATGTCATGGGCGATCTGAGAGATTCATCCGATTTGGTGGTCTTCCGATCTTC 837
QY 1214 AAGCTTCCCGGACATCAAGAGGCGCTGCAAAATTTGGGCGAGAGCGTTGGGCGCTCATG 1273
Db 838 AAGCTTCCCGGACATCAAGAGGCGCTGCAAAATTTGGGCGAGAGCGTTGGGCGCTCATG 897
QY 1274 CGTGAGCTGGGCTCTCTCATCTTTTCTCTTATCGGTGTGCTCTTTTTCAGAGCGC 1333
Db 898 CGTGAGCTGGGCTCTCTCATCTTTTCTCTTATCGGTGTGCTCTTTTTCAGAGCGC 957
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QY	1574	GCTGGGATTTAGGCAATGTGACATMGACGCTTGTGGGCCCATCTGAGAGGGCAAGGCCAAT	1633
Db	1198	GCTGGGATTTTAGCCATATGTGACATMGACATGACGCTTGTGGGCCCATCTGAGAGGGCAAGGCCAAT	1257
QY	1634	GGGGGGCTGTGTGACAGGGGAGGTACTGTAGCTTACCACTTCACACTGTGGGACCCCCAG	1693
Db	1258	GGGGGGCTGTGTGACAGGGGAGGTACTGTAGCTTACCACTTCACACTGTGGGACCCCCAG	1317
QY	1694	GAACACCTGTGTACCCGAAGTGA	1717
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RESULT 5			
LOCUS	126643	1599 bp	DNA
DEFINITION	Sequence 9 from patent US 5559009.		linear
ACCESSION	126643		
VERSION	126643.1	GI:1606513	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1599)		
AUTHORS	Chandy,K.G., Kaiman,K., Chandy,G. and Gutman,G.A.		
TITLE	Voltage-gated potassium channel gene, KV1.7, vectors and host cells comprising the same, and recombinant methods of making potassium channel proteins		
JOURNAL	Patent: US 5559009-A 9 24-SEP-1996;		
FEATURES	Location/Qualifiers		
source	1..1599		
BASE COUNT	233 a 521 c 502 g 343 t		
ORIGIN	/organism="unknown"		
Query Match	61.2%, Score 1069; DB 6; Length 1599;		
Best Local Similarity	81.5%; Pred. No. 1.2e-137;		
Matches 1289; Conservative	0; Mismatches 280; Indels 12; Gaps 4;		
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QY	197	CCGCGCGGGGTGCACAGTGGCCCTCTCCCTGCGGCCCTTAGCGCGCGGCTATTTTAC	256
Db	91	CCCGGGGGGTAAACACGCGCCCTCCCGCGCCCTGTGGCGGACCTTTCATGCTATTTT	150
QY	257	GGCGGAGACCGGACACCGGACACCGGGCTGGGGCGCGGCTGGGGCCACACGTGGTTC	316
Db	151	ACCCGCGGACACCGGACACCGGACACCGGAGGTGGCTGCGGCTGGGGCCACACGTGGTTC	210
QY	317	GGGGGTGCGGGGGGTGGCGCGCGCCATGGAGCGGGGTGGCCGGCGCCCGGGGGGTGC	376
Db	211	ACCGGTGCGGGGGGTGGCGCGCGCCATGGAGCCACAGGTGCCCGCGCCCTG---CGTGC	267
QY	377	TGCGAGCGGCTGTGCTCAACGTGGCGGGGCTTGCTTGAAGACCGGGGCGGCGACGCTG	436
Db	268	TGCGAGCGGCTGTGCTCAACGTGGCGGGGTGGCTTGAAGACCGGGGCGGCGACGCTG	327
QY	437	GGCGGCTTCCGGACACTTCTGTAAGGGGACCCAGCGCGCGCGCGCTTCTAGACGAC	496
Db	328	GGCGGCTTCCGGACACTTCTGTAAGGGGACCCCGGTGCGCGCGCGCTTCTAGACGAC	387
QY	497	GGCGGCGCGGATATTTTCTGACACGGGACCGGGCCAGCTTGAAGCGGCTGCTACTAC	556
Db	388	GGCGGCGCGGATATTTTCTGACACGGGACCGGGCCAGCTTGAAGCGGCTGCTACTAC	447
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Db	448	TACCAAGTGGGGCGGCGGCTGAGACGGCCCGGCGCACGTGCCCCCTGAGCTCTTCTGGAG	507
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Db	508	GAGGTGCTCTTCTTACGGGGCTGGG---CGGCGGCTGGCGGGGCTGGGGAGGACGAGGCG	564
Qy	677	TGCCCCGTCGCCCGGAGCGCGCCCTGGCCCCCGCGGCTTGCCGCCAGCTGTGGCTG	736
Db	565	TGCGGGGgt---CGCGGAGCGGCGCGCTGCCCGCG---CCTTGGCGGTACGCTGTGGCTG	618
Qy	727	CTTTTCAGGTTTCCCGAGGCTCCACGGCGCGGCGGCTGGCGGTATGCTCCGTGGCTG	796
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Qy	797	GTCATCCGCTGCTCCATCGTGTCTTTCGCTGTGAGACGCTGCTGATCTTCGCGACGAC	856
Db	679	GTCATCCGCTGCTCCATCGTGTGCTTTCGCTGTGAGACGCTGCGAGACTTCCGCGACGAC	738
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Qy	917	AATGGCTCCAGCCAAATGCGCTGGAAATCCACCCCGCTGCTTCAATGACCCGTCTTC	976
Db	739	AATGGCTCCATCCCAATGCGGACGAGGCGCCCTCCCGGACGCTTCAAGCATCTATCTTT	858
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Db	919	TGCCCTAGCAAAAGCTGHTTCTTCAAGAAATGTATGAACCTTAATGACTTCGTGGCATT	978
Qy	1097	CTTCCCTACTTTGTGGGACGTGGGACCGGAGCTGGCCCCGACGAGGGGTGGGCGACGAG	1156
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Qy	1217	CTGTCCGGGCACTCAAAAGGCGTGCAAATCTTGGGCGAGGCTTCCGGGCTCCATGCGT	1276
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Qy	1277	GAGCTGGGCTCTCTCATCTTTTTCCTTTCATCGGTGTGGTCTCTTTTCCAGGCGCTC	1336
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Qy	1337	TACTTTGCGGAAGTTGAGCGGGGTGAGATCCCATTTTACTAGCATCCGTGAGTCTCTGG	1396
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Qy	1397	TGGGCGGTAGTCACCATGACTACAGTTGGCTATGAGACATGGACCGGCTCACTGTGGT	1456
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Qy	1577	GGGATGTTCACCCCATGTGAGCATGACGCTTGTGGCCCACTGGAGGGCAAGGCCAATGG	1636
Db	1459	GGGATGTACACCCATGTGAGCACACAGCCCTGGGGTACCTGTGAGGCAAGGCTATATGG	1518
Qy	1637	GGGCTGGTGAACGGGAGGACTGAGCTACGACCTCACTCTGGGCAACCCCGCAGGAA	1696

Db 1519 GGGCTGTGTGACTGTGAGTGCCTGAACTTCCTCCACACACTCTGACCCCTGACGAGGAAA 1578

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AF032099

LOCUS AF032099 1599 bp mRNA linear ROD 04-APR-1998

DEFINITION Mus musculus voltage-gated potassium channel Kv1.7 (Kvnc7) mRNA, complete cds.

ACCESSION AF032099

VERSION AF032099.1 GI:3004906

KEYWORDS

SOURCE Mus musculus.

ORGANISM Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1599)

AUTHORS Kalman, K., Nguyen, A., Tseng-Crank, J., Dukes, I.D., Chandy, G., Hustad, C.M., Copeland, N.G., Jenkins, N.A., Mohrenweiser, H.M., Brandriff, B., Cahalan, M.D., Gutman, G.A. and Chandy, K.G.

TITLE Genomic organization, chromosomal localization, tissue distribution, and biophysical characterization of a novel mammalian Shaker-related voltage-gated potassium channel, Kv1.7

JOURNAL J. Biol. Chem. 273 (10), 5851-5857 (1998)

MEDLINE 98157988

PubMed 9488722

REFERENCE 2 (bases 1 to 1599)

AUTHORS Kalman, K., Nguyen, A., Tseng-Crank, J., Dukes, I.D., Chandy, G., Hustad, C.M., Copeland, N.G., Jenkins, N.A., Mohrenweiser, H.M., Brandriff, B., Cahalan, M.D., Gutman, G.A. and Chandy, K.G.

TITLE Direct Submission

JOURNAL Submitted (30-OCT-1997) Physiology and Biophysics, University of California at Irvine, Irvine, CA 92697, USA

FEATURES

source 1..1599

gene /organism="Mus musculus"

gene /db_xref="taxon:10090"

gene 1..1599

gene /gene="Kvnc7"

gene 1..1599

gene /note="similar to Shaker"

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BASE COUNT 234 a 520 c 502 g 343 t

ORIGIN

Query Match 61.0%; Score 1065.8; DB 10; Length 1599;
Best Local Similarity 82.8%; Pred. No. 3,3e-137;
Matches 1269; Conservative 0; Mismatches 252; Indels 12; Gaps 4;

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Db 139 CATGCAATTTTACCGCGACACCGGACACCGGAGTGGGCGGCGGTGCGGGGCC 198

QY 305 ACAAGTGGTTTCGGGGTGCACGGGGCTGCGCGGACCATGAGACCGGCGTGGCCGCC 364

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QY 425 GCGCGACAGCTGGGCGGCTTCCGGACACTCTCTAGGGGACCCAGCGCGCGCGCCG 484

Db 316 GCGCGACAGCTGGGCGGCTTCCGGACACTCTCTAGGGGACCCAGCGCGCGCGCCG 375

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QY	1585	GCGCAAGAGCGCTGGGATGTTCAGCCATGTGGACATGCAAGCTTTGGGCCCACTGGAAGGC	1624
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QY	1625	AAGGCAATGGGGGCTGTGTGACCGGGAGAGTACCTAGACTTACCACTTCACTCTGGGCA	1684
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LOCUS	AC008687/c
DEFINITION	AC008687 Homo sapiens chromosome 19 clone CTF-60918, complete sequence.
ACCESSION	AC008687
VERSION	AC008687.5 GI:15887249
KEYWORDS	HTG.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens

REFERENCE	1 (bases 1 to 157633)
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE	Direct Submision
JOURNAL	Unpublished
REFERENCE	2. (bases 1 to 157633)
AUTHORS	DOE Joint Genome Institute.
TITLE	Direct Submision
JOURNAL	Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE	3 (bases 1 to 157633)
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE	Direct Submision
JOURNAL	Submitted (27-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE	4. (bases 1 to 157633)
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE	Direct Submision
JOURNAL	Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT	On Oct 3, 2001 this sequence version replaced gi:10312243.

COMMENT
On Oct 3, 2001 this sequence version replaced g1:10312243.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% Of Sequence;
Estimated Total Number of Errors is 0.2.
STS Content:
SHGC-15869 G153229
SHGC-15864 G15325
SHGC-5822 G14090
SHGC-58615 G42524.

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Best Local Similarity	99.1%;	Pred. No. 3.7e-107;			
Matches 849;	Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0

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QY	1131	CCGGGCAAGGAGGGGGTGGGGCCAGAGGCCATGTACTGTGGCCATCTCTAGAGTATCCGAT	1190
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Db	81537	ACGGGGAGACAGAGGGCGGAAGAGGCTGGGATGTTTACGACATGTGGACATCGACCTTTGG	81478
QY	1611	GCCCACTGAGAGGCAAGGCAATGGGGGGCTGGTGGAGGAGGGAGGTACTGTGACTACAC	1670
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Db	81357	TCGTGAGGAGACTTCACAC	81341

LOCUS	OCU38240	1551 bp	DNA	linear	MAM 30-JUN-1999
DEFINITION	Oryctolagus cuniculus glibenclamide-sensitive voltage-gated potassium channel (Kv1.3-glib) gene, complete cds.				

ACCESSION U38240
 VERSION 038240.1 GI:3264840
 KEYWORDS
 SOURCE Oryctolagus cuniculus.
 ORGANISM Oryctolagus cuniculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 REFERENCE
 1 (bases 1 to 1551)
 Yao, X., Chang, A.Y., Boulipaep, E.L., Segal, A.S. and Desir, G.V.
 Molecular cloning of a glibenclamide-sensitive, voltage-gated
 potassium channel expressed in rabbit kidney
 J. Clin. Invest. 97 (11), 2525-2533 (1996)
 JOURNAL
 MEDLINE
 PUBMED 8647945
 REFERENCE
 2 (bases 1 to 1551)
 Desir, G.
 Direct Submission
 Submitted (10-OCT-1995) Gary Desir, Medicine, Yale, 2074 LMP 333
 Cedar Street, New Haven, CT 06510, USA
 On Jun 29, 1998 this sequence version replaced gi:1033191.
 COMMENT
 FEATURES
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 Db 400 GGCATGAGAGATTCGCGGAGAGAGAGGCTTCTGCGGAGAGAGAGCGCGCTGCCC 459
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 DEFINITION Homo sapiens chromosome 1 clone RP1-183f4 map p13.3-21.2, ***
 SEQUENCING IN PROGRESS ***, 4 unordered pieces.
 ACCESSION AL513469

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RESULT 10
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 DEFINITION Human DNA sequence from clone RP11-284N8 on chromosome 1, complete
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 ACCESSION AL365361 AC025151
 VERSION AL365361.11 GI:13160295
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 155343)
 AUTHORS Mashreghi-Mohammadi, M.
 TITLE Direct Submission
 JOURNAL Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On or before May 15, 2001 this sequence version replaced
 gi:7283305, gi:12718091.

COMMENT

During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em: EMBL; Sw:
 SWSMSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
 database can be found at
 http://www.sanger.ac.uk/projects/c_elegans/wormpep
 This sequence was generated from part of bacterial clone contigs of human
 chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
 group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chrl
 RP11-284N8 is from the library RPCT-11.1 constructed by the group
 of Pieter de Jong. For further details see
 http://www.chori.org/bacpac/home.htm

VECTOR: PBACE3.6
 IMPORTANT: This sequence is not the entire insert of clone
 RP11-284N8. It may be shorter because we sequence overlapping
 sections only once, except for a 100 base overlap.
 The true left end of clone RP11-284N8 is at 1 in this sequence. The
 true left end of clone RP1-24465 is at 155244 in this sequence. The
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DEFINITION L23499
ACCESSION L23499.1 GI:385222
VERSION KCNA3 gene; potassium channel; voltage-gated potassium channel.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1836)
AUTHORS Folander, K., Lin, S., Koo, G. and Swanson, R.
TITLE Assignment of the gene encoding Kv1.3, a voltage gated potassium
channel, to human chromosome 1
JOURNAL Unpublished (1993)
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Best local Similarity 70.4%; Pred. No. 1,2e-78;
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VERSION	M55515			
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SOURCE	potassium channel protein.			
ORGANISM	Human DNA.			
REFERENCE	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (sites)			
JOURNAL	Phillipson, L. H., Lamendola, J., Bell, G. I. and Steiner, D. F.			
REFERENCE	Genomic sequence of a human potassium channel related to RCK3			
REFERENCE	2 (bases 1 to 1820)			
REFERENCE	Unpublished (1990)			
REFERENCE	Phillipson, L. H., Hice, R. E., Schaefer, K., Lamendola, J., Bell, G. I.,			
REFERENCE	Nelson, D. J. and Steiner, D. F.			
REFERENCE	Sequence and functional expression in Xenopus oocytes of a human			
REFERENCE	insulinoma and islet potassium channel			
REFERENCE	Proc. Natl. Acad. Sci. U.S.A. 88 (1), 53-57 (1991)			
REFERENCE	91093456			
REFERENCE	1986382			
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Db	250	CGCGCGGGGGGAGACGAGACTGTGCGGGGAGCGCGTGGTCATCAATCATCTCGGGCTGC	309						
QY	411	GCTTCGAGAGCGCGGGCGCGACGCTGGCGCGCTTCGCCGAGCACTCTGCTAGGGGACCCAG	470						
Db	310	GCTTCGAGAGCGCACCTAGAACCCTTTGGCAGTTCCCGGAGCGCTGCTGGCGACCCCA	369						
QY	471	CGCCCCCGCGCGCTTTACGACGACGCGCGCGGACGATTTCTTCGACACGGACCGCG	530						
Db	370	AGCGGCGCATAGAGTACTTTCGACCCCGTCCGCAACGAGTACTTTCGACCCGACACCGCG	429						
QY	531	CCAGCTTCGACGCGCGCTCTACTACTACCAAGTCGGGTGGCGGCGCTGCGCGCGCGCGCG	590						
Db	430	CCAGCTTCGAGCGCATCTCTACTACTATCAGTCGGGGGCGCATTCGCGCGCGGTCAC	489						
QY	591	ACGTGCCGCTGACGCTTCTCTGSAAGAGTGGCTTTTACGCGGCTGGCGCGCGCGCGCG	650						
Db	490	ACGTGCCCATCAGACTTTTCTCCGAGAGATCCGCTTACCGAGCTGGCGGAGAGGCCA	549						
QY	651	TGGCAGCGCTCGCGGAGAGAGAGGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	710						
Db	550	TGGAGAAAGTTCGCGGAGAGAGAGGCGTCTCGCGGAGAGAGAGCGCGCGCGCGCGCG	609						
QY	711	GCGCGCTTCGCGCGCGCACGTCGTGCTTTCAGTTTCCGAGAGCTTCACAGCGCGCG	770						
Db	610	GCGACTTTCAGCGCGCAGGTGTGGGTGCTTTCAGTACCCCGAGACTCCGGGCGCGCGCG	669						
QY	771	GCGTGTCCGCCGTAGTCTCCGTGCTGTCTACTCTCGTCTCCATCGTCGTTCTGCTCG	830						
Db	670	GGGCGATCAGCATGTCGTCGCTGTGTCACCTCAATCTCATCTTCTGCGCTGG	729						
QY	831	AGAGCGTCCGCACTTCGCGGAGAGACCGCGACCGGCGTGTGCTGCGACCGCGAG	890						
Db	730	AGAGCGTCCGCACTTCGCGGAGAGAGAGACCCCGCTCGACGTCGACAGGACTCAT	789						
QY	891	CCGCGCGGTGTTCGCCGCTCCGCTGATGGCTCCACGCAAAATGCTGGAATAATCAACCC	950						
Db	790	TTCGAAGCAG-----CCGCGCAACACACATCGGGGTCCCGCGCAGAG	831						
QY	951	GCTGCGCTTCATGACCCGCTCTCTGCTGTGAGAGCGCTGTGTATTTTGTTGGTCTCCT	1010						
Db	832	CCTCAGCTTCTCCGATCCCTCTCTGCTGTGAGAGCGCTGACATCATCTGTTCTCCT	891						
QY	1011	TTGAGCTGCTGTAGCGCTCTCTGTCTGTCTCAAGCAAGGCTATCTTCTTCAAGAACTGA	1070						
Db	892	TTCGACGCTGTGTGTCGGTCTTCTGCTGTGCTCTGCAAAAGCACCTTCTGCGCAATCA	951						
QY	1071	TGACACCTCATGATTTTGTGGCTATGCTCCCTACCTTTTGGGCACTGGGCAACGAGCTGG	1130						
Db	952	TGAACCTGATGACATTTGTGGCCATCTTCTTATTTTATCACTCTGCGGTACCGAGCTGG	1011						
QY	1131	CCCGGACGAGGGGTGGGCCAGCAGGCCATGTCACTGGCCATCTGAGAGCTATCCGAT	1190						
Db	1012	CGGAACGACAGGGCAATGAGACAGAGCCATGTCTCTGGGCATCCGTGAGGGTCAATCCGCC	1071						
QY	1191	TGTGTGCTGTCTTCGCGATTTCAAGCTGTCCCGGCACTCAAAAGGCGCTGCAAAATCTTGG	1250						
Db	1072	TGTGTAAGGCTTCCGATCTTCAAGCTGTGCGGCCATCAAGGGGCGTGCAGATCTGCG	1131						

Oy	1251	GCACAGCGTTGGGCGCTTCACATGCGTGAAGACTGGGGCTCCATCTTTTTCCTTCATCG	1310
Db	1132	GGCAAAAGCCTGAAGCGCTGCATCGCGGAACTGGGATGCTCACTCTTCTCCCTTTATG	1191
Oy	1311	GTGTGTCCTCTTTTCCACAGCGCGTCTACTTTTGCCGAAGTTGACCGGGGTGCATCCCAT	1370
Db	1192	GGGTATCTCTTTTTCACACGCGGGGTCTACTTTGGCCGAGGACACACCCCATCTTAGGTT	1251
Oy	1371	TCACTAGCATCCCTCAGACCTCTCTGTGGGCGGTAGTGCACCTAGCATCAGTTGGCTATG	1430
Db	1252	TCAGCAGCATCCCGGATGCTCTTGTGGTGGCAGTGGTAAACATAGAACAGTGGGTTACG	1311
Oy	1431	GAGACATGGCACCCCTCACACTGTGGGTGCGAAGATAGTGGGCTCTCTGTGTGCCATTTGGG	1490
Db	1312	CGCATATGCACCAATGACCATATGAGGGGGGAAATATGTGGGATCTCTGTGTGCCATTCGCG	1371
Oy	1491	GGCTCTCACTATTTTCCCTGCGCAGTGGCCCGTATTTGTCCCAATTTAGACTACTTTATC	1550
Db	1372	GTGTCTTGCCATTCGCATATGGCAGTTCCCGTATTTGTTTCCAACTTCATTTACTTCTAC	1431
Oy	1551	ACCGGAGACAGAGGGCCGAAGAGCGCTGGGATGTTTACGATCTGG	1595
Db	1432	ACCGGAGACAGAGGGGAGAGCATCCCATATCATGACGTGG	1476

RESULT 15					
AC073711/c					
LOCUS	AC073711	208632 bp	DNA	linear	HTG 18-JUL-2000
DEFINITION	Mus musculus clone RP2-133A10,	WORKING	DRAFT	SEQUENCE,	7 ordered

ACCESSION	AC073711.1
VERSION	AC073711.2 GI:9256763
KEYWORDS	HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE	Mus musculus.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathia; Muridae; Murinae; Mus
AUTHORS	1 (bases 1 to 208633)
TITLE	DOE Joint Genome Institute.
JOURNAL	Sequencing of Mouse
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 208632)
TITLE	DOE Joint Genome Institute.
JOURNAL	Direct Submission
COMMENT	Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:8810328.

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Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1810994
Center clone name: RPCI-23_193A10
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Summary Statistics
Consensus quality: 204234 bases at least Q40
Consensus quality: 207322 bases at least Q30
Consensus quality: 207805 bases at least Q20
Estimated insert size: 221930; agarose-fp estimation
Estimated insert size: 208382; sum-of-contigs estimation
Quality coverage: 8.77 in Q20 bases; agarose-fp estimation
Quality coverage: 9.34 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
  consists of 7 contigs. Gaps between the contigs
  are represented as runs of N. The order of the pieces
  is believed to be correct as given, however the sizes
  of the gaps between them are based on estimates that have
  been provided by the submittor.
  This sequence may be replaced
  by the finished sequence as soon as it is available and

```

Query Match	Best Local Similarity	Matches	Score	DB	Length
870	GGCTGCTGCTCAGCCGCGCGCCGGTTCCTCCCGCTCGGTGATGAGCTCCAGCC	93558	contig of 93558 bp in	length	929
72171	GGCTCCCTGACCCCTTCTGCTCCCTTTCGACTTCTCGCGAGATGAGCTCCAGCC	93559	contig of 93558 bp in	length	929
930	AAATCCCTGGAAATCCACCCCGCCCTTCAATGACCCGTTCTTCTGCTGAGAGCC	94751	contig of 1093 bp in	length	989
72111	CCATCCGACGAGACCCCTCCCGACAGCCCTTCAACGATCATTCTTTGGTGAGAGCC	94752	gap of unknown length		72052
990	TGTGATTTGTTGGTTCCTCTTGAGCTCTGTGAGCCCTCGGTGCTGCTCAAGAGG	118285	contig of 2343 bp in	length	1049
72051	TGTGATTTGTTGGTTCCTCTTGAGCTCTGTGAGCCCTCGGTGCTGCTCAAGAGG	118286	contig of 2343 bp in	length	71992
1050	CTATCTTCTTCAAGAACGATGATGAACCTCATCGATTTTGTGCTATCTTCCCTCACTTG	118385	gap of unknown length		11909
71991	CTGTGTTCTTCAAGATGATGATGAACCTCATCGATTTTGTGCTATCTTCCCTCACTTG	118386	gap of unknown length		71932
1110	TGGGACCTGGGACCGAGCTGGCCCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	157043	contig of 3658 bp in	length	1169
71931	TGGGACCTGGGACCGAGGATGAGCCCGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGG	157044	gap of unknown length		71872
1170	CCATCTGAGATCAATCCGATGATGAGCTGTTCGCTCCGATCTTCAAGAGCTGCCGCACT	157144	contig of 7418 bp in	length	1229
71871	CCATCTGAGATCAATCCGATGATGAGCTGTTCGCTCCGATCTTCAAGAGCTGCCGCACT	164561	gap of unknown length		71812
1230	CAAGGCGCTGCAAAATCTTGGGCGAGAGCGCTTCGGGCTTCATGCTGAGCTGGGCTTC	164662	gap of unknown length		1289
71811	CAAGGCGCTGCAAAATCTTGGGCGAGAGCGCTTCGGGCTTCATGCTGAGCTGGGCTTC	176791	contig of 12130 bp in	length	1469
1290	TCATCTTCTTCTTCAATCGGCTGTGAGCTGTTCCTTTCACGAGCCGCTCACTTTCGCGAAG	176792	gap of unknown length		1349
71751	TCATCTTCTTCTTCAATCGGCTGTGAGCTGTTCCTTTCACGAGCCGCTCACTTTCGCGAAG	176892	contig of 31741 bp in	length	71692
1350	TTGACCGGCTGAGCTCCCAATTCACATGACATCCCTGATCTTCTTGTGAGGCGGTAGTCA	176892	contig of 31741 bp in	length	1409
71691	TTGACCGGCTGAGCTCCCAATTCACATGACATCCCTGATCTTCTTGTGAGGCGGTAGTCA	176892	contig of 31741 bp in	length	71632
1410	CCATGACATCAATGTTGGCTATGAGAGCATGAGACCCGCTCACTGTGGGTGAGAGATATGAG	176892	contig of 31741 bp in	length	1469
71631	CCATGACATCAATGTTGGCTATGAGAGCATGAGACCCGCTCACTGTGGGTGAGAGATATGAG	176892	contig of 31741 bp in	length	71572
1470	GCTCTCTGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	176892	contig of 31741 bp in	length	1529
71571	GCTCTCTGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	176892	contig of 31741 bp in	length	71512
1530	CCAAATTTAGGCTACTTTTATACCGGAGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG	176892	contig of 31741 bp in	length	1589

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Db 71511 CTACTTTAGCTACTTTTACCAACGGGAGACAGAGGGCGGAAGAGCGAGGATGTACAGCC 71452
QY 1590 ATGTGGACATGCAGCCTTGTGSCCACTGGAGGGCAAGGCCAATGGGGGCTGTGGACG 1649
||||| ||||| ||| | ||||| ||||| ||||| ||||| |||||
Db 71451 ATGTGGACACACAGCCCTGGGCTACCTGGAGGGCAAGGCTAATGGGGGCTGTGGACT 71392
QY 1650 GGGAGGTACCTGAGCTACCACTCTGACCTGTGGGCACCCCGAGGGAACACCTGTGCACCG 1709
||||| ||||| || | ||||| ||| | ||||| ||||| |||
Db 71391 CTGAGGTGCCCTGAACCTCTCCACACACTCTGGCCCCCTGCAGGGAACACATGTTGACTG 71332
QY 1710 AAGTGTGAGGAACAGTTGAGGTCTGCAGG 1738
| ||||| || | ||||| ||||
Db 71331 AGGTGTGAGGGTCAACTGGGGTCTCCAGG 71303

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Search completed: February 20, 2003, 09:59:47
 Job time : 5512.86 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2003, 23:59:06 : Search time 418.075 Seconds
(without alignments)
9410.374 Million cell updates/sec

Title: US-09-804-014a-7

Perfect score: 1747

Sequence: 1 gaagcctgattctgacgaaa.....agctcgcagcaccacac 1747

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1747	100.0	1747	22	AAS13338	Human cDNA encoding
2	1420.2	81.3	1792	24	AAD37899	Human ion channel
3	1333.6	76.3	1686	23	AAS78540	DNA encoding novel
4	1321.6	75.6	1341	24	ABL57038	Human potassium ch
5	1068	61.1	1598	16	AA04953	Mouse Kv1.7 voltag
6	601.4	34.4	691	24	AAD28734	Human ion channel
7	596.2	34.1	2867	24	ABN95856	Gene #2354 used to
8	596.2	34.1	2867	24	ABL65917	Lung cancer relate
9	588.2	33.7	1836	22	AAH21452	Human Kv1.5 DNA.

10	546	31.3	3147	24	AB19654	Mouse ischaemic co
11	508.6	29.1	994	24	AB019704	Oligonucleotide fo
12	508.6	29.1	994	24	AB019705	Oligonucleotide fo
13	506.6	29.0	994	24	AB019702	Oligonucleotide fo
14	506.6	29.0	994	24	AB019703	Oligonucleotide fo
15	367.4	21.0	7642	24	AB133117	Human immune syste
16	348.2	19.9	7642	24	AB133116	Human immune syste
17	340.4	19.5	8758	24	AB133119	Human immune syste
18	311.4	17.8	2157	22	AAS29512	Human endocrine po
19	311.4	17.8	2159	23	ABK43428	DNA encoding novel
20	303.4	17.4	2237	23	AB133285	Drosophila melanog
21	296.6	17.0	7488	24	AB133112	Human immune syste
22	291.4	16.7	7488	24	AB133112	Human immune syste
23	262.8	15.0	8758	24	AB133118	Human immune syste
24	233.8	13.4	492	22	ABR06356	Human cDNA seq ID
25	233.8	13.4	492	22	AAS28936	cDNA encoding for
26	233.8	13.4	492	22	AAS29636	DNA encoding rena
27	233.8	13.4	492	22	AAS30165	DNA encoding novel
28	233.8	13.4	492	23	ABK43751	Human immune syste
29	228.8	13.1	7500	24	AB133114	Human immune syste
30	215.6	12.3	2064	24	ABR84401	Human Kv4.3 potass
31	215.6	12.3	2072	19	AAV61572	Human Kv potassium
32	215.6	12.3	2104	19	AAV61571	Human Kv potassium
33	215.6	12.3	2121	24	ABR84400	Human Kv4.3 potass
34	213.6	12.2	2578	22	AAH99538	Human protein enco
35	213.6	12.2	2711	22	AAH21246	Human Kv4.1 cDNA.
36	213.2	12.2	3424	20	AAZ11901	Human potassium ch
37	212.4	12.2	2104	19	AAV61573	Human Kv potassium
38	205.2	11.7	1521	24	ABQ49288	Oligonucleotide fo
39	205.2	11.7	1521	24	ABQ49289	Oligonucleotide fo
40	191	10.9	998	22	ABA43164	Human breast cell
41	191	10.9	998	22	ABA53583	Human foetal liver
42	191	10.9	998	22	ABR23338	Human foetal liver
43	191	10.9	998	22	AAK01849	Probe #1804 for ge
44	191	10.9	998	22	AAK27308	Human brain expres
45	191	10.9	998	22	AA11882	Human bone marrow Probe #1815 for ge

ALIGNMENTS

RESULT 1	
AAS13338	
ID	AAS13338 standard; cDNA: 1747 BP.
AC	AAS13338;
XX	
DT	18-DEC-2001 (first entry)
DE	Human cDNA encoding NOV4 protein.
XX	
KW	Human: NOV4; ss; cytosolic; neurotrophic; neuroprotective; vulnary;
KW	cerebroprotective; antiparkinsonian; hypotensive; antisthmatic;
KW	antidiabetic; antipsoriatic; antiinflammatory; immunosuppressive;
KW	antithrombotic; dermatological; cancer; neurological disorder;
KW	Parkinson's disease; diabetes mellitus; asthma; enamel defect;
KW	immune disorder; autoimmune disease; respiratory disorder;
KW	bone disorder; musculoskeletal disorders; leukemia; lymphoma;
KW	cell growth regulation disorder; lesional psoriatic skin;
XX	atherosclerosis; abdominal aortic aneurysm.
OS	Homo sapiens.
XX	
PH	
FT	key
FT	5'UTR
FT	Location/Qualifiers
FT	1..37
FT	/*tag= a
FT	CDS
FT	38..1717
FT	/*tag= b
FT	/*product= "NOV4"
FT	3'UTR
FT	1718..1747
FT	/*tag= c
PN	WO200168851-A2.

XX 20-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-US07735.
XX
PR 10-MAR-2000; 2000US-0188377.
XX
PR 10-MAR-2000; 2000US-0188316.
PR 14-MAR-2000; 2000US-0189139.
PR 14-MAR-2000; 2000US-0189140.
PR 17-MAR-2000; 2000US-0190231.
XX
PR 17-MAR-2000; 2000US-0190401.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Vernet CM, Fernandes E, Shinkets RA, Spaderina SK;
PI Majunder K, Li L;
XX
DR WPI: 2001-570869/64.
DR P-PSDB; AA008660.
XX
XX Novel polypeptides and nucleic acids homologous to members of collagen,
PT potassium channel, tufelin family of proteins for diagnosing, treating
PT cancer, atherosclerosis, neurological, skin and enamel defect disorders
PT
XX
XX
PS Claim 9; Page 15-16; 128bp; English.
XX
XX The invention relates to isolated NOVX (NOVX-11) polypeptides and
CC the polynucleotides that encode them. NOVX polypeptides, polynucleotides
CC and anti-NOVX antibodies are useful for treating or preventing a
CC pathology associated with NOVX polypeptide in humans and for treating a
CC syndrome associated with human disease e.g. disorders characterised by
CC altered cell motility, proliferation and migration e.g. cancer,
CC angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.
CC episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's
CC disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,
CC asthma, hypertension and seizure (NOV4), enamel defects, such as
CC amelogenesis imperfecta and disorders involving enamel defects,
CC including hypoplasia and hypomeliorisation (NOV5-7), paraneoplastic
CC neurological disorders, e.g. paraneoplastic limbic of brain-stem
CC encephalitis occurring during testicular cancer, diabetes, reproductive
CC health, metabolic and endocrine disorders, gastrointestinal disorders,
CC immune disorders and autoimmune diseases, respiratory disorders, bone
CC disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell
CC growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and
CC atherosclerosis, abdominal aortic aneurysm and neurological disorders
CC (NOV11). NOVX polypeptide is also useful for identifying an agent that
CC binds to it and a cell expressing NOVX polypeptide is useful for
CC identifying a therapeutic agent for use in treatment of a NOVX related
CC pathology. The antibodies and a polypeptide having 95% sequence identity
CC to NOVX polypeptide are useful for treating a pathological state in a
CC mammal. The present sequence encodes NOV4, a possible voltage gated
CC potassium channel.
XX
SQ Sequence 1747 BP; 255 A; 582 C; 575 G; 335 T; 0 other;

Query Match 100.0%; Score 1747; DB 22; Length 1747;
Best Local Similarity 100.0%; Pred. No. 2.8e-312;
Matches 1747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 CCGTGTGCGCCCTCCGCGCGCGGCGGTCACAGTCCCTCCCTGCGCCTACGCGCC 240
OY 241 TGCCGGGCTATTTTACGCGGAGACCGGACACCGGAGTGGGGGCGGCTCG 300
Db 241 TGCCGGGCTATTTTACGCGGAGACCGGAGACCGGAGTGGGGGCGGCTCG 300
OY 301 GGGCAGACGTCGTTGCGGGGTGCGCGGGGTGCGCGCGCCATGAGCCGCGGTC 360
Db 301 GGGCAGACGTCGTTGCGGGGTGCGCGGGGTGCGCGCGCCATGAGCCGCGGTC 360
OY 361 CGCCCGGTCGCGGTCGCGGAGCGGCGGTCGCGGAGCGGCGGCGGCGGTCGAGAC 420
Db 361 CGCCCGGTCGCGGTCGCGGAGCGGCGGTCGCGGAGCGGCGGCGGCGGTCGAGAC 420
OY 421 GCGGCGCGGCGGTCGCGGAGCGGCGGTCGCGGAGCGGCGGCGGCGGTCGAGAC 480
Db 421 GCGGCGCGGCGGTCGCGGAGCGGCGGTCGCGGAGCGGCGGCGGCGGTCGAGAC 480
OY 481 CGCGCTTACGAGACGCGCGCGCGGAGTATTTCTGACCGGACCGCGCGGCTTGA 540
Db 481 CGCGCTTACGAGACGCGCGCGCGGAGTATTTCTGACCGGACCGCGCGGCTTGA 540
OY 541 CGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 600
Db 541 CGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 600
OY 601 CGAGCTTTCCTGGAAGAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 660
Db 601 CGAGCTTTCCTGGAAGAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 660
OY 661 GCGGAGAGAGAGGCGGCGCGCGGTCGCGCGCGCGCGCGCGCGCGCGCGCTTGC 720
Db 661 GCGGAGAGAGAGGCGGCGCGCGGTCGCGCGCGCGCGCGCGCGCGCGCGCTTGC 720
OY 721 CGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 780
Db 721 CGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 780
OY 781 CGTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 840
Db 781 CGTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 840
OY 841 TGACTTTCGCGGAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 900
Db 841 TGACTTTCGCGGAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 900
OY 901 GTTCCCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 960
Db 901 GTTCCCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 960
OY 961 CAATGACCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1020
Db 961 CAATGACCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1020
OY 1021 GGTACGCTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1080
Db 1021 GGTACGCTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1080
OY 1081 CGATTGTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1140
Db 1081 CGATTGTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1140
OY 1141 AGGGTGGGCGGAGGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1200
Db 1141 AGGGTGGGCGGAGGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1200
OY 1201 CTTTCGCGATCTTCAAGCTGTCCGCGGCTCAAGAGGCGCTCAAACTTCTTGAGCGACGCT 1260
Db 1201 CTTTCGCGATCTTCAAGCTGTCCGCGGCTCAAGAGGCGCTCAAACTTCTTGAGCGACGCT 1260
OY 1261 TCGGGGCTCCATGCGTGTAGCTGGGCTGCTGATCTTTTCTCTTATCGGTGTGCTCT 1320
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Db 1261 TGGGGCTCCATGCGTAGCTGGGCTCCCTCATCTTTTCTCTTCATGCGTGCTCT 1320
 QY 1321 CTTTTCACGCGGCTACTTTGCGAGTTGACGGGGGAGTCCCATTTCTGCTAGCAT 1380
 Db 1321 CTTTTCACGCGGCTACTTTGCGAGTTGACGGGGGAGTCCCATTTCTGCTAGCAT 1380
 QY 1381 CCGTGAATCTTCTGTGGGCGGTAGTCAACATGACTAGTGGCTATGAGACATGCG 1440
 Db 1381 CCGTGAATCTTCTGTGGGCGGTAGTCAACATGACTAGTGGCTATGAGACATGCG 1440
 QY 1441 ACCCGTCACTGTGGGCGGCAAGATAGTGGCTCTGTGCTCCATTGCGGGCTGCTGAC 1500
 Db 1441 ACCCGTCACTGTGGGCGGCAAGATAGTGGCTCTGTGCTCCATTGCGGGCTGCTGAC 1500
 QY 1501 TATTTCCCTGACAGTCCCGTCAATGTCACATTTACGTAATTCACCGGGAGAC 1560
 Db 1501 TATTTCCCTGACAGTCCCGTCAATGTCACATTTACGTAATTCACCGGGAGAC 1560
 QY 1561 AGAGGGCGAAGAGGCTGGGATGTTTCAGCATGTGACATGACGCTTGTGGCCACTGGA 1620
 Db 1561 AGAGGGCGAAGAGGCTGGGATGTTTCAGCATGTGACATGACGCTTGTGGCCACTGGA 1620
 QY 1621 GGGCAAGGCAATGGGGGCTGTGTGACGGGAGGTAACCTGACCTTCCACTCTG 1680
 Db 1621 GGGCAAGGCAATGGGGGCTGTGTGACGGGAGGTAACCTGACCTTCCACTCTG 1680
 QY 1681 GGCACCCCGGAGGACCTGTGTGACGGGAGGTAACCTGAGGAGTGTGAGGAGTGTGACGAGAC 1740
 Db 1681 GGCACCCCGGAGGACCTGTGTGACGGGAGGTAACCTGAGGAGTGTGAGGAGTGTGACGAGAC 1740
 QY 1741 CTCACAC 1747
 Db 1741 CTCACAC 1747

RESULT 2

AAD37899
 ID AAD37899 standard; cDNA; 1792 BP.

AC AAD37899;

DT 10-SEP-2002 (first entry)

DE Human ion channel protein encoding cDNA.

XX Human: novel human protein; NHP; ion channel protein; forensic biology;

KM pharmacogenomic; drug screening; mental disorder; biological disorder;

KM symptomatic manifestation; phenotypic manifestation; medical disorder;

OS gene; ss.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 93..1463 /tag= a /product= "Human ion channel protein"

FT /note= "This region is specifically claimed as

FT SEQ ID NO: 1 in claim 1 of the specification"

PN WO200231150-A2.

PD 18-APR-2002.

PF 10-OCT-2001; 2001WO-US31900.

PR 10-OCT-2000; 2000US-239623P.

PA (LEXI-) LEXICON GENETICS INC.

PI Friddle CJ, Hilbun E, Gerhardt B, Turner CA;

DR WPI; 2002-452348/48.

DR P-PSDB; AAE23655.

XX Novel human ion channel polynucleotide encoding protein sharing
 PT structural similarity with mammalian ion channel proteins, e.g.
 PT potassium channels useful in therapeutic, diagnostic and
 PT pharmacogenomic applications -
 PS
 XX Disclosure; Page 36; 36pp; English.
 CC The present invention relates to novel human proteins (NHPs), human ion
 CC channel proteins and polynucleotides encoding such proteins. Sequences of
 CC the invention are useful in therapeutic, diagnostic and pharmacogenomic
 CC applications. They are useful for the identification of protein coding
 CC sequences, for mapping a unique gene to a particular chromosome, as
 CC additional DNA markers for restriction fragment length polymorphism
 CC (RFLP) analysis and in forensic biology, for screening libraries,
 CC isolating clones, preparing templates for cloning and sequencing, as
 CC hybridisation probes, in microarrays or other assay formats, to screen
 CC collections of genetic material from patients who have a particular
 CC medical condition, to identify mutations associated with a particular
 CC disease and also as a diagnostic or prognostic assay. NHPs are useful
 CC for the detection of mutant human proteins or inappropriately expressed
 CC proteins for the diagnosis of disease, for the generation of antibodies,
 CC for screening for drugs effective in the treatment of symptomatic or
 CC phenotypic manifestations of perturbing the normal function of the
 CC protein in the body, for identification of other cellular gene products
 CC related to the protein and as reagents in assays for screening for
 CC compounds that can be used as pharmaceutical agents in the therapeutic
 CC treatment of mental, biological or medical disorders and diseases. The
 CC present sequence is a cDNA encoding human ion channel protein.
 XX
 SQ Sequence 1792 BP; 265 A; 534 C; 592 G; 399 T; 2 other;

Query Match 81.38; Score 1420.2; DB 24; Length 1792;

Best Local Similarity 99.18; Pred. No. 3.3e-252;

Matches 1450; Conservative 0; Mismatches 8; Indels 5; Gaps 2;

QY 285 CTGGGCGGCGGCTCGGGGCGACACAGTGGCTTCGCGGGCTGCGCGGCATG 344
 Db 36 CGGGGCGGCGGCTCGGGGCGACACAGTGGCTTCGCGGGCTGCGCGGCATG 95
 QY 345 GAGCGGCGGCTCGGGGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGG 404
 Db 96 GAGCGGCGGCTCGGGGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGG 153
 QY 405 GCGTGGCTTCGAGACGCGGGGCGGCGGCTGCGGCGGCTTCGCGGACCTCTAGGG 464
 Db 154 GCGTGGCTTCGAGACGCGGGGCGGCGGCTGCGGCGGCTTCGCGGACCTCTAGGG 213
 QY 465 ACCCAGCGCGCGCGCGCGCTTACGACGACGCGCGCGAGATATTTCTGACCGGC 524
 Db 214 ACCCAGCGCGCGCGCGCGCTTACGACGACGCGCGCGAGATATTTCTGACCGGC 273
 QY 525 ACCGCGCCAGCTTCGACGCGCGCTCTACTACAGTCCGGTGGGCGGCTGCGCGGC 584
 Db 274 ACCGCGCCAGCTTCGACGCGCGCTCTACTACAGTCCGGTGGGCGGCTGCGCGGC 333
 QY 585 CGCGCGACGCGCGCGCTTCGACGCTTCTCTGGAAGAAGTGGCTTCTAGGGCTGGGCGG 644
 Db 334 CGCGCGACGCGCGCGCTTCGACGCTTCTCTGGAAGAAGTGGCTTCTAGGGCTGGGCGG 393
 QY 645 CGGCGCTGGCAGCGCTGCGGCGGAGAGAGGCTGCGCGGCTGCGCGCGCGCGCTGCG 704
 Db 394 CGGCGCTGGCAGCGCTGCGGCGGAGAGAGGCTGCGCGGCTGCGCGCGCGCGCTGCG 453
 QY 705 CGCGCGCGCTTCGCGCGCGAGCTGCGCTTCTGATTTCCGAGAGCTCTAGG 764
 Db 454 CGCGCGCGCTTCGCGCGCGAGCTGCGCTTCTGATTTCCGAGAGCTCTAGG 513
 QY 765 CGCGCGCGCTTCGCGCGCGAGCTGCGCTTCTGATTTCCGAGAGCTCTAGG 824
 Db 514 CGCGCGCGCTTCGCGCGCGAGCTGCGCTTCTGATTTCCGAGAGCTCTAGG 573
 QY 825 GCTCGAGAGAGCTGCTGACTTCGCGAGACCGGCGAGCGGCGCTGCTGCGAG 884

Db	574	GCCTGAGAGCGCTGCTGACGCTTCGGGAGACGACCGGACGCGGAGCGGGGCTTGGCTGCGAG	633
Oy	885	CCGCAAGCCGGCCGGGTGTTTCCCGGCTCCGCTGAATGGCTCCAGCCAAATGCTCGAATC	944
Db	634	CCGCAAGCCGGCCGCCC--GTTCCCGGCTCGGCTGAATGGCTCCAGCCAAATGCGTGGAAATC	690
Oy	945	CACCCGCGCTCCCTTCGAATGACCCGCTTCGATGGGAGACGCTGTCAATTTGGT	1004
Db	631	CACCCGCGCTCCCTTCGAATGACCCGCTTCGATGGGAGACGCTGTCAATTTGGT	750
Oy	1005	TCCTCTTTGAGCTCTGCTGACGCTCCGCTGCTGCTCCAAAGCAAGCTATCTTCTCAAGA	1064
Db	751	TCCTCTTTGAGCTCTGCTGACGCTCCGCTGCTGCTGCTCCAAAGCAAGCTATCTTCTCAAGA	810
Oy	1065	ACGTGATGAACTTATGATTTTGTGGCTATCCTTCCCTACTTTGTGGCACTGGCAGCG	1122
Db	811	ACGTGATGAACTTATGATTTTGTGGCTATCCTTCCCTACTTTGTGGCACTGGCAGCG	870
Oy	1125	AGCTGGCCCGGCGACGAGGGGTGGGCGACGAGCCATATGCTACGCGGCTCTGAGAGTCA	1188
Db	871	AGCTGGCCCGGCGACGAGGGGTGGGCGACGAGCCATATGCTACGCGGCTCTGAGAGTCA	930
Oy	1185	TCCGATTTGCTGCTGTCTTCCGACTTTCAGCTGTCCCGGCACTCAAAAGGCGTCGAAA	1244
Db	931	TCCGATTTGCTGCTGTCTTCCGACTTTCAGCTGTCCCGGCACTCAAAAGGCGTCGAAA	990
Oy	1245	TCCTGGGGCAGACGCTTCGGGCGCTCCATGGGTGAGCGTGGGCGCTCCCATCTTTTCTCT	1304
Db	991	TCCTGGGGCAGACGCTTCGGGCGCTCCATGGGTGAGCGTGGGCGCTCCCATCTTTTCTCT	1050
Oy	1305	TCATGCGTGTGCTCTCTTTTCCAGCGCGCTCTACTTTTGGCGAATGTGACCGGGGTGACT	1364
Db	1051	TCATGCGTGTGCTCTCTTTTCCAGCGCGCTCTACTTTTGGCGAATGTGACCGGGGTGACT	1110
Oy	1365	CCCATTTTCACATGATGCTCGTAGAGTCTTTCGATGGGCGGTGAGTCAACATGACTACAGTTG	1422
Db	1111	CCCATTTTCACATGATGCTCGTAGAGTCTTTCGATGGGCGGTGAGTCAACATGACTACAGTTG	1170
Oy	1425	GCTATGAGACATGGACACCGGCTGACTGTGGGTGGCAAGAATAGTGGGCTCTGTGTGCCA	1484
Db	1171	GCTATGAGACATGGACACCGGCTGACTGTGGGTGGCAAGAATAGTGGGCTCTGTGTGCCA	1230
Oy	1485	TTTGGGGGCGTCTACTATTTTCCCTGGCAATGGCCGCTCATTTGCTCCAAATTTACGTA	1544
Db	1231	TTTGGGGGCGTCTACTATTTTCCCTGGCAATGGCCGCTCATTTGCTCCAAATTTACGTA	1290
Oy	1545	TTTATACACCGGAGACAGAGGGCGCAAGAGCTGGAGTTTCACGCTTGTGGCATTCAGC	1604
Db	1291	TTTATACACCGGAGACAGAGGGCGCAAGAGCTGGAGTTTCACGCTTGTGGCATTCAGC	1350
Oy	1605	CTTGTGGCCACTGTGAGGGCAAGGCCAATGGGGGCTGTGGACGGGAGGTACTGAGC	1664
Db	1351	CTTGTGGCCACTGTGAGGGCAAGGCCAATGGGGGCTGTGGACGGGAGGTACTGAGC	1410
Oy	1665	TACACGCTCCACTTGTGGGCAACCCCGAGGAAACCTTGTCACCGAATGTGAGGACAG	1724
Db	1411	TACACGCTCCACTTGTGGGCAACCCCGAGGAAACCTTGTCACCGAATGTGAGGACAG	1470
Oy	1725	TTTGAAGTCTGACGAGCACTCACAC	1747
Db	1471	TTTGAAGTCTGACGAGCACTCACAC	1493
RESULT 3			
AAS78540			
ID AAS78540 standard; cDNA; 1686 BP.			
XX AAS78540;			
XX 13-FEB-2002 (first entry)			
DE DNA encoding novel human diagnostic protein #14344.			

KW	Human: Chromosome mapping; gene mapping; gene therapy; forensic;
XX	food supplement; medical imaging; diagnostic; genetic disorder; ss.
OS	Homo sapiens.
PN	WO200175067-A2.
PD	11-OCT-2001.
PF	30-MAR-2001; 2001WO-US08631.
PR	31-MAR-2000; 2000US-0540217.
PR	23-AUG-2000; 2000US-0649167.
PA	(HYSE-) HYSEO INC.
PI	Drimanac RT, Liu C, Tang YT;
DR	WP1: 2001-639362/73. P-PSDB: ABG14353.
PT	New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
PS	Claim 1; SEQ ID NO 14344; 103pp; English.
XX	The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
SQ	Sequence 1686 BP; 236 A; 545 C; 562 G; 343 T; 0 other:
Query Match	76.3%; Score 1333.6; DB 23; Length 1686; Best Local Similarity 99.3%; Pred. No.2.7e-236;
Matches 1361;	Conservative 0; Mismatches 4; Indels 5; Gaps 2.
OY	285 CTGGGCGCGCGGTCCGGGCCACAGCTCGGTTGGCGGCTGCCGGCGGCATG 344
Db	1 I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
OY	322 CGGGGCGGGGCTCGGGGCGCACACTCGGTTGCGGGTCCGGCGGGCGGCCCAAG 381
Db	1 I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
OY	345 GAGCGCGGTGGCCCCCGCCCCTCGTGCGGTGTGGAGAGGAGTGGTGCATCATGTGACC 404
Db	1 I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
OY	382 GAGCGCGGATGCCCGC--CCGTCCGGCTGCTGGAGAGGAGTGGTGTCTCATCATGTGACC 439
Db	1 I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
OY	405 GGCTGCGCTTCAGAGAGCGGCGCGCACGCTGGGCGCTTCCGGACACTGCTAGGGG 464
Db	1 I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
OY	440 GGCTCGCTTCAGAGAGCGGCGCGCACGCTGGGCGCTTCCGGACACTGCTAGGGG 499
Db	1 I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
OY	465 ACCGAGCGCGCGCGCGCTTCTAAGAGAGAGCGCGCCCGAGATATTCTTCGACCGGC 524
Db	1 I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
OY	500 ACCGAGCGCGCGCGCGCTTCTAAGAGAGAGCGCGCGCGAGATATTCTTCGACCGGC 559
Db	1 I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I

QY	525	ACGGCCGACGCTTGAGAGCCGCTCTCTACTACACAGTCGCTGGGGGGCTCGGGGGCG	584
Db	560	ACCGGCCACGCTTCGAGCGGCTCTCTACTACACAGTCGCTGGGGGGCTCGGGGGCG	619
QY	585	CGGCGCACGTCGCGCTGACGCTTCTCTGGAGAGGTGGGCTCTTACAGGGGCTGGGCGGG	644
Db	620	CGGCGCACGTCGCGCTGACGCTTCTCTGGAGAGGTGGGCTCTTACAGGGGCTGGGCGGG	679
QY	645	CGGCGCTTGCGACGCTTCGCGGAGAGACGAGGGCTGCCGGTCCGCCACAGCGCCCTGCG	704
Db	680	CGGCGCTTGCGACGCTTCGCGGAGAGACGAGGGCTGCCGGTCCGCCACAGCGCCCTGCG	739
QY	705	CCGCGCGCGGCTTGGCGCGCGCACGCTGGCTGCTTTCGAGTTTCCGACAGCTCTCAGG	764
Db	740	CCGCGCGCGGCTTGGCGCGCGCACGCTGGCTGCTTTCGAGTTTCCGACAGCTCTCAGG	799
QY	765	CCGCGCGCGGCTTGGCGCGCGCTGAGTCTCCGCTGCTGGTCTACTCCGCTCCATCGTCGCTCT	824
Db	800	CCGCGCGCGGCTTGGCGCGCGCTGAGTCTCCGCTGCTGGTCTACTCCGCTCCATCGTCGCTCT	859
QY	825	GCGCTCGAGACGCTTCGACTTCGCGGACACCGCGAGCGGACGSGGGCTTGCTGCTCGAG	884
Db	860	GCGCTCGAGACGCTTCGACTTCGCGGAGACCGCGACGSGGCGCTTGCTGCTCGAG	919
QY	885	CCGCGAGCGGGCGGGGTTCGCCGCTCCGCTGAATGGCTCCAGCCCAATGGCTGGAAATC	944
Db	920	CCGCGAGCGGGCGG---GTTCGCCGCTCCGCTGAATGGCTCCAGCCCAATGGCTGGAAATC	976
QY	945	CACCCGCGCTGCGCTTCATGATGACCCGCTCTTGCTGGTGAGACGCTGATATTGTTGGT	1004
Db	977	CACCCGCGCTGCGCTTCATGATGACCCGCTCTTGCTGGTGAGACGCTGATATTGTTGGT	1036
QY	1005	TCCTCTTGAAGCTCTGGTACGCGCTTCGCTGTCTGTCCAAAGCAAGGCTATCTTCTTCAAGA	1064
Db	1037	TCCTCTTGAAGCTCTGGTACGCGCTTCGCTGTCTGTCTGTCCAAAGCAAGGCTATCTTCAAGA	1096
QY	1065	ACGCGATGAACCTTCATCGATTTTGTGTGGCTATCTTCCCTACTTGTGGCATGCGGACCG	1124
Db	1097	ACGCGATGAACCTTCATCGATTTTGTGTGGCTATCTTCCCTACTTGTGGCATGCGGACCG	1156
QY	1125	AGCTGGCGCCGCGACGAGGGGTGGGGCGACAGGCCATGTCATCTGGCCATCTCGAGAGTCA	1184
Db	1157	AGCTGGCGCCGCGACGAGGGGTGGGGCGACAGGCCATGTCATCTGGCCATCTCGAGAGTCA	1216
QY	1185	TCCGATTGATGCGTGTCTTCCGATCTTCAAGCTGTCCCGGCACTCAAAAGGGCTCGCAAA	1244
Db	1217	TCCGATTGATGCGTGTCTTCCGATCTTCAAGCTGTCCCGGCACTCAAAAGGGCTCGCAAA	1276
QY	1245	TCCTTGGGCGACAGCGCTTCGGGCTCCATCGCTGAGCTGGGGCTCCTCATCTTCTTCTCT	1304
Db	1277	TCCTTGGGCGACAGCGCTTCGGGCTCCATCGCTGAGCTGGGGCTCCTCATCTTCTTCTCTCT	1336
QY	1305	TCATCGGTGGTGCCTCTTTCGAGGGCGGCTACTTTCGGAACCTGAACCGGGTGGACT	1364
Db	1337	TCATCGGTGGTGCCTCTTTCGAGGGCGGCTACTTTCGGAACCTGAACCGGGTGGACT	1396
QY	1365	CCCATTTCACTATGATCCCTGATCTCTTCTGGTGGGCGGTATGTACCATGTACTAGATGTC	1424
Db	1397	CCCATTTCACTATGATCCCTGATCTCTTCTGGTGGGCGGTATGTACCATGTACTAGATGTC	1456
QY	1425	GCTATGAGACATGAGCACCCGCTCATCTGTGGGTGGCAAGATAGTGGGCTCTCTGTGGCA	1484
Db	1457	GCTATGAGACATGAGCACCCGCTCATCTGTGGGTGGCAAGATAGTGGGCTCTCTGTGGCA	1516
QY	1485	TTGGGGGCGGTGACATATTTCCCTGGCCGATCGCTCCGCTCATTTCTTCACATTTACACTACT	1544
Db	1517	TTGGGGGCGGTGACATATTTCCCTGGCCGATCGCTCCGCTCATTTCTTCACATTTACACTACT	1576
QY	1545	TTTATTCACCGGGAGACAGAGGGCGAGAGGCTGTTCAGCCATGTGACATGACGAC	1604
Db	1577	TTTATTCACCGGGAGACAGAGGGCGAGAGGCTGTTCAGCCATGTGACATGACGAC	1636
QY	1605	CTTGTGGCCACTGTGAGGCGCAAGGCCAATGGGGGCTGTGTGACGGGGAG	1654

[illegible]

acid. The ion flux-related disorders include: potassium channel associated disorders, such as neurological disorders and central nervous system disorders such as cognitive and neurodegenerative disorders e.g. Alzheimer's disease, Parkinson's disease, senile dementia, Huntington's disease, Gilles de la Tourette's syndrome, multiple sclerosis, progressive supranuclear palsy, epilepsy, Jacob-Creutzfeldt disease, autonomic function disorders such as hypertension and sleep disorders, neuropsychiatric disorders such as depression, schizophrenia, mania, anxiety disorders or phobic memory loss, learning or memory disorders, amnesia or age-related memory loss, attention deficit disorder, obsessive-compulsive disorder, migraine or obesity; cardiac-related disorders such as arteriosclerosis, ischemia reperfusion injury, restenosis, arterial inflammation, tachycardia, congestive heart failure, myocardial infarction and arrhythmia. The polypeptides and nucleic acids are also useful as diagnostic targets and therapeutic agents for: controlling cellular proliferative and/or differentiative disorders e.g. haematopoietic neoplastic disorders, carcinoma and sarcoma; disorders associated with bone metabolism such as osteoporosis, rickets, osteopenia, cirrhosis, hyperparathyroidism, idiopathic hypercalcaemia; immune disorders such as autoimmune disorders, diabetes mellitus, arthritis, including rheumatoid arthritis, osteoarthritis and psoriatic arthritis; multiple sclerosis, myasthenia gravis, autoimmune thyroiditis, ulcerative colitis, psoriasis, Sjogren's syndrome, dermatitis, Crohn's disease, asthma, allergic asthma, conjunctivitis, aplastic anaemia, Grave's disease, chronic active hepatitis, autoimmune uveitis, scleroderma; liver disorders including storage disorders such as Gaucher's disease, glycogen storage disease, haemochromatosis and porphyria; disorders; viral diseases; pain; or metabolic disorders such as obesity, anorexia nervosa, cachexia, lipid disorders and diabetes.

Sequence 1341 BP; 190 A; 443 C; 411 G; 297 T; 0 other;

Query Match 75.6%; Score 1321.6; DB 24; Length 1341;

Best Local Similarity 95.5%; Pred. No. 4.3e-234;

Matches 1337; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

374 TGTGCGAGCGGCTGTGCTCAAGTGGCGCGGCTTTCGAGACGCGGCGCGACG 433
 1 TGTGCGAGCGGCTGTGCTCAAGTGGCGCGGCTTTCGAGACGCGGCGCGACG 60
 434 CTGGGGCGGCTTCCCGACACTCTGTAGGAGCCAGCGCGCGCGCTTCTACGAC 493
 61 CTGGGGCGGCTTCCCGACACTCTGTAGGAGCCAGCGCGCGCGCTTCTACGAC 120
 494 GACCGCGCGCGAGTATTTCTTGACGCGGCGCGCGCTTTCGAGACGCGGCTTCTAC 553
 121 GACCGCGCGCGAGTATTTCTTGACGCGGCGCGCGCTTTCGAGACGCGGCTTCTAC 180
 554 TACTACAGTCCGCTGGGCGGCTGGGCGCGCGAGCGAGTCCGCTTCTCTG 613
 181 TACTACAGTCCGCTGGGCGGCTGGGCGCGCGAGCGAGTCCGCTTCTCTG 240
 614 GAAAGGTGCGCTTCTACGCGGCTGGGCGCGCGCTTTCGAGACGCGGCTTCTCTG 673
 241 GAAAGGTGCGCTTCTACGCGGCTGGGCGCGCGCTTTCGAGACGCGGCTTCTCTG 300
 674 GCGTCCCGGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCTTTCGAGACGCGGCTTCTG 733
 301 GCGTCCCGGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCTTTCGAGACGCGGCTTCTG 360
 734 CTGCTTTTCAGTTTCCGAGAGCTCTACGCGCGCGGCTTTCGAGACGCGGCTTCTCTG 793
 361 CTGCTTTTCAGTTTCCGAGAGCTCTACGCGCGCGGCTTTCGAGACGCGGCTTCTCTG 420
 794 CTGCTTTTCAGTTTCCGAGAGCTCTACGCGCGCGGCTTTCGAGACGCGGCTTCTCTG 853
 421 CTGCTTTTCAGTTTCCGAGAGCTCTACGCGCGCGGCTTTCGAGACGCGGCTTCTCTG 480
 854 GACCGCGCGCGAGGCGGCTTTCGAGAGCTCTACGCGCGCGGCTTTCGAGACGCGGCTTCTG 913
 481 GACCGCGCGCGAGGCGGCTTTCGAGAGCTCTACGCGCGCGGCTTTCGAGACGCGGCTTCTG 537

914 CTGAATGGCTCCACCAAAATCCCTGGAATCCACCCGCGCTTTCATATGACCGCTTC 973
 538 CTGAATGGCTCCACCAAAATCCCTGGAATCCACCCGCGCTTTCATATGACCGCTTC 597
 974 TTGCTGGTGGAGACGCTGTATTTTGTGTTCTTTCGAGCTGCTGCTGCTGCTG 1033
 598 TTGCTGGTGGAGACGCTGTATTTTGTGTTCTTTCGAGCTGCTGCTGCTGCTG 657
 1034 GTCTGTCACCAAGGAGGCTATTTCTTCAGAACGATGATGATGATGATGATGATG 1093
 658 GTCTGTCACCAAGGAGGCTATTTCTTCAGAACGATGATGATGATGATGATGATG 717
 1094 ATCTTCCCTACTTTTGTGACCTGAGGACCGAGCTGGCGCGGACGAGGCGGCTG 1153
 718 ATCTTCCCTACTTTTGTGACCTGAGGACCGAGCTGGCGCGGACGAGGCGGCTG 777
 1154 CAGGCGATGTACGTGCGCATCTCTGAGAGTATCCGATTTGTGCTGCTTCCGATCTTC 1213
 778 CAGGCGATGTACGTGCGCATCTCTGAGAGTATCCGATTTGTGCTGCTTCCGATCTTC 837
 1214 AAGCTGTCGCGGCACTCAAAAGGCGCTGGAATTTGGGCGAGAGCGCTTCCGATG 1273
 838 AAGCTGTCGCGGCACTCAAAAGGCGCTGGAATTTGGGCGAGAGCGCTTCCGATG 897
 1274 CGTAGGCTGGGCTCTCATCTTTTCTCTTCATCGGTGCTGCTTTCGAGCGCC 1333
 898 CGTAGGCTGGGCTCTCATCTTTTCTCTTCATCGGTGCTGCTTTCGAGCGCC 957
 1334 GTCTACTTTTGGCGAAGTTGACCGGGGTGAGCTCCCATTTCTACTAGATCCCTGATCTTC 1393
 958 GTCTACTTTTGGCGAAGTTGACCGGGGTGAGCTCCCATTTCTACTAGATCCCTGATCTTC 1017
 1394 TGTGCGGCGGTAGTACCATGATGATGATGATGATGATGATGATGATGATGATG 1453
 1018 TGTGCGGCGGTAGTACCATGATGATGATGATGATGATGATGATGATGATGATG 1077
 1454 GGTGGCAAGATATGAGGCTCTGTGTGTCATGTCGCGGCGGTGCTATTTCCCTGCCA 1513
 1078 GGTGGCAAGATATGAGGCTCTGTGTGTCATGTCGCGGCGGTGCTATTTCCCTGCCA 1137
 1514 GTGCGCGGCTATGCTCCAAATTTGACGCTTATATACCGGGAGACAGAGGGGAGAG 1573
 1138 GTGCGCGGCTATGCTCCAAATTTGACGCTTATATACCGGGAGACAGAGGGGAGAG 1197
 1574 GCTGGGATGTTTCAACCATGTTGACATGAGGCTTGTGGCCCATGAGAGGCGCAAT 1633
 1198 GCTGGGATGTTTCAACCATGTTGACATGAGGCTTGTGGCCCATGAGAGGCGCAAT 1257
 1634 GGGGGGCTGTGACGCGGGAGGTAAGTACCTGAGTACCACTCTGAGGACCGCCAGG 1693
 1258 GGGGGGCTGTGACGCGGGAGGTAAGTACCTGAGTACCACTCTGAGGACCGCCAGG 1317
 1694 GAACACCTGTGACCGAAGTGA 1717
 1318 AAACACTGTGTACCGAAGTGA 1341

RESULT 5

AAT04953 standard; cDNA; 1598 BP.

AAT04953;

11-APR-1996 (first entry)

Mouse Kv1.7 voltage-gated potassium channel coding sequence.

Mouse Kv1.7 voltage-gated potassium channel;

insulin antagonist drug screening; insulin agonist drug screening;

non-insulin-dependent diabetes mellitus; ds.

Mus musculus.

XX	Key	Location/Qualifiers
EH	1..1598	
FT	CDS	
FT		/*tag=a
FT		/note="specification states sequence is 1599.
FT		Incomplete stop codon given"
XX		
PN	W095523858-A1.	
XX		
PD	08-SEP-1995.	
XX		
PE	23-FEB-1995; 95MO-US02221.	
XX		
PR	10-AUG-1994; 94US-0288405.	
XX	04-MAR-1994; 94US-0207401.	
PA	(RGC) UNIV CALIFORNIA.	
XX		
PI	Chandy G, Chandy KG, Gutman GA, Kalman K;	
DR	WPI; 1995-320573/41.	
DR	P-PSDB; AAR82937.	
XX		
PT	New voltage-gated potassium channel gene - used to identify	
PT	material(s) which can increase insulin release e.g. for treating	
PT	non-insulin dependent diabetes mellitus.	
XX		
XS	Claim 1; Page 22-23; 38pp; English.	
XX		
CC	The DNA encodes a mouse Kvl.7, which is a Shaker-related voltage	
CC	gated potassium channel. It may be used in drug screening for	
CC	identification of therapeutics which modulate the channel and,	
CC	therefore, modulate insulin secretion. Selective antagonists	
CC	increase insulin release and thereby reduce hyperglycaemia	
CC	associated with non-insulin-dependent diabetes mellitus.	
XX		
Q0	Sequence 1598 BP; 232 A; 521 C; 502 G; 343 T; 0 other;	

Query Match	61.1%;	Score 1068;	DB 16;	Length 1598;
Best Local Similarity	81.5%;	Pred. No. 1.8e-187;		
Matches 1288; Conservative	0;	Mismatches 280;	Indels 12;	Gaps 4

QY	137	CGGGGACAGGAGGAGGGGCGCTCCCGGACAGAGGGGCGGCGGTGCGCTTCGCGCTCCG	196
Db	31	CGGAAAGCGCGGGGTGGCAATGTTTCCACAGATGTGTGAACGGCAGAGGGCGCCCTAGC	90
QY	197	CCCGCGGGGGTTCACAGTCCCGCTCCCTCGCGCCCTAGCCGCCCTGCGGGGCTATTTTAC	256
Db	91	CCCGGGGGGTAAACACGGCCCGCTCCCGCGCCCTGGCGGAGCTTTCATGCTATTTT	150
QY	257	GGCGGGACACCGGACACCGGACACCGGGCTGGGGCGCGGTCGGGGGCACACGTGGTTC	316
Db	151	ACCGCGCGACACCGGACACCGCATGGGGGTGGCGCGGCGCTCGGGGCGACACGTCCGTTTC	210
QY	317	GGGGTTCGCGGGGCTGGCGCGCGCATAGAGACCGCGGTGGCCGGCGCCCGCTCGGCTGC	376
Db	211	ACCGGTCCCGGGGCTGTGGCGCGCATAGAACCAACGGTGGCCGCGCGCTG---CGTGC	267
QY	377	TGCGAGCGGGTGTGCTCAACGTGGCGCGGCGTGGCTTTCAGAGACGGGGCGCGCACGCTG	436
Db	268	TGCGAGCGGGCTGTGCTCAACGTGGCGGGGTGGCTTTCAGAGACCGCGCGCACGCTTC	327
QY	437	GGCGGCTTCCGGACACGTCTTAGGGGACCCACGGGCGCGCGCGCTTCTACAGAGAC	486
Db	328	GGCGGCTTCCGGACACGTCTTAGGGGACCCCGGTGGCGCGACCGCTTCTACAGAGGCG	387
QY	497	GGCGCGCGCGATATTTTCTTGACCGGACCGCGCCACGTTTCGACGGCGCGTCTACTAC	556
Db	388	GGCGCGCGCGATATTTTCTTGACCGAGACCGCGCCACGTTTCATGGGGGTCTACTAC	447
QY	557	TACACAGTCCGGTGGCGGCGCTGGCGGCGCGGACGACGTCGCGCTTCGACGTCCTTGAGAA	616
Db	448	TACACAGTCCGGCGCGCGCTAGAGCGCGCGCGACGCTGGCCCTTCGACGTCCTTCGAG	507

QY	617	GAGTGGCCCTTTCTACGGGCTGGCGCGGCGCCCTTGGACACGCTGCGGAGACGAGGCG	676
Db	508	GAGGATGTCCTTCTACAGGGGCTGGG---GGCGGGGCTGGCGCGGCTGGCGGAGACGAGGCG	564
QY	677	TGCCGGGGCGCGCGAGGCGCCCTGTGCCCGCGCGGCGCCCTGTGGCCCGGAGCTGGGGCG	736
Db	565	TGCGGGG---CGCGAGCGCGGCTGTCCCCG---CCTTGGCGGTAGCTCTGGGCTG	618
QY	737	CTTTTGGATTTCGAGAGCTCTCAGAGCGCGCGGCTGTGCTGCCTATGCTCCGTGCG	796
Db	619	CTCTTCGAAATTTCTGAGAGGTGCGACAGCTGGCGGGTGTGTGCGGTCTTCGTAATC	678
QY	797	GTCATCTCTGTCTCCATGCTGTCTTGTGCTTGGAGACGCTGCTAGCTTTCCGCGACGAC	856
Db	679	GTCATCTCGGTCTCCATGCTGTGCTTTTGGCTTGAGACACTGCCACACTTTCCGCGACGAC	738
QY	857	CGCGACGGCAGGGGGCTTGCTGTGCGACCGCGACCGCGCCCGGTGTTCGCCGCTCCGCTG	916
Db	739	CGCGATGACCCGGGGGCTGTGCGCGCGGTGAGCGGCTGTACTGTGCTGTCTCGCTCGCTC	798
QY	917	AATGGCTTCAGCAAAATGCGCTGGAAATTCACCCCGGCTGGCCTTCAATACCGCTTTCTC	976
Db	799	AATGGCTTCAGTCCCATGCGACGAGGACGCCCTTCCCGACAGGCTTTACAGATCATTTCTTT	858
QY	977	GTTGGAGAGCGCTGTATTATTGTTGGTTCTCTTTGAGTGTGCTGTATGACCTCTGTGTC	1036
Db	859	GTTGGAGAGACCTGTGTATGCTGTGTCTCTTTGAGTGTGTGTATGTGTATGTGGTGGGC	918
QY	1037	TGTCCAGACAGGCTATCTTCTTCAGACGTGATGAACTCATGATTTTGTGCTATC	1096
Db	919	TGCCCTACCAAGCTGTGTTCTTCAAGAAATGATGAACCTTAATGACTTCCGTGGCACATC	978
QY	1097	CTTCCCTATTGGGACAGTGGGACGAGCGACGACTGGCGGAGGAGGAGGGGTGGGCCACAG	1156
Db	979	CTGCCCTTACTTGTGGGCTGTGGGACGAGATTAAGCCGGAGGGGTGTGGGCCACGCG	1038
QY	1157	GCCATGTACCTGGGCATCTGAGAGTATCCGAAATGGTGGCTGTCTTCCGATCTTTCAAG	1218
Db	1039	GCTATGTCCCTGGGCATCTGTAAGGCTATCCGAAATGGTGTGTCTTCCGCAATCTTTCAAG	1098
QY	1217	CTGTCCGCGCACTAAGAGGCTGTCAAAATCTTGGGCGACAGCGTTTCGGGCTTCATGCGT	1278
Db	1099	CTCTCTCAGGCAATTCGAAGGGGTCTCAGAATCTTGGGTAGACACTGTGGGGCTTCCATGCGT	1158
QY	1277	GAGCTGGGCGCTCACTCTTTTCCCTTATGAGGTGTGTCTCTTTTCCAGGCGCGTC	1338
Db	1159	GAGCTAGGTCTCTCATCTCTCTCTCTCTTATTTGGGTGTCTCTTTTCCAGGCGAGTC	1218
QY	1337	TACTTTGGCGAAGTTGACCGGGTGGAGCTCCCATTTACTAGCATCTCTAGTCTTCTTG	1398
Db	1219	TACTTTGGTGAAGTGGAGCGGGGTGTGACCACTTTCACAGCATTCGGGAGTCTTTTGG	1278
QY	1397	TGGGCGGTAGTACCATGACTACAGTTGGCTATGAGACATGGCACCGCTCACTGTGGT	1458
Db	1279	TGGGCGGTAGTACCATGACTACAGCGTTGGCTATGAGGACATGGCACCGCTCACTGGGT	1338
QY	1457	GGCAGATAGTGGGCTCTGTGTGGCATTTGGCGGCGTGTGTACTTTTCCCTGCGCAGTG	1518
Db	1339	GGCAGATAGTGGGCTCTGTGTGGCATTTGGCATGAGGTGTGTCTTCCATCTCTGTGCTGG	1398
QY	1517	CCCGCATTTGCTCCAAATTTAGTACTTTTATCACCGGAGACAGAGGCAAGAGCT	1578
Db	1399	CCGTGATTTGTCTACTTACTTACTTATTTTACACCGGAGACAGAGGCGCAAGAGCA	1458
QY	1577	GGGATGTTACGCCATGTGACATGACGCTTGTGGCCCACTGGAGGGCAAGGCCAATGGG	1638
Db	1459	GGGATGTTACGCCATGTGACACACAGACCCCTGGGTATACCTGGAGGGCAAGGCTAATGGG	1518
QY	1637	GGGCTGTGTGACGGGAGAGTACTGTAGACTACACCTTCATCTGTGGGCAACCCCGCAGGAA	1698
Db	1519	GGGCTGTGTGACCTGTGAGAGTCTGGAAGCTCTCTCCACACTGTGGGCCCTCTCTCAGGAAA	1578

XX 02-OCT-2001; 2001WO-US30589.
 XX
 XX 02-OCT-2000; 2000US-237054P.
 XX
 XX (GENE-) GENE LOGIC INC.
 XX
 XX Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
 DR WPI: 2002-426119/45.
 XX
 PT Diagnosing and detecting the progression of liver cancer,
 PT hepatocellular carcinoma or metastatic liver tumor in a patient,
 PT involves detecting the level of expression of two or more genes in a
 PT liver tissue sample
 XX
 PS Claim 1: SEQ ID NO 2354; 298bp; English.
 XX
 XX The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
 CC tumor in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in ABN93503-ABN97455 in a
 CC tissue sample. The method of the invention has hepatotropic, and
 CC cytostatic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 2867 BP; 565 A; 839 C; 845 G; 618 T; 0 other;
 XX
 Query Match 34.1%; Score 596.2; DB 24; Length 2867;
 Best Local Similarity 68.6%; Pred. No. 9,7e-101;
 Matches 873; Conservative 0; Mismatches 358; Indels 42; Gaps 2;

Db 1033 TTGGAGACCTGCGCTGATGAGGATGAAGTGAAGTGTGCTCCGCCACCTCCGGGCCCC 1092
 QY 887 GCAAGCCGGCCGGTGTTCCTCCCGCTCCGCTGAATGG-----CTCC 925
 Db 1093 CACCAGCCTCCCGCGCCGCCCTGGGGCCAGCGGGGTCAATGAGCCCGCCCTCT 1152
 QY 926 AGCCAAATGGCTGGAAATTCACCCCGCCCTGCTCAATGACCGGTCTTGTTGGAG 985
 Db 1153 GGCCTTAAGGTGGACCGCTCTCCAGAGACCTGGCCGACCTTCTTCAATGAGAG 1212
 QY 986 ACGTGTGATTTTGGTTCCTCTGCTGAGCTGCTGTAGCCCTCTGCTGTCAAGC 1045
 Db 1213 ACACAGTGCCTCAATGTGTTCACCTTGACCTGTGTGGCTTCTTGCTGCTGCCAGC 1272
 QY 1046 AAGGCTATCTTCTTCAAGAAAGTGAAGTGAACCTCATGATTTTGGCTATCTCTAC 1105
 Db 1273 AAGGCAAGGTTCTCCCGGAACATCATGATCATGATGTGGTGGCCATCTCCCTAC 1332
 QY 1106 TTTGTGGACATGGGACACGAGCTGGCCGCGGACGAGGAGGAGGCTGGGCTGAG 1150
 Db 1333 TTCAATACCTTGGGACCGAAGTGGACAGAGACGAGGAGGAGGAGGAGGAGGAG 1392
 QY 1151 -----CAGCAGGACATGTCACTGAGCTGAGCTGAGATTCAGATTTGGCTGTCTTC 1204
 Db 1393 AATGGGACGAGGAGCATGTCTCCGAGCATCTCGAATCATCCGCTGTGCTGGGTCTTC 1452
 QY 1205 CGCATCTTCAAGCTGTCCCGGCACTCAAGAGGCTGTCAATCTTGGGCGCAGAGCTTCGG 1264
 Db 1453 CGCATCTTCAAGCTGTCCCGGCACTCAAGAGGCTGTCAATCTTGGGCGCAGAGCTTCGG 1512
 QY 1265 GCGCTCAATGGTGAAGCTGGGCGCTGCTGATCTTCTCTTCAATGAGGCTGTGCTCTT 1324
 Db 1513 GCTTCATGAGGAGAGCTGGGCTGCTGATCTTCTCTTCAATGAGGCTGTGCTCTT 1372
 QY 1325 TCCAGGCGCTTCACTTGTGCGAAGTGAACCGGAGTGAATCCATTTCACTAGCATCTCT 1384
 Db 1573 TCCAGTCCGCTTCACTTGTGCGAAGTGAACCGGAGTGAATCCATTTCACTAGCATCTCT 1632
 QY 1385 GATGCTTCTGTGGGAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1444
 Db 1633 GAGGCTTCTGTGGGAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1692
 QY 1445 GTCACTGTGGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1504
 Db 1693 ATCACTGTGGGAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1752
 QY 1505 TCCCTGCAAGTGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1564
 Db 1753 GCGCTGCTGTGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1812
 QY 1565 GCGGAGAGGCTG 1577
 Db 1813 CACGAGAGAGCGG 1825

RESULT 8
 ABL65917
 ID ABL65917 standard; DNA: 2867 BP.
 AC ABL65917;
 XX
 DE 15-MAY-2002 (first entry)
 XX
 XX Lung cancer related gene sequence SEQ ID NO:4254.
 XX
 XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 XX gene; ds.
 XX
 XX Homo sapiens.
 OS
 XX

PN W0200194629-A2.
 XX
 PD 13-DEC-2001.
 PF 30-MAY-2001; 2001MO-US10838.
 XX
 PR 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-23133P.
 PR 18-SEP-2000; 2000US-231617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 20-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 28-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237588P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 XX
 PA (AVAL-) AVALON PHARM.
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Sopet DR, Weaver Z;
 XX
 DR WPI; 2002-188264/24.
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set -
 XX
 PS Claim 1; SEQ ID 4254; 44pp; English.
 XX
 CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical

CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.
 XX
 SQ Sequence 2867 BP; 565 A; 839 C; 845 G; 618 T; 0 other;
 Query Match 34.1%; Score 596.2; DB 24; Length 2867;
 Best Local Similarity 68.6%; Pred. No. 9,7e-101;
 Matches 873; Conservative 0; Mismatches 358; Indels 42; Gaps 2;
 QY 347 GCCGCGGTGCCCGCCCGCCGCTGCGAGCGGCTGCTCAACGTCGGG 406
 DB 553 GACCAGGCTCTGGGACGCGGCTCCCTGACACACGAGCGGCGTCACATCATCTCCGG 612
 QY 407 CTGGCTTCGAGACGGGGGCGGACCGCTGGCGGCTTCCCGACACTCTGTAGGGAG 466
 DB 613 CTGGCTTTTAGACGAGCTGGGACCCAGGCGAGTTCCCAACACACTCTGGGGGAC 672
 QY 467 CCAGCGCGCGCGCGCGCTTCTTACGACGAGCGCGCGAGTATTTCTTGACCGGAC 526
 DB 673 CCCGCCAAGCGGCTGCGGTACTTGACCCCTGAGAACGAGTACTTTCGACCGCAC 732
 QY 527 CGGCGAGCTTCGACGCGGCTGCTTACTTACTTACAGTCCGCTGGCGGCGCG 586
 DB 733 CGGCGAGCTTCGACGAGTATCTTACTTACTTACTTACAGTCCGCGGCGCGCGGAGCG 792
 QY 587 GCGGAGCTGCGGCTGACGCTTCTTCTGGAAGAGGTGGCTTTCAGAGGCTGGCGGCG 646
 DB 793 GTCAACGCTTCTCTGAGAGGTTCTGCGAGAGTATCTTCTTCTTCTTCTTCTTCTTCT 852
 QY 647 GCCCTGCGAGCGCTGCGCGAGGAGAGAGGCGTCCGCGCGCGCGCGCGCGCGCG 706
 DB 853 GCCATGAGCGGCTTGGCGGAGATGAGGGCTTCAATTAAGAACGAGAACCGCTGTC 912
 QY 707 CGCGCGCTTGGCGCGCGAGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 766
 DB 913 CGCAACGAGTTCAGCGCGCGAGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 972
 QY 767 GCGGCGTGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 826
 DB 973 GCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1032
 QY 827 CTGAGAGCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 886
 DB 1033 TTGAGAGCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1092
 QY 887 GCAGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 925
 DB 1093 CACGAGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1152
 QY 926 AGCCAAATGCTGGAATTCACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 985
 DB 1153 GGCCTACGGTGGCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1212
 QY 986 ACGCTGTATTTTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1045
 DB 1213 AACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1272
 QY 1046 AAGGCTATCTTCTTCAAGAACGTGATGACCTTCGATTTTGGCTATCTTCTTCTTCT 1105
 DB 1273 AAGGACAGGTTCTCCGACATCATCATCATCATCATCATCATCATCATCATCTTCC 1332
 QY 1106 TTGTGCACTGGGACACGAGCTGGCGCGGACGAGGAGGTGGC----- 1150
 DB 1333 TTCAATCCCTTGGGACCGAATCGAGACGAGGACGAGGAGGAGGAGGAGGAGGAGG 1392
 QY 1151 -----CAGCAGGCGATGATGAGGCGATCTGAGTCAATCGATGAGTGGCGGTCTT 1204
 DB 1393 AATGGGACGAGGCGATGCTCCCTGGCCATCTCCGAGTCAATCCGCTGCTGCTGCTGCT 1452

QY 1205 CGCATCTTCAGCTGTCCCGGCACTCAAGGGCTGCAATCTTGGGCGAGCGCTTCGG 1264
|||||
DB 1453 CGCATCTTCAGCTGTCCCGGCACTCAAGGGCTGCAATCTTCCTGGCAAGACCTTCGAG 1512
QY 1265 GCTTCATGCGTGTGAGCTGGGCTCTCTCATCTTTTCTCTTCTGCTGTGCTCTTT 1324
|||||
DB 1513 GCTTCATGCGTGTGAGCTGGGCTCTCTCATCTTTTCTCTTCTGCTGTGCTCTTT 1572
QY 1325 TCCGAGCGGCTGTACCTTTCGCAAGTTCGACGGGGTGGACTCCCATTTTCACTGACATCCG 1384
|||||
DB 1573 TCCGAGCGGCTGTACCTTTCGCAAGTTCGACGGGGTGGACTCCCATTTTCACTGACATCCG 1632
QY 1385 GAGTCCTTCTGTGTGGCGGTAGTCAACATGACTACAGTGTGGTATGAGACATGGACCC 1444
|||||
DB 1633 GAGTCCTTCTGTGTGGCGGTAGTCAACATGACTACAGTGTGGTATGAGACATGGACCC 1692
QY 1445 GTCACTGTGTGGCGGTAGTCAACATGACTACAGTGTGGTATGAGACATGGACCC 1504
|||||
DB 1693 ATCACTGTGTGGCGGTAGTCAACATGACTACAGTGTGGTATGAGACATGGACCC 1752
QY 1505 TCCGAGCGGCTGTACCTTTCGCAAGTTCGACGGGGTGGACTCCCATTTTCACTGACATCCG 1564
|||||
DB 1753 GCTTCATGCGTGTGAGCTGGGCTCTCTCATCTTTTCTCTTCTGCTGTGCTCTTT 1812
QY 1565 GCGGAGAGGCTG 1577
|||||
DB 1813 CACGAGAGGCTG 1825

RESULT 9
AAH21452
ID AAH21452 standard; DNA: 1836 BP.

AAH21452;

18-SEP-2001 (first entry)

Human Kv1.5 DNA.

Inhibitor; eukaryotic; potassium channel; TRK1; TRK2; TOK1;
activator; ds.

Homo sapiens.

MO200151519-A2.

19-JUL-2001.

05-JAN-2001; 2001WO-EP00055.

11-JAN-2000; 2000DE-1000651.

(AVET) AVENTIS PHARMA DEUT GMBH.

Leberer E, Leeuw T, Ritscher A;

WPI: 2001-442137/47.

Identifying inhibitors and activators of eukaryotic potassium channels,
for use as pharmaceuticals, comprises using yeast cells that express
heterologous, but no endogenous, potassium channels -

Disclosure: Page 45-46; 78pp; German.

This sequence represents a novel method for identifying inhibitors or
activators (A) of a eukaryotic potassium channel (KC) by applying a test
compound to a mutant *Saccharomyces cerevisiae* cell in which: (1) the
three endogenous KC (TRK1, TRK2 and TOK1) are not expressed; but (1i) a
eukaryotic KC is expressed heterologously, where the effect of the
compound on the eukaryotic KC is then determined. The method is used to
identify inhibitors or activators (A) of a eukaryotic potassium channel.
(A) are potentially useful as pharmaceuticals. The method is easily
automated for parallel processing of many samples, using either different

CC concentrations of test compounds and/or different levels of heterologous
KC gene expression. It allows identification of compounds that inhibit human
KC selectively. This sequence represents the human Kv1.5 encoding DNA
described in the method of the invention.

Sequence 1836 BP; 323 A; 614 C; 580 G; 319 T; 0 other;

Query Match 33.7%; Score 588.2; DB 22; Length 1836;

Best local similarity 68.7%; Pred. No. 2.8e-99; Mismatches 353; Indels 45; Gaps 3;

QY 347 GCCGCGTCCCGCCCGCCCGGCTGCGTGGAGCGGCTGTCTCAACGTGGCGGG 406
|||
DB 322 GACACAGCTCTGGGACGAGGCTCTGACACACACGCGGTCCATCAACATCTCCGG 381
QY 407 CTGCGCTTGGAGACGCGGCGCGGACGCTGGCGGCTTCCCGACACTCTGCTAGGGGAC 466
|||||
DB 382 CTGCGCTTGGAGACGCGGCTGGCGGACCTTGGCGGCTTCCCGACACTCTGCGGGGAC 441
QY 467 CCAGCGCGCGGCGGCTTCTACGACGACGCGCGGAGATTTCTTCAGCGGAC 526
|||
DB 442 CCGCGCAAGCGCTGCGCTACTTCTGACCCCTGAGAGAGAGTCTTCTGACCGCAC 501
QY 527 CCGCGCGCTTGGACGCGCTGCTCTACTACTACATCCGCTGGCGGCTGCGCGCGG 586
|||||
DB 502 CCGCGCGCTTGGACGCGTATCTCTACTACTACAGTCTCGGGGCGCGCTGCGAGG---G 558
QY 587 GCGCAGCTGCGCTGACGCTTCTCTGAGAGAGTGGCTTCTACGGGCTGGCGCGGCG 646
|||
DB 559 GTCAACGCTCTCCCTGAGAGGCTTGGCGGAGATAGCTTCTACAGCTGGCGGGGAG 618
QY 647 GCCCTGGACAGCGCTGGCGGAGAGAGGCTGGCGGCTGGCGGCGCGCGCGCTGGCC 706
|||
DB 619 GCGCTGAGAGCGCTTCCGCGGAGATGAGGCTTATTAAGAGAGAGAGAGAGCGCTGCC 678
QY 707 CCGCGCGCTTGGACGCGGCTGCTCTACTACTACATCCGCTGGCGGCTGCGCGCGG 766
|||
DB 679 CCGCAGAGTTCAGGCGGCGGAGGCTGCTTATCTTCTGAGATATCGGAGAGCTGTGGCTC 738
QY 767 GCGCGGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 826
|||||
DB 739 GCGCGGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 798
QY 827 CTGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 886
|||||
DB 799 TTGAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 858
QY 887 GCAGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 925
|||
DB 859 CACGAGCTGCTGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 918
QY 926 AGCCAAATGCTTGAAGATCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 985
|||||
DB 919 GCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 978
QY 986 AGCGTGTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1045
|||
DB 979 ACCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1038
QY 1046 AAGGCTATCTTCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1105
|||||
DB 1039 AAGGAGAGGCTTCCGGAACATGATGATGATGATGATGATGATGATGATGATGATGATG 1098
QY 1106 TTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1150
|||
DB 1099 TTGATCACTTCCGGAACATGATGATGATGATGATGATGATGATGATGATGATGATG 1158
QY 1151 -----CAGAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1204
|||||
DB 1159 AATGGCAGAGGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1218
QY 1205 CGCATCTTCAGCTGTCCCGGCACTCAAGGGCTGCAATCTTGGGCGAGCGCTTCGG 1264
|||||

Db 1219 CGGATCTTCAAGCTCTCCGCCACACTCCAGAGGGCTGAGATCTTGGGCAAGACCTTGCAG 1278
 Qy 1265 GCCCTCATGGCTGAGTGGGCGCTCCATCATCTTTTCTTTCATCGGTGATCTCTTT 1324
 Db 1279 GCCTCCATGAGGAGAGCTGGGGCTGCTATCTTCTTCTTCATCGGGGTCATCTCTTC 1338
 Qy 1325 TCCAGCGCCGCTTCACTTGGCGAAGTTGACCGGGTGACCTCCACTTCACTAGCATCTCT 1384
 Db 1339 TCCAGTCCGCTTCACTTGGCGAAGTTGACCGGGTGACCTCCACTTCACTAGCATCTCT 1398
 Qy 1385 GAGTCTCTTGTGTTGGGGGATGATCACCATGATCACTTGGCTATGAGACATGGCACCC 1444
 Db 1399 GAGGCTCTTGTGTTGGGGGATGATCACCATGATCACTTGGCTATGAGACATGGCACCC 1458
 Qy 1445 GTCACTGTGGTGGCAAGATAGTGGGCTCTGTGTGCTCACTTGGCGGCTGCTAGTAT 1504
 Db 1459 ATCACTTGTGGGCAAGATAGTGGGCTCTGTGTGCTCACTTGGCGGCTGCTAGTAT 1518
 Qy 1505 TCCCTGCGAGTGGCGGCTTGTCTCCAAATTTGACCTATTTATCAACGGGAGACAGAG 1564
 Db 1519 GCCCTGCTGTGGCGGCTGATCTGCTCACTTCACTTCACTTCACTTCACTTCACTT 1578
 Qy 1565 GCGGAGAGAGCTG 1577
 Db 1579 CACGAGAGAGCTG 1591

RESULT 10

ABI99654
ID ABI99654 standard; cDNA: 3147 BP.

AC ABI99654;
 DT 07-MAR-2002 (first entry)

XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:683.

XX Mouse: ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
 XX Mus musculus.

XX WO200186188-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001MO-JP04192.

XX 18-MAY-2000; 2000JP-0145977.

XX (UNIV-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX WPI; 2002-034733/04.

XX P-PSDB; ABB57250.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or
 PT by determining the expression profile of a gene group comprising these
 PT genes -

XX Claim 2; Page 1705-1709; 2690pp; English.

XX The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (1) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (1). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI9912, encoding
 CC the protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The

CC expression levels or expression profiles produced by these genes are
 CC used as an indicator when screening for ischaemic condition-improving
 CC drugs or therapeutics for ischaemic diseases. ABI9913 and ABI9914
 CC represent PCR primers for a mouse ischaemic condition related sequence,
 CC which are used in the exemplification of the present invention.

XX Sequence 3147 BP; 704 A; 859 C; 887 G; 697 T; 0 other;

Query Match 31.3%; Score 546; DB 24; Length 3147;

Best Local Similarity 66.7%; Pred. No. 1,6e-91;

Matches 833; Conservative 0; Mismatches 370; Indels 45; Gaps 2;

Qy 352 GGTGCCCCCGCCCGCTGCGGCTGCTGAGCGGCTGCTCAAGCTGCGCGGCTGCG 411
 Db 1537 GCGGAGACGAGACAGACACCAAGATGCTCGAGCGGCTGATATCAATCTCCGGGCTGCG 1596
 Qy 412 CTTCGAAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 471
 Db 1597 CTTCGAAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1656
 Qy 472 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 531
 Db 1657 GAACGCGATGCGCTACTTTGACCCCTGAGAGACGATCTTCTTTACCGCAACGCGCC 1716
 Qy 532 CAGCTTGCAGCGCGGCTGCTACTTACAGTCCGCTGCGGCGGCGGCGGCGGCGGCGGCA 591
 Db 1717 CAGCTTGCAGCGCGGCTGCTACTTACAGTCCGCTGCGGCGGCGGCGGCGGCGGCGGCA 1776
 Qy 592 CTTGCGGCTGAGCTCTCTCTGGAAGAGTGGCTTCTTACAGGCTGCGGCGGCGGCGGCT 651
 Db 1777 CTTGCGGCTGAGCTCTCTCTGGAAGAGTGGCTTCTTACAGGCTGCGGCGGCGGCGGCT 1836
 Qy 652 GCGAGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 711
 Db 1837 GCGAGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1896
 Qy 712 GCGCTTGCAGCGCGGCTGCTACTTACAGTCCGCTGCGGCGGCGGCGGCGGCGGCGG 771
 Db 1897 GCGCTTGCAGCGCGGCTGCTACTTACAGTCCGCTGCGGCGGCGGCGGCGGCGGCGG 1956
 Qy 772 CTTGCGGCTGAGCTCTCTCTGGAAGAGTGGCTTCTTACAGGCTGCGGCGGCGGCGGCT 831
 Db 1957 GCGCTTGCAGCGCGGCTGCTACTTACAGTCCGCTGCGGCGGCGGCGGCGGCGGCGGCT 2016
 Qy 832 GAGCGCTGCTGACTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 891
 Db 2017 GAGCTTGCAGCGCGGCTGCTACTTACAGTCCGCTGCGGCGGCGGCGGCGGCGGCGG 2055
 Qy 892 CCGCGCGGCTTCCCGCTGCGGCTGGAATGGCTCCAGCCAAATGCTTGAATCCACCCG 951
 Db 2056 -----CACCATCCACCGCATGACCAACACCACTCATATATTC 2097
 Qy 952 CCGCGCTTCAATGACCGCGGCTTCTGAGGAGACGCTGATTTGTTGGTCTCTCTT 1011
 Db 2098 CACATCTTCAAGACCGCTTCTTCTTATGGAACCTTGTATCTATCTGTTCTCTT 2157
 Qy 1012 TGAAGCTGCTGCTGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1071
 Db 2158 TGAAGCTGCTGCTGCTTCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2217
 Qy 1072 GAACTCATGATTTTGGCTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1131
 Db 2218 GAACTCATGATTTTGGCTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277
 Qy 1132 CCGGCGAGAGG-----GGTGGGCGAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1185
 Db 2278 TGACGAGAGGAGAAATAGAAAGGCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2337
 Qy 1186 CCGATTTGCTGCTTCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1245
 Db 2338 CCGTGTGTAAAGGTGTTCAAGATCTTCAAACTCTCCGCGCATCAAGAGGCGCTTCAAGAT 2397
 Qy 1246 CTTGGGCGAGAGCTTGGGCGCTCCAGTGCAGCTGGGCTCTCTCATCTTTTCTCTT 1305

Db 2398 CCGGGGACAGACCCCTCAAGCTATGAGGGAGTTAGGGCTCATCTTTTCCCTT 2457
 QY 1306 CATTGGTGGTCCCTTTTCCAGGCCCTCTACTTTGCCAGATTGACCGGTGACATC 1365
 Db 2458 CATTGGGTCATCTTTTCTTCTAGCCAGTACTTGGCGAGCGGAGAACCTAGTC 2517
 QY 1366 CCATTTCATAGCATCCCTGAGTCTTCTGTTGGCGGTAGTACCATGACTACATGG 1425
 Db 2518 GCACCTCTCCAGTATCCCGATCTTCTGTTGGCGGTAGTACCATGACTACATGG 2577
 QY 1426 CTATGGAGCATGAGACCCCTGACTGTGGGTGAGAAATAGTGGCTCTCTGTGCCAT 1485
 Db 2578 ATACGGTGACATGTACCTGTGACATTTGAGGCAAGATCGTGGCTCTGTGTGCAT 2637
 QY 1486 TGGGGGCGTGTACTATTTCCCTGCAATGCCCGCATTTGTCCAAATTTACGACTT 1545
 Db 2638 CGCTGGTGTGACAAATTTGCCCTGCCCTGACTGTCTGTCATTTTCAACTATTT 2697
 QY 1546 TTATCACCGGAGACAGAGGCGGAGAGGCTGGATGTTTACGCCATGT 1593
 Db 2698 CTACCAACGAGAACTGAGGGGAGAGACAGCTCAGTTCTCATGT 2745
 RESULT 11
 ABQ19704
 ID ABQ19704 standard; DNA; 994 BP.
 XX
 AC ABQ19704;
 DT 12-JUL-2002 (first entry)
 XX
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 6295.
 XX
 KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200218632-A2.
 XX
 PD 07-MAR-2002.
 XX
 PE 01-SEP-2001; 2001WO-EP10074.
 XX
 PR 01-SEP-2000; 2000DE-1043826.
 PR 05-SEP-2000; 2000DE-1044543.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K, Guelzig D;
 DR WPI; 2002-371829/40.
 PT Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA
 PS Claim 12; 56pp + sequence listing; 56pp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 CC and the degree of hybridisation to both classes is determined from the
 CC label on the amplicon. From the ratio of labels hybridised to the two
 CC classes of oligomers, the degree of methylation is calculated. The method
 CC is used: (i) for diagnosis and/or prognosis of side effects of

CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations or single nucleotide
 CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
 CC types and for investigating cell differentiation. The method allows the
 CC methylation status of many C residues to be determined simultaneously.
 CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
 CC method for determining the degree of cytosine methylation described in
 CC the disclosure of the invention.
 XX
 SQ Sequence 994 BP; 131 A; 152 C; 380 G; 331 T; 0 other;
 Query Match 29.1%; Score 508.6; DB 24; Length 994;
 Best Local Similarity 74.3%; Pred. No. 1.2e-84;
 Matches 705; Conservative 0; Mismatches 194; Indels 50; Gaps 3;
 QY 1 GAAGCCTGATTTGACGAAACACACGACACGAAACATGAGAGACGACAGCATC 60
 Db 33 GAAGTTGATTTTACGAAATATACGATATACGGAATTTGAGAGACGATAGATGAT 92
 QY 61 CCGGCGGCAAGAGACGAGAGAGAAAGGGACCCCGGAGCGGAGAAAGCGCAGAGCGC 120
 Db 93 TCGGCGGTAGAGACGAGAGAGAAAGGGATTTTCGGAGCGGAGAAAGCGCTAGAGTGGC 152
 QY 121 CCGGCGGCGCGCGCGCGCGAGCGAGCGCGCGCTCCCGCAGAGGCGCGCGTGC 180
 Db 153 CCGGCGGCGCGCGCGCGCGCGGTAGCGTAGCGGCGGCTTTCGTAGAGGCGCGCGTGC 212
 QY 181 CCCTGTGCCCCCGCGCGCGCGGTACAGTGCCTCCCTCCGCGCCCTAGCCGCC 240
 Db 213 TTTTGTGCTTTTTCGTTTCGCGGGTATAGTGTATTTTTCGCGTTTATGTCGTT 272
 QY 241 TCGCGGGCTA-TTTTACGCGCGGACACCGGACACCGGACCGGCGTGGGGCGCG- 295
 Db 273 TGTGGGTTATTTTACGCGCGGATATCGATATCGGATTCGGGTTGGGCGCGCGCG 332
 QY 296 -----GTGCGGGCCACAGCTCG 312
 Db 333 CCGCGGTCAAGCGCGGTGAGGCGGGGTCTGATCGGGGTGCGGCTTTATTCGTCG 392
 QY 313 GTTCCGGGTGCGCGGGGCTGCGCGCGCATGAGCGCGGTCGCCCGCCCGCTGCGG 372
 Db 393 GTTCCGGGTGCGCGGGGTGCGCGCGGTATGAGTGCGGGTGTCGTGCG-TCGTGCGG 450
 QY 373 CTGCTCGAGCGCGCTGCTCAACGTGCGCGGCTGCGCTTGAGACGCGGCGCGAC 432
 Db 451 TTGTTTCGAGCGGTTGTTTAACTGTTGCGGTTGCGTTGAGACGCGGCGCGTAC 510
 QY 433 GCTGGGCGCTTCCGCGACCTGCTGATGAGGAGCCAGCGCGCGCGCGCTTACGA 492
 Db 511 GTTGGGTGTTTTTTCGATATTTTGTAGGGGATTTAGCGCGTGCAGTCTTACGA 570
 QY 493 CGACGCGCGCGGATTTTTCGACCGGACCGGCGCCAGCTTGAGCGCTGCTCTA 552
 Db 571 CGACGCGCGCTCGGAGATATTTTTCGATGCGATTCGTTAGTTGAGACGCTGTTTA 630
 QY 553 CTACTACAGTCCGTTGGGCGCTGCGGCGCGCGGACGTCGCTCGAGCTTTCCT 612
 Db 631 TTATTTATGTTTCGTCGCGCGGCTTGCAGCGCTGCTGACGCTTTT 690
 QY 613 GGAAGAGTGGCTTCTACGGGCTGGGCGGCGCGCGCTTGAGCGCTGGGAGAGCA 672
 Db 691 GGAAGAGTGGTTTTTACGGGTTGGCGGGGTTTTGGTAGCTTTGGCAGAGCA 750
 QY 673 GCGCTCCGCGTGGCGCGCGGCGCGCCCTGCGCGCGCTTGCGCCCGCAGCTGTG 732
 Db 751 GCGTTTGGTGGTGCTTGAGAGCGTTTGTGTCGCGGTTTGGTTGTTAGTTGTG 810
 QY 733 GCTGCTTTTCGATTTCCGAGAGCTCAGCGCGCGCGCTGCGCTAGCTTCCT 792
 Db 811 GTTGTTTTCGATTTTTCGAGAGTTTAAAGTTCGCGCGCGCTGCTGCTAGTTTCGT 870
 QY 793 GCTGTATCTGCTGCTCATGCTGCTTCTGCTTCGACGAGCGCTCCGACTCCGGCA 852

Db	871	GTGGTATTATTTCTGTTTATTCGTCGTTTTTTTGTTCGAGACGTTGTTTATTTTCGCA	930
0y	853	GCACCGCGCAGCGAGGCGCTTCGTCCTGCAGCCGCGACGCCGCGTG	901
Db	931	CGATCGCGACGGTACGCGGTTGTTGTTGTAGTCGATGTCGTTGCGTG	979
RESULT 12			
ID	ABQ19705/C		
XX	ABQ19705 standard: DNA; 994 BP.		
AC	ABQ19705;		
XX			
D7	12-JUL-2002 (first entry)		
XX			
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 6296.		
KM	Human; cytosine methylation: 5'-CpG-3'; uracil; cytosine; diagnosis;		
KW	drug; side effect; cancer; central nervous system; cardiovascular;		
RW	gastrointestinal; respiratory system; single nucleotide polymorphism;		
XX	SNP; cell differentiation; ds.		
OS	Homo sapiens.		
XX			
PM	WO200218632-A2.		
XX			
PD	07-MAR-2002.		
XX			
PF	01-SEP-2001; 2001WO-EP10074.		
XX			
PK	01-SEP-2000; 2000DE-1043826.		
PR	05-SEP-2000; 2000DE-1044543.		
XX			
PA	(EP1G-) EPIGENOMICS AG.		
PI	Olek A, Plepenbrock C, Berlin K, Guetig D;		
XX			
DR	WPI: 2002-371829/40.		
PT	Determining the degree of cytosine methylation in genomic DNA, useful		
PT	for diagnosis and prognosis, comprises selective hybridization of		
PT	amplicons from chemically treated DNA -		
XX			
PS	Claim 12; 56pp + Sequence Listing; 56pp; German.		
XX			
CC	This invention describes a novel method for determining the degree of		
CC	methylation of a particular cytosine in a motif 5'-CpG-3', present in a		
CC	genomic sample of DNA. The sample is treated chemically to convert		
CC	cytosine (C) but not methylated C, to uracil, then part of the genomic		
CC	DNA that contains the target C is amplified to form a labeled amplicon.		
CC	The amplicon is hybridised to two classes, each with at least one		
CC	member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers		
CC	and the degree of hybridisation to both classes is determined from the		
CC	label on the amplicon. From the ratio of labels hybridised to the two		
CC	classes of oligomers, the degree of methylation is calculated. The method		
CC	is used: (i) for diagnosis and/or prognosis of side effects of		
CC	therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders		
CC	of the central nervous, cardiovascular, gastrointestinal and respiratory		
CC	systems etc., particularly by detecting mutations or single nucleotide		
CC	polymorphisms (SNP's); and (ii) for differentiation of cell or tissue		
CC	types and for investigating cell differentiation. The method allows the		
CC	methylation status of many C residues to be determined simultaneously.		
CC	AB013410-AB054121 represent genomic DNA sequences used to illustrate the		
CC	method for determining the degree of cytosine methylation described in		
CC	the disclosure of the invention.		
XX			
XX	Sequence 994 BP; 331 A; 380 C; 152 G; 131 T; 0 other;		

OY	1	GAAAGCTGATTTGTGAACAAACACGCACAGCGAAGAATGGAGAGACCAGACAGAGATC	60
Db	962	GAAATTGATTTTTCACGAATAATTAAGTATACGGAATTTGGAGAGACTTAGATAGATT	90
OY	61	CCGGCGCGAAGAAAGACGAGAGAAAGGGGACCCTGGGACGGGAAAGGCCAGACAGCGC	120
Db	902	TGCGCGGTAAAGAACGACGAGAGAAAGGGGATTTTCGGACGCGGAAAGCGGTAGAGTAGCG	84
OY	121	CGGGGCGCGCGCGCGCGCGCGAGGGCGACGGGGCGGCGTCCGCGAGAGGGCGCGGTG	180
Db	842	CGGGCGCGCGCGCGCGCGGGGTAGGGGTAGGGCGGGCGTTTGCGTAGAGGGCGCGGTG	78
OY	181	CCCTGTACGCCCTCCGCCCGCGGGGTACAAGTGCCTCCCCTCCCTCGCCCTTACCGGCC	240
Db	782	TTTTTGTCTTTTTCGTTTCGTCTCGCGGTTATAGTGTTTTTTTTTTTCGCTTTTAGTCGTTT	72
OY	241	TGCCCGGCGTA-TTTTACGCGCGGACACCGGACCCGACACCGAGCTGGGGCGCG--	29
Db	722	TGTCGGGTATTTTACGGCGCGATATCGGATATCGGATATCGAGTTTGGGGTGGCGGCGCG	66
OY	296	-----GTCCGGGGCCACACGTG	31
Db	662	CGCGCGTCGAGCGGTCTAGCGCGGGGTCTATCGGGGTCTGGGCGTCTGGGGTTATACGTG	60
OY	313	GTTTCGGGGTCCGCGGGGCTGCGCGCGCATGAGACCGCGGGTCCCGCGCGCGCGTGGG	37
Db	602	GTTTCGGGGTCTCGGGGTTGCGCGCGTATAGGATCTCGGGTTCGCG--TCTGCGG	54
OY	373	CTGCTGCGAGCGGCTGTGCTCAACGTAGGCGCGGCTGCGCTTCGAGACGCGGCGCGCAC	43
Db	544	TGTGTTCCAGCGGTTGGTGTTAACGTGGTTCGGGTTGGGTTTCGAGACGCGGGCGGTAC	48
OY	433	GCTGGCGCGTCCCGACACTCTCTAGGGAGCCAGCGCGCGCGCGCGCTCTACGA	49
Db	484	GTTGGCGGTCTTTTCGGGATATTTTGTAGGGGATTTTACCGCGTCTCGGCTCTTTTACGA	42
OY	493	CGACGCGCGCGCGAGTATTTCTTGACCGCGGACCGCGGCCACAGCTCGACGGCGCTCTA	55
Db	424	CGACGCGCGCGAGATTTTTCGATCGGATCGGTTTAGTTCGACGTCGTGTTTTA	36
OY	553	CTACTACAGTCCGGGTGGGCGGCTCGGCGCGCGGACGAGCTGGCGCTCGACGTCCTCT	61
Db	364	TTATTATTAGTTCCGTTGGGCGGTGCGGCGGTGCGGCGTACGATGTCGACGTTTTTTT	30
OY	613	GGAAGAGGTGCTTCTACGGGCTGGGCGCGCGGCGCTTGGACGCTTCGCGAGAGACA	67
Db	304	GGAAGAGGTGCTTTTACGGGCTGGGCGCGCGGCTTTTGGTACGTTTTCGCGAGAGACA	24
OY	673	GGGCGCGCGGCGCGCGCGGACGCGCCCTGCCCCGCGCGGCTTCGCGCGGACGCTG	73
Db	244	GGGTGTTTCGGGTCTGCGACGTTTTTTTGTTCGCGCTTTTCGTTCTGTAGTGTG	18
OY	733	GCTGCTTTTCAGTTTCCCGAGAGCTCTACGCGCGCGCGGTGCTCGGCTAGTCTCCGT	79
Db	184	GTTGTTTTCAGTTTTCGAGAGCTTTTAGTTCGCGCGCGGTTCGTCGTATAGTTTTCG	12
OY	793	GCTGTCATCTGCTCTCATCGTGTCTTGCCTCGAGACGCTGCTGACTTCCGCGA	85
Db	124	GTTGGTATTTTCGTTTATATCGTGTGTTTTTGTTCGACGAGCTGTGATTTCGCGA	65
OY	853	CGACCGCGAGCGACAGGGGCTGTGCTGACGCGGACCGGCGCGCGGTG	90
Db	64	CGATCGCGAGCTACGGGGTTGTGTGTATGTCCTACTCGGTTCCGTTG	16
RESULT 13			
ABO19702/c			
ID	ABO19702 standard; DNA: 994 BP.		
XX	ABO19702;		
AC			
DT	12-JUL-2002 (first entry)		

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 6293.
 XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 XX drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 OS Homo sapiens.
 XX MO200218632-A2.
 XX PD 07-MAR-2002.
 XX PF 01-SEP-2001; 2001WO-EP10074.
 XX PR 01-SEP-2000; 2000DE-1043826.
 XX PR 05-SEP-2000; 2000DE-1044543.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;
 XX WPI: 2002-371829/40.
 XX DR
 XX PT Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA -
 XX
 XX PS Claim 12: 56pp + Sequence Listing: 56pp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 CC and the degree of hybridisation to both classes is determined from the
 CC label on the amplicon. From the ratio of labels hybridised to the two
 CC classes of oligomers, the degree of methylation is calculated. The method
 CC is used: (i) for diagnosis and/or prognosis of side effects of
 CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations or single nucleotide
 CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
 CC types and for investigating cell differentiation. The method allows the
 CC methylation status of many C residues to be determined simultaneously.
 CC ABO13410-ABO54121 represent genomic DNA sequences used to illustrate the
 CC method for determining the degree of cytosine methylation described in
 CC the disclosure of the invention.
 XX
 XX SO Sequence 994 BP; 129 A; 152 C; 354 G; 359 T; 0 other;

Query Match 29.0%; Score 506.6; DB 24; Length 994;
 Best Local Similarity 74.2%; Pred. No. 2.7e-84;
 Matches 703; Conservative 0; Mismatches 194; Indels 50; Gaps 3;

OY 2 AAGCCGATTCTGACGAACACACGACGAAACATGTGAGAGAGAGAGAGATCC 61
 DB 961 AAGCCTAATTTACGAAACACACGACGAAACCTTAAACAAACGCAAAATAATCC 902
 OY 62 CGCGCGCAG 121
 DB 901 CGACGCAAAAAACGCAAAAAACGCAAAAAACGCAAAAAACGCAAAAAACGCA 842
 OY 122 GGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 181
 DB 841 GAAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 782
 OY 182 CCTGTGCGCCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 241
 DB 781 CCTATGCGCCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 722

OY 242 GCCGGCTA-TTTTACGCGCGGACACCGGACACCGGCGTGGGCGCG- 295
 DB 721 ACCGAATATTTTACGCGCGGAGACCGAACCAGAACCGAATATTTTAAACGAGACG 662
 OY 296 -----GTGGGGCGACAGTCCG 313
 DB 661 GACGACCGAAACGACCGAAACGACCGAACCGAACCGAACCGAACCGAACCGACG 602
 OY 314 TTGCGGGGTGCGGGGCTGCGCGCGCATGAGCGCGGCTGCGCGCGCGCGCGCGCG 373
 DB 601 TTGCGAATGCGCGAATGCGCGCGCATGAGCGCGCGCATGAGCGCGCGCGCGCG 544
 OY 374 TGCTGCGAGCGGCTGCTGCTCAACGTCGCGCGGCTGCTGCTGCGAGCGCGCGCG 433
 DB 543 TACTAGAACGACTAATACACGACGACGACGACGACGACGACGACGACGACGACG 484
 OY 434 CTGGCGCGCTTCCCGGACACTGTGTAGGGGACCCAGCGCGCGCGCGCGCTTACG 493
 DB 483 CTAACCGCTTCCCGAACAACCTTACTAATAAAACCAACGCGCGCGCGCGCTTACG 424
 OY 494 GACGCGCGCGGAGTATTTCTTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCTTAC 553
 DB 423 GACGCGCGCGGAGTATTTCTTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCTTAC 364
 OY 554 TACTACAGTCGCGTGGGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTAC 613
 DB 363 TACTACCAATCCGATTAACGACGACGACGACGACGACGACGACGACGACGACG 304
 OY 614 GAAGAGTGCGCTTACGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 673
 DB 303 AAAAAATATACCTTTACGACGACGACGACGACGACGACGACGACGACGACGACG 244
 OY 674 GCGTGGCGGCG 733
 DB 243 AACTTACCGCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 184
 OY 734 CTCTTTTTCAGTTTCCCGGACGCTGTCAGCGCGCGCGCGCGCGCGCGCGCG 793
 DB 183 CTACTTTTTCAGTTTCCCGGAAACGCTGTCAGCGCGCGCGCGCGCGCGCG 124
 OY 794 CTGCTATCTCTGCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 853
 DB 123 CTATATATCTCTGCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 64
 OY 854 GACCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
 DB 63 GACCGGAGCGGCGGAACTTACTACTACACCGCAACCGACCGCGCAT 17

RESULT 14
 ABO19703
 ID ABO19703 standard; DNA: 994 BP.
 AC ABO19703;
 XX
 XX 12-JUL-2002 (first entry)
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 6294.
 XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 OS Homo sapiens.
 XX MO200218632-A2.
 XX PD 07-MAR-2002.
 XX PF 01-SEP-2001; 2001WO-EP10074.
 XX PR 01-SEP-2000; 2000DE-1043826.

PR 05-SEP-2000; 2000DE-1044543.
 XX (EPiG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K, Guetig D;
 XX WPI; 2002-371829/40.
 DR
 XX
 PT Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA -
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 PS Claim 12; 56pp + Sequence Listing; 56pp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
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 CC DNA that contains the target C is amplified to form a labeled amplicon.
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 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 CC and the degree of hybridisation to both classes is determined from the
 CC label on the amplicon. From the ratio of labels hybridised to the two
 CC classes of oligomers, the degree of methylation is calculated. The method
 CC is used: (i) for diagnosis and/or prognosis of side effects of
 CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations or single nucleotide
 CC polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue
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 XX
 XX Sequence 994 BP; 359 A; 354 C; 152 G; 129 T; 0 other;
 Query Match 29.0%; Score 506.6; DB 24; Length 994;
 Best Local Similarity 74.2%; Pred. No. 2,7e-84;
 Matches 703; Conservative 0; Mismatches 194; Indels 50; Gaps 3;

QY 434 CTGGCCGCTTCCGGACACTCTGCTAGGGAGCCAGCGCGCGCGCTTACGAC 493
 DB 512 CTAAACCGCTTCCGGAACACTCTATAAAACCAACGCGCGCGCTTACGAC 571
 QY 494 GAGCGCGCGCGGAGTATTTCTTACGCGGAGCGCGCGAGCTTGAGCGCGCTCTAC 553
 DB 572 GAGCGCGCGCGGAGTATTTCTTACGCGGAGCGCGCGAGCTTGAGCGCGCTCTAC 631
 QY 554 TACTACCAAGTCCGGTGGCGGCTGCGCGCGCGCGCGAGCTGCGCTGAGCGTCTCTG 613
 DB 632 TACTACCAATCCGATTAACAGACTACGAGACCGAGCGAGCTGCGCTGAGCGTCTCTA 691
 QY 614 GAAGAGGTGCGCTTCTACGCGGCTGGCGCGCGCGCGCTGCGAGCGCTGCGGAGAGAC 673
 DB 692 AAAAATAATCACTTCTACGAACTTAACGCGAGCCCTTACACCGCTTACGAGGAAACGAA 751
 QY 674 GCGTCCCG 733
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 QY 734 CTGCTTTGAGATTCCCGAGAGCTCTAGGCGCGCGCGCGCGCTGCGCGCTAGTCTCCGTG 793
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 QY 854 GACGCGGAGCGGCGGCGGCTTGTCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
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RESULT 15
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 ID ABL33117 standard; DNA: 7642 BP.
 AC ABL33117;
 XX 26-MAR-2002 (first entry)
 DT
 XX
 DE Human immune system associated gene SEQ ID NO: 1090.
 XX
 KW Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antianaemic; cytosolic; noctropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antihemetic; antirheumatic; antidiabetic; antipsoriatic;
 KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 KW gene; ds.
 KW
 OS Homo sapiens.
 XX
 PN WO20020928-A2.
 PD 03-JAN-2002.
 PE 02-JUL-2001; 2001WO-EP07537.
 PR 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX
 PA (EPiG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2002-130909/17.
 DR
 XX Nucleic acid comprising fragment of chemically modified gene, useful
 PT for diagnosis and treatment of diseases associated with abnormal
 PT cytosine methylation -
 XX

PS Claim 1; SEQ ID NO 1090; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anemia, cancer, acute myeloid leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.

XX Sequence 7642 BP; 1881 A; 279 C; 1925 G; 3557 T; 0 other;

Query Match 21.0%; Score 367.4; DB 24; Length 7642;

Best Local Similarity 57.8%; Pred. No. 1.2e-58; Matches 684; Conservative 0; Mismatches 481; Indels 18; Gaps 1;

QY 381 AGCGCTGTCTCAACGTCGGCGGCTGCGCTTCGAGACGCGGCGCGACGCTGGGCC 440
 DB 2401 AAGCGCTAATCATCAACATCTCCGAACTACGCTTCGAAACGCACTAATAAACCTTTACC 2342
 QY 441 GCTTCCGGACACTGTGTAGGGGACCCGCGCGCGCGCTTCTACGACGACGCGC 500
 DB 2341 AATTCCCGAAACGCTACTAAGACGACCCCAAGACGACATATAATCTTCGACCCGCTCC 2282
 QY 501 GCCGCGAGTATTTCTGACACGCGCGCGCGCTTCGACGCGCGCTGCTACTACAC 560
 DB 2281 GCACGAAATATCTTCTGACGCGACGCGACCGCACTTCGACGCACTCTACTATATC 2222
 QY 561 AGTCGCGTGGCGGCTGCGCGCGCGCGACGTCGCGCGCTGACGCTTCTCGAAGAG 620
 DB 2221 AATCCGAAACGCGCATCTCCGCGACGATCAACGATACCATCCGATTTCTCCGAAAAA 2162
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 DB 2161 TCGGCTTACCACTAAGGAAAAAATTAATAAATTCGCGGAAACGAAACCTTCC 2102
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 DB 2101 TACGAAAAAAGAAAGACCCCTTACCGCGCGCGCGCTTCCAGCGCAATATATCTACT 2042
 QY 741 TCGAGTTTCCGAGAGCTCTCAGCGCGCGCGCGCTGCTGCGCTGCTGCTGCTGCTA 800
 DB 2041 TCGAATATCCCGGAAACCTCGAAGCGAGCAACATCGCATGATCTCGTACTATCA 1982
 QY 801 TCGTGTCCGACGCTGCTGCTGCTGCTGAGAGCGTGCCTGACTCCGCGAGACGCGC 860
 DB 1981 TCGTCACTGCAATATATCTTCTTACTTAAACGCTACCGAATTCGCGGAGAAAAA 1922
 QY 861 ACGGCAAGGCGCTTCTGCTGCGAGCGCGCGCGCGGCTTCCCGCGCTCGCTGATG 920
 DB 1921 ACTACCGCGCTGCGAGCTGCGAAACTCATTTGAAACCAACCGCAACACGCTGCAAT 1862
 QY 921 GCTCAGCAAAATGCTGGAATTCACCCGCGCTGCGCTTCAATGACCGCTTCTGCTG 980
 DB 1861 CCGGCGCAAAAA-----CTTCCAACTTCTCGGATTCCTTCTGTTAA 1820
 QY 981 TGGAGACGCTGTATTTGTGTGCTTCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCT 1040
 DB 1819 TAAAAAGCTATACATCATCTAATTTCTCTGAACTACTAATAGATTTCTTCTGCTATC 1760
 QY 1041 CAAGCAAGCTATCTTCAAGAACGTATGAACTCATGATTTTGTGGCTATGCTTC 1100
 DB 1759 CTAAACAAACGACCTTCTGCGGAAACATATAAAGCTAATCGACATTTATACCATCAT 1700
 QY 1101 CCTACTTTGTGCACTGGGACGAGCTGCGCGCGCGAGCGAGGCGTGGCGCAGAGCCCA 1160
 DB 1699 CTATATTTTATCACTTAATACGAACTAACGAGACGAAACAAATTAACAAACCA 1640
 QY 1161 TGTCACTGGCATCTCGAGAGGATCATGATTTGCTGCTGCTGCTGCTGCTGCTGCTG 1220
 DB 1639 TATCTCTAACCATCTTAATAATCATCTCGCTTATATAAATCTTCCGATCTTCAAACTAT 1580

QY 1221 CCGGCACTCAAGAGGCGCTGCAAAATCTTGGGCCAGACGCTTCGGGCTCCATGCTGAGC 1280
 DB 1579 GCGGCACTCTCAAAAAAAGCTACAAATCTCTGAGACAAAGCTTAAAAAGCTATACGAAAC 1520
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 QY 1401 CGGTAGTCACTAGTACTACATGTTGGCTATGAGACATGGCACCGCTGCTGCTGCTGCTG 1460
 DB 1399 CAATTAATACCATTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1340
 QY 1461 AGATAGTGGGCT 1520
 DB 1339 AAATTAATTAATCT 1280
 QY 1521 TCAATGCTCTCAATTTTCTAGTACTTTTATATCAGCGGAGACAGA 1563
 DB 1279 TAAATTTTCCAACTTCAATTTTCTTACCAACGCAAAAAACAAA 1237

Search completed: February 20, 2003, 06:32:00
 Job time : 456.075 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2003, 02:24:22 ; Search time 71.815 Seconds
(without alignments)
7460.705 Million cell updates/sec

Title: US-09-804-014A-7
Perfect score: 1747
Sequence: 1 gaagcgtatcttgacgaaa.....agctctgcagcactcacac 1747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1069	61.2	1599	1 US-08-288-405A-9	Sequence 9, Appli
2	614.2	35.2	1994	1 US-08-527-152-1	Sequence 1, Appli
3	215.6	12.3	2064	4 US-09-178-109-3	Sequence 3, Appli
4	215.6	12.3	2072	4 US-09-142-791A-3	Sequence 3, Appli
5	215.6	12.3	2104	4 US-09-142-791A-1	Sequence 1, Appli
6	215.6	12.3	2121	4 US-09-178-109-1	Sequence 1, Appli
7	213.2	12.2	3124	4 US-09-336-643A-9	Sequence 9, Appli
8	212.4	12.2	2104	4 US-09-142-791A-5	Sequence 9, Appli
9	212	12.1	271	1 US-08-288-405A-19	Sequence 19, Appli
10	187.4	10.7	696	1 US-07-955-916-5	Sequence 5, Appli
11	173.8	9.9	1805	1 US-07-955-916-6	Sequence 6, Appli
12	161	9.2	2127	5 US-08-464-340A-1	Sequence 1, Appli
13	161	9.2	2127	5 PCT-US94-08449A-1	Sequence 1, Appli
14	152.8	8.7	2483	5 US-08-464-340A-3	Sequence 3, Appli
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16	130.8	7.6	2293	4 US-09-336-643A-5	Sequence 5, Appli
17	130.8	7.5	196	1 US-08-288-405A-18	Sequence 18, Appli
18	128.4	7.3	1927	4 US-09-336-643A-3	Sequence 3, Appli
19	128	7.3	3102	4 US-09-336-643A-17	Sequence 17, Appli
20	106.4	6.1	3080	4 US-09-336-643A-7	Sequence 7, Appli
21	97.4	5.6	139	1 US-07-961-268-3	Sequence 3, Appli
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23	79.4	4.5	896	4 US-09-105-058C-1	Sequence 1, Appli
24	68.2	3.9	1926	4 US-09-249-585A-4	Sequence 2, Appli
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26	63.4	3.6	2353	5 PCT-US92-06840-1	Sequence 1, Appli
27	62.8	3.6	8438	1 US-07-945-283-1	Sequence 1, Appli

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29	62.6	3.6	4257	4 US-09-259-821A-1	Sequence 1, Appli
30	62.6	3.6	4257	4 US-08-843-659-1	Sequence 1, Appli
31	62	3.5	12001	1 US-08-458-568A-11	Sequence 11, Appli
32	61.8	3.5	44377	2 US-08-804-227C-7	Sequence 7, Appli
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34	61.2	3.5	2721	6 5215881-2	Patent No. 5215881
35	60.6	3.5	2150	2 US-08-318-837-1	Sequence 1, Appli
36	60.4	3.5	1312	5 PCT-US94-02389-1	Sequence 1, Appli
37	60.4	3.5	1312	5 US-08-205-506A-1	Sequence 1, Appli
38	60.2	3.4	2028	4 US-09-634-920-1	Sequence 1, Appli
39	60.2	3.4	2734	3 US-09-135-021-79	Sequence 79, Appli
40	60.2	3.4	2821	4 US-09-135-010A-115	Sequence 115, App
41	60.2	3.4	2821	4 US-09-597-735-115	Sequence 115, App
42	60.2	3.4	2821	4 US-09-597-733-115	Sequence 115, App
43	60.2	3.4	3181	3 US-09-135-021-1	Sequence 1, Appli
44	60.2	3.4	3181	4 US-09-135-020-1	Sequence 1, Appli
45	60.2	3.4	3181	4 US-09-135-010A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
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; Sequence 9, Application US/08288405A
; Patent No. 5559009
; GENERAL INFORMATION:
; APPLICANT: Chandu, Kanianthara G.
; APPLICANT: Kalman, Katalin
; APPLICANT: Gutman, George A.
; APPLICANT: Gutman, George A.
; TITLE OF INVENTION: A No. 5559009ei Voltage-Gated Potassium Channel
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
; ADDRESSEE: Attn: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,405A
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,431
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-59844-1/MHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1599
; US-08-288-405A-9


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; SEQ ID NO 3
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: human
US-09-178-109-3

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Best Local Similarity	52.8%	Pred. No. 1.2e-33		
Matches 622	Conservative 0	Mismatches 499	Indels 57	Gaps 5

QY	380	GAGGGGCTGGTGGCTCAACGTGGGCGGGGCTGGCTCTGAGAGCGGGGCGGACGCTGGGC	439
Db	190	GAGCTGATTTCCTCAACCTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCAAGCTGGAG	249
QY	440	CGCTCCCGGACACTCTGGTAGGGAGCCAGCGCGCGCGCGCGCTTCTACGAGGAGCG	499
Db	250	CGCTACCGGACACCTGGTGGGCAACACGAGAGAGAGATTCTTCTCAAGAGGACAC	308
QY	500	CGCCGCGAGTATTTCCTTCGACGGGACACGGGCCAGCTTCGACGCCGTGCTACTACTAC	559
Db	309	--CAAGAGAGTACTTCTTCGACCGGGGACCCCGAGGTTGTCGCTGGTGTCTCAACTTCTAC	366
QY	560	CAGTCCGGTGGGGGCGGGCGGGCGGCGGCGACGTCGGCGTGGACGTCTTCTGGAAGAG	619
Db	367	C---GCACGGGGGAAGCTGCACTACCGCGCTACGAGTGAATCTTGCTTACGAGACGAG	423
QY	620	GTCGCTTCTACGAGGGCTGGGGCGGGCGGCCCTTGGACGCGTTCGCGAGAGGAGGGCTGC	679
Db	424	CTGGCTTCTACGGCATCTCCCGGAGATCATCGGGGACATGCTGTCTTACGAGAGTACAAG	483
QY	680	CGGTCGGCGCCGACGGCGCCCTCGCCCGCGCGCTTCGCCCGCACTGTGGTGGCTT	739
Db	484	GACCGCAAGGAGGAGAACCGCGAGC-----GGCTCATG	516
QY	740	TTGAGATTCCCGAGAGCTCTGAGCGCGCGCGCTGGCTGAGCTGATCTCCGTGGTGTG	799
Db	517	GAGGACACAGACTCTGGAGAACACACAGAGTGCATATCCCTGGCTAGCTTCCGCAAGCC	576
QY	800	ATCTCTGCTCATCTGTCGTGTTCTTCTGCTCGAGAGCGTGCCTGACTTCGCGAGACAGCGC	859
Db	577	ATTGGGCGGGCCTTTCGAGAACCCCGACACAGACGCTGACCCCTGGTCTTCTACTACGTG	636
QY	860	GAGCGGACGGGGCTTGCTGCTGTGACGCCGACGCCGCGGCTTTCGCCGTCCGTCAAT	919
Db	637	ACTGGCTTCTTCATCGCTGCTGCTGGTCATACACAGTGAGAGACGTCGCCGCGCGC	696
QY	920	GGCTCCAGCCAAATGCTGGAAATTCACCCCGCGCCCTTCAATGAGCCGCTTCTGCTG	979
Db	697	ACGCTCCCGGGGACAGAGAGAGCTGCCGCGGGGAGCGCTACTCGGTGGCTTCTTCTGCG	756
QY	980	GTCGAGAGCGCTGTGTATTTGTTGGTTCTCTCTTGGAGCTGGTGAAGCCTCTCGTGTGT	1039
Db	757	CTGGACACGGGCGTGCATGATCTTCACACGTCGGAGTACTCTCGGCTCTTCGCGGCT	816
QY	1040	CCAGCAAGGCTATCTTCTTCAAGAGACGATGAGAACCTATGATTTGTGGCTATCTCT	1099
Db	817	CCGAGCGGTACGCTTCAATCCGACAGTCATGATGATATGAGAGTGGTGGCCATATG	876
QY	1100	CCCTACTTGTGGACACTGGGACACGAGCTGGCCCGGACAGAGGGGTGGGCGACAGGCC	1159
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QY	1460	AAGATAGTGGGCTCTCTGTGTGGCAATTCGGGGGCTGTCTACATATTTCCCTGTGCATGGCC	1519
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RESULT 4
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: Patent No. 6368823
: GENERAL INFORMATION:
: APPLICANT: Antoine Michel Alain Bril
: APPLICANT: Thierry Paul Gerard Calmels
: APPLICANT: Jean-Francois Simon Pierre Faivre
: APPLICANT: Jean-Luc Javre
: APPLICANT: Sabine Roualet
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GH-30012
: CURRENT APPLICATION NUMBER: US/09/142, 791A
: CURRENT FILING DATE: 1999-02-02
: PRIOR APPLICATION NUMBER: PCT/EP98/01901
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: UK 9706377.0
: PRIOR FILING DATE: 1997-03-27
: PRIOR APPLICATION NUMBER: EP 97402971.2
: PRIOR FILING DATE: 1997-12-09
: PRIOR APPLICATION NUMBER: EP 97403007.4
: PRIOR FILING DATE: 1997-12-11
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 1072
: TYPE: DNA
: ORGANISM: HOMO SAPIENS
US-09-142-791A-3

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Query Match	12.3%;	Score 215.6;	DB 4;	Length 2072;
Best Local Similarity	52.8%;	Pred. No. 1.2e-33;		
Matches 622;	Conservative	0;	Mismatches 499;	Indels 57;
				Gaps 5;

OY	380	GAGGGGCTGGTGGTCAACGTGTGGCGGGGTGGCTTTCAGAGAGCGGGGCGCCACAGTGGG	439
Db	118	GAGCTGATTGTCTCAACGTAGTGGGCGGAGGTTCCAGACCTTGGAGGACACGCTTGAG	177
OY	440	CGCTTCCCGGACACTCTGTAGGGGACCCAGCGCGCCGCGGCGCTTCTACAGACGCG	499
Db	178	CGCTACCCGGACACCTGTGGGAGCAGCAGAGAGAGTCTTCTTCAACGAGGAGAC	236
OY	500	CGCGCGGATTTTCTTCGACCGGACCGGCGCCAGCTTCAGCGCGGTCTACTACTAC	559
Db	237	--CAAGGAGTACTTCTTCGACCGGGGACCCGAGGTTGTTCCGCTGCGTCAACTTCTAC	294
OY	560	CAGTCCGCTGGGCGCTGCGGGCGCGGCGACGTGCCCTCGACGTCTTCTTGGAAAG	619
Db	295	C---GCAGGGGGAAGCTGCATACCCCGGCTACGACAGTCTCTGTGCCTACGACGAG	351
OY	620	GTTGGCCTTCAGAGGAGCTGGGCGGCGGCGGACCTGTGCACGCCCTGCGCAGAGACGAGGCTGC	679
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QY 1220 TCCCGGCACTCAAGGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1279
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QY 1460 AAGATAGTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1519
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Db 1201 GTGATTTCTCCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1238

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; Sequence 1, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Bril
; APPLICANT: Thierry Paul Gerard Calmels
; APPLICANT: Jean-Francois Simon Pierre Falvire
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
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; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2104
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-142-791A-1

Query Match 12.3%; Score 215.6; DB 4; Length 2104;
Best Local Similarity 52.8%; Pred. No. 1.2e-33;
Matches 622; Conservative 0; Mismatches 499; Indels 57; Gaps 5;
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QY 380 GACGCGCTGCTCTCAACGTCGCGGCTGCTCTGAGACGCGGCGCGACGTCGGC 439
Db 118 GAGCTATTGTCTCTCAACGTCGCGGAGGCTTCCAGACCTGAGACCAACGCTGAG 177
QY 440 CCGTCCCGGACACCTCTGCTGAGGAGACCAAGCGCGCGCGCGCTCTCAACGACGCG 499
Db 178 CGCTACCGGACACCTCTGCGGCGGACGAGAGAGTCTCTCTCAACGAGGACAC- 236
QY 500 CGCGCGAGTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 559
Db 237 --CAAGAGTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 294
QY 560 CACTCCGGTGGCGCTGCGGCGCGCGCGACGTCGCTCTCTCTCTCTCTCTCTCT 619
Db 295 C--GCAGCGGAGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 351
QY 620 GTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 679
Db 352 CTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 411
QY 680 CGGCTCCCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 739
Db 412 GACCGCAAGAGGAGAAAGCGCGAGC-----GGCTCATG 444
QY 740 TTGGAATTTCCGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 799
Db 445 GACGACAAAGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 504
QY 800 ATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 859
Db 505 ATGTGGCGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 564
QY 860 GACGCGACGGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 919
Db 565 ACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 624
QY 920 GGCTCCAGCAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 979
Db 625 ACGGTCCCGGCGAGCAAGAGCTGCGTCCGGGAGCGCTACTCGCTGCTCTCTCT 684
QY 980 GTGAGACGCTGTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1039
Db 685 CTGGACACGGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 744
QY 1040 CCAAGCAAGGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1099
Db 745 CCCAGCGCTACCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 804
QY 1100 CCTACTTTGTGCACTGGGCAACCGAGCTGGCCGCGGACGAGGGGTGGGCGCAC 1159
Db 805 CCTACTACATGCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 843
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QY	1160	ATGTCATGGGCAATCCGAGACATGATCCGATATGGTGGCCGGTCCGATCTTTCACAGCTG	122.19
Db	844	GTGTCCGGCGCCCTTCGTA---CGTCCGGGCTTTCCGGCTTTGAGGATCTTCAAGTTT	900
QY	1220	TCCCGGCACTCAAAAGGGCCCTGCAAAATCTTGGGCGAGACGCTTTGGGGCCCTCCATGCGTAG	127.99
Db	901	TCCCGGCACTCCAGGGCCCTGGGGAATCTGGGGTACACACTGAAGCTGTGGCTCCGAA	960
QY	1280	CTGGGGCCTCCTCATCTTTTTCCTTCATCGGTGTTGGTCTCTTTTCCAGCGCGCTTAC	133.99
Db	961	CTGGGCTTTTCTCTCTCTCTCCCTACACATGGCCATCATCTTTGGCACATGTGATGTTT	1020
QY	1340	TTTGCCGAAGTACACGGGGTGGAGTCCCAATTTACATAGATCCCGATGCTCTTCGGGG	139.99
Db	1021	TATCCGAGGAAGGGCTCTCGGGCCACAGATTCACAGAGATCCCTGCTCTTTTGGTAC	1080
QY	1400	GGCGTAGTCACATGACATGACTAGTTGGCTATGAGACATGGCACCCGTCACCTGTGGGTGC	145.99
Db	1081	ACCATTTGCACACATGACACACACTGGGATACGGAGACATGTGTCCTTAAGACGATTCGAA	1140
QY	1460	AAGATAGTGGGCTCTCTGTGTGCCATTTGCGGGCGTGTGATATTTTCCCTGGCAGTGGCC	151.99
Db	1141	AAGATCTCGGGCTCCATCTGCTCTCTTGAAGGGGCTCTGTGATTTAGCCCTGGCAGTCCCT	1200
QY	1520	GTCATGTCACAAATTCACACTACTTTTACACCGGGA	155.7
Db	1201	GTGATGTGTTTCAACCTTTAGCCGGATTTTACACACAA	1238

RESULT 6
US-09-17

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: Sequence 1, Application US/09178109
: Patent No. 6395477
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: GENERAL INFORMATION:
:
: APPLICANT: Cockett, Mark I.
: APPLICANT: Dilks, Daniel W.
: APPLICANT: Chang Ling, Hual-Ping
: APPLICANT: Sokol, Patricia T.
:
: TITLE OF INVENTION: Human Potassium Channel Polypeptides and
: FILE REFERENCE: ahp-98089
:
: CURRENT APPLICATION NUMBER: US/09/178,109
:
: CURRENT FILING DATE: 1998-10-23
:
: NUMBER OF SEQ ID NOS: 4
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 1
:
: LENGTH: 2121
:
: TYPE: DNA
:
: ORGANISM: human
:
: US-09-178-109-1

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Query Match	12.3%	Score 215.6	DB 4	Length 2121
Best Local Similarity	52.8%	Pred. No. 1.2e-33		
Matches 622	Conservative	0	Mismatches 499	Indels 57
				Gaps 5

QY	380	GAGGCGCGTGGTGTCAACGTGTGGCGGGCTGTGGCTTTCAGGACCGGGGGCGCCACGCTGGG	4.39
Db	190 <td>GAGCTGATTTGTCTCAACGTAAGTAGGGCGGAGGTTCCAGACCTGTAGAGACCACGCTGAG<td>24.9</td></td>	GAGCTGATTTGTCTCAACGTAAGTAGGGCGGAGGTTCCAGACCTGTAGAGACCACGCTGAG <td>24.9</td>	24.9
QY	440 <td>CGCTTCCCGGACACTCTGTAGGGAGCCAGCGCGCCGCGCTTCTAAGACGACGG<td>4.99</td></td>	CGCTTCCCGGACACTCTGTAGGGAGCCAGCGCGCCGCGCTTCTAAGACGACGG <td>4.99</td>	4.99
Db	250 <td>CGCTACCCCGGACACCTCTCTGTGGAGACAGGAGGAGGATTTCTTTCACGAGGACAC-<td>30.8</td></td>	CGCTACCCCGGACACCTCTCTGTGGAGACAGGAGGAGGATTTCTTTCACGAGGACAC- <td>30.8</td>	30.8
QY	500 <td>CGCGCGAGTATTTCTTCGACCGGCGACCGGGCCGAGCTTTCGACGCGCTGTCTACTATAC<td>55.9</td></td>	CGCGCGAGTATTTCTTCGACCGGCGACCGGGCCGAGCTTTCGACGCGCTGTCTACTATAC <td>55.9</td>	55.9
Db	309 <td>--CAAGGAGTACTTCTTCGACCGGAGACCCGAGGTGTTCCGCTCGTGTCAACATTTTAC<td>3.66</td></td>	--CAAGGAGTACTTCTTCGACCGGAGACCCGAGGTGTTCCGCTCGTGTCAACATTTTAC <td>3.66</td>	3.66
QY	560 <td>CAGTCCGATGGGCGGCTGTGGCGGCGCGCGGCGGACGTGTGCGACGTCCTTCGTGGAGAG<td>61.9</td></td>	CAGTCCGATGGGCGGCTGTGGCGGCGCGCGGCGGACGTGTGCGACGTCCTTCGTGGAGAG <td>61.9</td>	61.9
Db	367 <td>C---GCACGGGGGAAGTGTCACTACCCGCGCTACGAGTGTCACTCTGCTTCAGACGACGAG<td>4.23</td></td>	C---GCACGGGGGAAGTGTCACTACCCGCGCTACGAGTGTCACTCTGCTTCAGACGACGAG <td>4.23</td>	4.23
QY	620 <td>GTGGCTTTTCAGGGGCTGTGGCGGCGGCGGCGCTGTGACGACCTTGGCGGAGGAGGGCTGC<td>67.9</td></td>	GTGGCTTTTCAGGGGCTGTGGCGGCGGCGGCGCTGTGACGACCTTGGCGGAGGAGGGCTGC <td>67.9</td>	67.9

Db	424	CTGGGCTTTCTACGGCATCTCTCCGGAGATCATGGGGAGCTGCTGACAGAGATCAAG	483
Oy	680	CCGGTGGCCGCCAAGCGCCCTTCGCCCGCGGCTTGCCCGGACAGCTGTGGCTGCT	739
Db	484	GACCGCAAGAGGGGAACGGCGAGC-----GGCTCATG	516
Oy	740	TTTCGATTTTCCCGAGAGCTCTCGAGGCGCGCGGCTGCTGGCGTATGCTCCGTGTGATC	799
Db	517	GACGACACAGACTCGGAGAAACACAGAGATCCATCCCTCGCTCAGCTTCGGCAGAC	576
Oy	800	ATTCCTGCTTCATCGTCTGCTCTTGTGCTCGAGACGCTGCTGACTTCCGACAGCAGC	859
Db	577	ATGTGGGGGGGCTTCGAGAAACCCCAACAGCAGCGTGGCCCTGGTCTTACTACGTG	636
Oy	860	GACGGCACGGGGCTTGTCTGCTGACGCCGACGCCGGCCGGTTCCTCCGCTCCCTGAAT	919
Db	637	ACTGGCTTCTTCATCGCTGCTGTCTGTGATCACCACAGTGTGGAGACGGTGGCGGCG	696
Oy	920	GGCTCCAGCCAAATGCGCTGGAAATTCACACCCCGCGCTCCCTTCATAGACCCGTTCTGCTG	979
Db	697	ACGGTCCGGGGACACAGAGACTGCGGTGCGGGGAGCGTACTCGGTGGCTCTTCTTCTGC	756
Oy	980	GTGGAGACGCTGTGATTTTGTGGTTCTCTCTTGTAGCTGCTGGTACGCCCTCCGTGCTGT	1039
Db	757	CTGGACACGGCGTGCATGATCTTCACCGTGAATACCTCTCGGGGCTCTTCTCGCGCT	816
Oy	1040	CCAGCAAGGCTATCTTCTTCCAAAGACGTGATATACCTATGATTTTGTGGCTATCCTT	1099
Db	817	CCGACCGGCTACCGCTTCATCCGAGGCTCATGAGATCATGACGTGGTGGCCATCATG	876
Oy	1100	CCCTACCTTTTGGGACACTGGGGCACCGAGGTGGCCCGGACGAGAGGGGTGGCCAGCAGCC	1159
Db	877	CCCTACTACATCGGTCTGGTCAAT-----GACACACAGCAGGAC	915
Oy	1160	ATGTCACTGGCCATCTCGAAGATCATCCGATTTGGTGCGTCTCCGATCTTCAAGCTG	1219
Db	916	GTGTCCGGCGGCTTCGTCGA---GCGTCCGGGTCTTCGGGTCTTCAGAGATCTTCAAGTTT	972
Oy	1220	TCCCGGCACATCAAGGGCTGCAAAATCTTGGGCGAGAGCCTTGGGGCTCCATGCGCTAG	1279
Db	973	TCCCGCACATCCGAGGGCTGCGGATCTCTGGGTACACACTAAGAGGCTGTGCCCTCCAA	1032
Oy	1280	CTGGGGCTCCCTCACTTTTTCCTCTTCATCGGTGTGGTCTCTCTTTTCCAGGGCGGCTTAC	1339
Db	1033	CTGGGCTTTCTCTCTCTCTCTCCCTCCACATGGCCATATCATCTTTGGCACTGTGATGTTT	1092
Oy	1340	TTTGGCGAAGTTGACCGGGGAGATCCCATTTCACTAGACATCCCTGAGTCTCTTCTGATGG	1399
Db	1093	TATGCCGGAAGGGCTCTCTGGGCGAGAGTTTACAAGATCCCTCGTTCCTGTTTGGTAC	1152
Oy	1400	GGCGTAGTCACCATGACTACAGTTTGGCTATGAGACATGGACCCCTGCACCTGTGGTGGC	1459
Db	1153	ACCATTTGACATGACACACACTGGGATACGGAGACATGTGCTCTTAAGACGATTTGCAAGG	1212
Oy	1460	AAGATAGTGGGCTCTCTGTGTGCATTTGGGGGGGTCTGACATTTTCCCTGGCAATGGCC	1519
Db	1213	AAGATCTTCGGCTTCATCTCTCTCTTGAAGTGGGTCTGTGCATTTGCCCTGCACATCCCT	1272
Oy	1520	GTCAATGTGCAATTTTCACTACTTTTATCAGCCAGGGA	1557
Db	1273	GTGATTTTTCACACTTTTACCGGAGATTTTACCAACAGAA	1310

RESULT 7
US-09-336-643A-9

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: sequence 9, Application US/09356
: Patent No. 6399761
:
: GENERAL INFORMATION:
:
: APPLICANT: Miller, Andrew P.
: APPLICANT: Curran, Mark Edward
: APPLICANT: Hu, Ping
: APPLICANT: Rutter, Marc
: APPLICANT: Wang, Jian-Wang

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; TITLE OF INVENTION: No. 6399761e1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3424
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (257)...(2195)
; OTHER INFORMATION: K+Hnov12
US-09-336-643A-9

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Query Match      12.2%; Score 213.2; DB 4; Length 3424;
Best Local Similarity 52.3%; Pred. No. 3.8e-33;
Matches 616; Conservative 1; Mismatches 519; Indels 42; Gaps 5;

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QY 380 GAGCGGCTGCTCAACGTGGCGGGCTGCGCTTGAAGAGCGGGCGGCGACGCTGGGC 439
DB 374 GAGGCTTCTGTGTGACAGTGAAGCGGCGGCTTTGAAGATGAGATGACGCTGGAC 433
QY 440 CGCTTCCCGGACACTGTCTAGGAGGAGCGGCGGCGGCGGCGCTTCAACGACGCG 499
DB 434 CGCTACCCGACACCTTGTCTGGGACGCTCGGAGAG--GAATTTCTTACGATGCTGAC 490
QY 500 CGCCCGAGATATTTCTTCACGGGACCGGCGGCGGCGGCGCTTCAACTCTAC 559
DB 491 TCAGGCGATCTTCTTCATGCGCCCTGACATGTTCCGATGCTGGAACCTCTAC 550
QY 560 CAGTCCGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCTGCGATGCTTCCGAGAG 619
DB 551 CGAAC--GGGCGGCTGATGCTCCGACGAGAGTGCATCAGGCTTCCGACGAGAG 607
QY 620 GTGGCTTCTACGGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGC 679
DB 608 CTGGCTTCTACGGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGC 667
QY 680 CGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGC 739
DB 668 GACCGAAGAGAGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGC 721
QY 740 TTGAGTTTCCGAGAGCTCTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGC 799
DB 722 -GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGC 780
QY 800 ATCTGCTCTCATGCTGCTTCTTCTGCGCTGAGAGCGCTGCTGCTTCCGACGACCG 859
DB 781 CTTCAGAAATCCACACAG-----AGCACGCGAGCGCTGCTTCTTCAATATGAGCGG 835
QY 860 GACGCGACGCGGCTGCTCTGACGCGGCGGCGGCGGCGGCTTCCCGCTCGCTGAAT 919
DB 836 TTCTTATGCGGCTGCTCATGCGCAATGCTGAGAACCATCCATCCGCGGCGCTCT 895
QY 920 GGCCTCAGCAATGCTGGAATCCACCGCGCTGCTGCTCAATGACCGCTTCTCGG 979
DB 896 GCACGCGAGTCTCAAGSAGACGCTTGGCGAAGCTTCCACAGCGCTTTTCTGCG 955
QY 980 GTGAGAGCGCTGATTTGTTGTTCTCTTGAAGCTGCTGAGCGCTTCTGCTGTCT 1039
DB 956 ATGACACAGCTGTGTACTCATATTCACAGGTAATACCTCTCTGCGGCTGTTGCGGCG 1015
QY 1040 CCAACGAGGCTATCTTCTTCAAGAACGATGAGAACCTATGATTTTGTGCTATCTT 1099
DB 1016 CCCAGCGCTTGTCTCTGCGAGGTGATGAGCTCATGACGCTGTTGCGCAATCTG 1075

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QY 1100 CCTACTTTGTGCACTGGGACCGAGCTGGCCCGGAGGAGGGGCGGACGAGGCC 1159
DB 1076 CCTACTACTTTGGCTTT-----GGTGGCAAGAACGAC 1111
QY 1160 ATGTACATGCGCATCTGAGAGTATCCGATTTGTGCTGCTTCCGATCTTCAAGCTG 1219
DB 1112 GATGCTCTGGCGCTTTGTACCTGCGGTGTGCTCGGGGTGTTTGCATCTTCAAGTTG 1171
QY 1220 TCCCGGACCTCAAGGCGCTGCAATCTTGGGCGAGACGCTTGGGCGCTTCATGCTGAG 1279
DB 1172 TCCAGGACACACAGGCGCTTGGAGATTCTGGGTACACACTCAAGAGCTGTGCTGAG 1231
QY 1280 CTGGGCGCTCTCATCTTTTCTTCTTCATGCGGTGCTGCTTTCAGCGCGGCTTAC 1339
DB 1232 CTGGGCTTCTCTCTTTTCTTCCCTTACCATGCGCATATCTTCTTCCACTGTGATTT 1291
QY 1340 TTTCGGAAGTTGACCGGCTGAGCTCCCATTTCTATGACATCCCTGATCTTGTGTTG 1399
DB 1292 TATGCTGAGAGGCGCAACAAACAGACCACTTACAAAGCATCCCTGGGCTTCTGTAT 1351
QY 1400 GCGGTAGTACCATGACTACATGATGATGAGATGSCACCGCTGCTGTGGTGC 1459
DB 1352 ACCATTGTCAACATGACACAGCGCTTGGCTAGGAGATGCTGCGACACCATTTGCTGGC 1411
QY 1460 AAGATAGTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1519
DB 1412 AAGATTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1471
QY 1520 GTGATTTGCTCAATTTACGCTACTTTTATCACCGGGA 1557
DB 1472 GTGATTTGCTCAATTTAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1509

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RESULT 8
US-09-142-791A-5
; Sequence 5, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Bril
; APPLICANT: Thierry Paul Gerard Carmels
; APPLICANT: Jean-Francois Simon Pierre Faivre
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2104
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-142-791A-5
Query Match      12.2%; Score 212.4; DB 4; Length 2104;
Best Local Similarity 52.6%; Pred. No. 5.1e-33;
Matches 620; Conservative 0; Mismatches 501; Indels 57; Gaps 5;
QY 380 GAGCGGCTGCTCAACGTGGCGGGCTGCGCTTGAAGAGCGGGCGGCGACGCTGGGC 439
DB 118 GAGCTTATTTGCTTCAACGTGAGTGGCGGAGGTTCCAGACCTGAGGACACGAGCGAG 177
QY 440 CGCTTCCCGGACACTGTCTAGGAGGACCGGCGGCGGCGGCGGCTTCAACGACGCG 499

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Db	178	CGTACCAGGACACCCCTGCTGGGACAGACGAGAAAGAGTCTTCTTCAACGAGACAC -	236
Qy	500	CGCCGCGAGATATTTTCTTCACACGGGCACCGGCCACAGTCTTGACGCGGTGCTCTACACTAC	559
Db	237	--CAAGAGATCTTCTTCGACCGGGGACCCCGAGTGTCCGGGTGGCTCAACTTCTTAC	294
Qy	560	CATGCGGGTGGGCGGCTGCGGGGCGGGGCGAGCTGCCTCGACTGAGCGTCTCTCGAAGAG	619
Db	295	C---GCACGGGGAAGCTGCACTACAGCGGTACAGATGATGATCTCTGTCCCTACGACGACGAG	351
Qy	620	GTGGCCTTCTTACGGGCTGGGCGCGGGCGCCCTTGACAGCCTTCGCGGAGAGACGAGGGCTGC	679
Db	352	CTGGCCTTCTTACGGCACTCTCCCGGAGATCATGGGGAGCTGGTGTCTACGAGAGATTAAG	411
Qy	680	CGGGTGGCGGCGGAGGGCCCCCTGGCCCCGGCGGCTTGCGCCGCGACGTGTGGGTGCTT	739
Db	412	GACCCGAAGAGGGGAACGGCCGAGC-----GGCTCATG	444
Qy	740	TTTCAGTTCCTCCGAGACTCTCAAGGCGCGCGGTGCTGCGCGTATGTCCTGTGCTG	799
Db	445	GAGCACAACAGCTGGAGAAACACAGAGATCATGCTCCCTCGTCAAGCTTCCGCGCAAGAC	504
Qy	800	ATCTCTGCTTCATCGTCGTCTTCTGCTTCGAGACGCTGCCTGACTTCCGCGACAGACGC	859
Db	505	ATGTGGCGGGCTTTCGAGAAACCCCAACACAGCACGCTGGCCCTGTGCTTCTTACTACGTG	564
Qy	860	GAGCGCACGGGGCTTCTGCTGTCAGCGCAGCGCGGGCGGGTGTGTCGCCGCTCGCGTAA	919
Db	565	ACTGGCTTCTTATCGCTGTCTGTGGTCTATCACCACAGTGTGGAGACGGTGGCGGCG	624
Qy	920	GGGTCCAGGCAATGCGCTGGAAAAATCCAGCCCGGCTCCCTTCAATGACCCGTTCTTCTG	979
Db	625	ACGGTCCCGGGGACAGAGAGCTGCCGTGGGGAGACGCTACGCGTGGCTTCTTCTGAC	684
Qy	980	GTGGAGACGCGTGTATTTTGTGGTTCCTCTTGAGCTGCTGTAGACGCTCTGCTGT	1039
Db	685	CTGGACACGGGGGTGCGATGATCTTACCGTGTGATACCTCTGTGGGCTCTTCCGCGCT	744
Qy	1040	CCAAGCAAGGCTATCTTCTTCAAGAACGTGATAAACCTATGATTTTGTGGCTATCCCTT	1099
Db	745	CCGACCGGCTACCGCTTATTCGCGAGGTCATGAGCATCATGAGCGTGGTGGCATTCATG	804
Qy	1100	CCCTACTTTGTGGCACTGGGCAACGAGCTGGCCCGGCAAGGAGGTGGGCGCAAGACGCC	1155
Db	805	CCCTACTTACATCGGTCTGGTCACT-----GACCAACAACAGAGAC	843
Qy	1160	ATGTGACTGGCCATCTCCGAGACGTACCCGATTTGGTGCAGTCTCCGCACTTTCACAGCG	1219
Db	844	GTGTCCGGCGGCTCTGCTGCA---CGCTCCGGGTCTTCCGGCTCTTCAAGATCTTCCAAGTTT	900
Qy	1220	TCGCGGCACTCAAAAGGCGCTGCAAAATCTTGGGCAAGAGCTTCGGGCTTCGATGCGTGA	1279
Db	901	TCGCGGCACTCCGAGGGCGCTGGCGGATCTTGGGCTACACACTGAAGAGCTGCTCCCGAA	960
Qy	1280	CTGGGCGCCGTCATCTTTCTTCCTTCATGCGGTGCTGCTCTCTTTCGAGCGCCGCTAC	1339
Db	961	CTGGGCTTTCTTCTCTCTCTCCCTACCATGGCCATATCATCTTGTGCACTGTATGTTT	1029
Qy	1340	TTTGGCAAGTTGACCGGGGTGAGCTCCCATTTCTACTAGACCTCCGTAGTCTTCTTGCTGG	1399
Db	1021	TATGCCGGAAGGGCTCTCTCGGCGAGAAATTCAACAAGCATCCGCTCGTTTTGGTAC	1080
Qy	1400	GCGGTACTCACATGACTACAGTTGGCTATGAGAGACATGAGCAACCCGTCACTGTGGGTGC	1459
Db	1081	ACCATTTCTACCATGACACACTGGGATAGGAGAACTGGTGCATAAGACGATTCAGAG	1140
Qy	1460	AAGATTAAGTGGGCTCTGTGTGCATATGCGGCGGTGCTCACTAATTTCCCTGCGACAGTCC	1519
Db	1141	AAGATCTTCCGCTCATCTCTCTCTCTTGAAGTGGGCTCTGTGTCATTTGCCCTTGCAATCC	1200
Qy	1520	GTCAATTGCTTCCAAATTCAGCTACTTTTATACCGGGA	1557

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RESULT 9
US-08-288-405A-19
; Sequence 19, Application US/08288405A
; Patent No. 5559009
; GENERAL INFORMATION:
; APPLICANT: Chandny, Kanianthara G.
; APPLICANT: Kalman, Katalin
; APPLICANT: Chandny, George A.
; APPLICANT: Gulman, George A.
; TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel
; TITLE OF INVENTION: Gene
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
; ADDRESSEE: Attn: Walter H. Dregler
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,405A
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,431
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-59844-1/WHO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEEX: 910 277299
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
;
; US-08-288-405A-19
;
; Query Match 12.1%, Score 212; DB 1; Length 271;
; Best Local Similarity 93.5%; Pred. No. 4.4e-33;
; Matches 232; Conservative 0; Mismatches 9; Indels 7; Gaps 14
;
; QY 1503 TTTCCTCCGACATGGCCGCGCATTTGCTCCCAATTTAGCTACTTTTATACCGCGAGACAG 1562
; Db 1 TTTCCTCCGACATGGCCGCGCATTTGCTCCCAATTTAGCTACTTTTATACCGCGAGACAG 60
;
; QY 1563 AGGGGGAAGAGGCTGGAGTGTTCACAGCATGTGAGCATGCAGGCTTGCGCCACATGGAGG 1622
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; QY 1623 G-----CAAGGCCAATGCGGGGCGCTGGTGTGACGCGGGGAGGTACCGAGCTACCACTTCA 1675
; Db 121 GNNCANGNCNANNNCAATGCGGGGCGCTGGTGTGACGCGGGGAGGTACCGAGCTACCACTTCA 180
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; QY 1676 CTCCTGGACACCCCGCAGGAGCAACCTGTGTCAACCGAAGTGTGAGAACAGTTGAGGCTTGC 1735
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; QY 1736 AGGACCTC 1743
; Db 1111 11

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Db      879  TCGAGGGGGTCTGGGTGGTCTGGTTACCTTGGAGTTCCTCATGGGTGTCGTTCTGCC  938
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Db      939  CCAACAGGTGGAGATTTATCATAGAACATCCCTCAATATCATATTTGAGGCAATTTCTCC  998
Qy      1101  CCTACTTTGTTGGACATGCGGACCGAGCTGGGCCCGGAGGAGGAGGGGTGGGCCAGAGGCCA  1160
Db      999  CTTTCTTACCTGGAGGTGG--CCTAAGCGGCTGTCTCTAANAAGCCGCCAAGGACGTT--  1054
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Qy      1281  TGGGCTGTCTCATCTTTTCTCTTCTCATGGGTGTGGTCTCTCTTTTCCAGCGCGCTACT  1340
Db      1170  TCTGCTGTCTATCATCTTCTCTGGCCCTGGGAGTGTCAATCTTTCCACCATGATCTACT  1229
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Db      1230  ACGCGAGAGAGATAGGGGCGACACACCCCATAGACCCCGCCAGCAGACACACACTTTA  1289
Qy      1374  CTACATCTCCCTGAGTCTTCTGTGGGCGGTAGTCACCATGACTACAGTTGGCTATGGAG  1433
Db      1290  AAAACATCCCATCGGCTTGTGGTGGGCTGTGTCACATGACGACACTGGGCTATGGAG  1349
Qy      1434  ACATGGACCCGCTACGTGTGGGTGGGAATAGTGGGCTCTGTGTGCCATTTGGGGCG  1493
Db      1350  ACATGTATCCCGACAGCGTGTCTGGAAATCTGGTGGAGCCTTGTGTCTCTGGCTGGTG  1409
Qy      1494  TGTGCTATTTCCCTGCGACAGTCCCGCTCATTTGTCTCCAAATT  1536
Db      1410  TGTGACCATTTGCCATGCCGTGCCGTGTCATGCTGAACATTT  1452

RESULT 12
US-08-464-340A-1
: Sequence 1, Application US/08464340A
: Patent No. 5710019
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: GENERAL INFORMATION:
:   APPLICANT: LI, ET AL.
:   TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
:   NUMBER OF SEQUENCES: 13
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
:     ADDRESSEE: CECCHI, STEWART & OLSTEIN
:     STREET: 6 BECKER FARM ROAD
:     CITY: ROSELAND
:     STATE: NEW JERSEY
:     COUNTRY: USA
:     ZIP: 07068
:
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: 3.5 INCH DISKETTE
:   COMPUTER: IBM PS/2
:   OPERATING SYSTEM: MS-DOS
:   SOFTWARE: WORD PERFECT 5.1
:
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/464 340A
:   FILING DATE: June 5, 1995
:   CLASSIFICATION: 435
:   PRIOR APPLICATION DATA:
:     APPLICATION NUMBER: PCT/US94/08449
:     FILING DATE: 28 JUL 1994
:     ATTORNEY/AGENT INFORMATION:
:       NAME: FERRARO, GREGORY D.
:       REGISTRATION NUMBER: 36,134
:       REFERENCE/DOCKET NUMBER: 325800-415
:     TELECOMMUNICATION INFORMATION:
:       TELEPHONE: 201-994-1700

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Query Match	Best Local Similarity	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length	DB 232
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TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2483 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; PCT-US94-08449A-3

Query Match 8.7%; Score 152.8; DB 5; Length 2483;
Best Local Similarity 53.0%; Pred. No. 2e-21;
Matches 350; Conservative 0; Mismatches 307; Indels 3; Gaps 1;

QY 980 GTGGAGACGCTGTATTTGTTGTTCTTCTTGTAGAGCTGTGTAGAGCTTCCCTGCTGTCTGT 1039
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QY 1040 CCAAGCAAGGCTATCTTCTTCAAGAGCTGATGAACTCATCGATTTTGTGCTATCTT 1099
Db 1417 CCAAGCAAGCTGTACTTCCGGCTGTCTTCTTCAATGATGTGACGTGCTGTGCGCATCTC 1476
QY 1100 CCGTACTTGTGTGACCTGTGGACCGAGCTGGCCGAGAGGGGTGGGCGCAGAGGCC 1159
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QY 1160 ATGTCACTGGCCATCCTGTAGAGATCCGATGTGTGTCTTCCGATCTTCAAGCTG 1219
Db 1537 GTGCAGACGCGGTGAG--GCGTGGGATCATCGCATGCGCGCATCTTCAAGCTG 1593
QY 1220 TCCCGGACCTCAAGGCGCTGCATATCTTGGCCAGACGCTTGGGCTTCATGCTGAG 1279
Db 1594 GCCCGCATCTCTCGGCGCTGAGACCTTACCTATGCCCTCAAGCGCAGCTTCAAGGAA 1653
QY 1280 CTGGGCTCTCTATCTTTTCTCTTCAATGCTGTGTGTCTTTCAGCGCGCTTAC 1339
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QY 1340 TTTGCCGAGTGTGACGGGTGACCTCCATTCATGATCCCTGATGCTGTGTGTG 1399
Db 1714 ACCATGAGACAGAGCATCCAGAGACCTGTTAAGACATCCCGCATGCTTCTGTGTG 1773
QY 1400 GCGGTAGTACCATGACTACAGTTGCTATGAGACATGAGACCCGCTCACTGTGGTGGC 1459
Db 1774 GGCATCATCAGCATGACACCGCTGAGGAGACATCTACCCCAAGACACGCTGAGC 1833
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Db 1834 AAGCTCAGCGGCGCATCAGCTTCTGTGTGTGTGCTATGCTGCGCCCTGCGCATCCAC 1893
QY 1520 GTCATGTCTCAATTTCAAGCTATTTTATCAACGGGAGACAGAGGGCGCAAGAGCTGG 1579
Db 1894 CCGATCATCAACACTTGTGTAGTACTACAAACAGAGGCGCTCTGTGAGACCGCGGCC 1953
QY 1580 ATGTTAGCCATGTGACATGAGCTGTGGCCACTGTGAGGCAAGGCCAATGGGGG 1639
Db 1954 AAGCAGAGACTGTGATGTGAACCTCACTCAGCAGCGGGGCGAAGGCAAGACCGGG 2013

Search completed: February 20, 2003, 06:35:04
Job time : 102.811 secs


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REFERENCE 3 (bases 1 to 1085)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.

FEATURES
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BASE COUNT 201 a 308 c 372 g 198 t 6 others

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Query Match 25.2% Score 439.8; DB 17; Length 1085;
Best Local Similarity 65.4%; Pred. No. 7.7e-76;
Matches 732; Conservative 4; Mismatches 321; Indels 62; Gaps 4;

QY 309 GTCGGTTCGCGGCTGCGCGGCGCTCCGCGCATGAGAGCGCGCGTCCGCGCGCT 368
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Db 1077 GTCGCGCTGCGGCTGCGCGGCGCTCCGCGCATGAGAGCGCGCGCTCCGCGCGCT 1018

QY 369 GCGGCTGCTGCGGCGCTGCTGCTCAACGTGGCGGCGCTGCTGCTGCGAGAGCGGCGCGC 428
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QY 548 CTCTACTACTACAGTCCGCTGCGGCGCGCGCGCGCGCGCGCGCTGCGCGCTGCGAGCTC 607
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QY 1028 CTCTGCTGCTGCTCAACAGGCTATCTTTCAGAGAGCGAGTCACTCATGATTTT 1087
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RESULT 2
LOCUS BM924998
DEFINITION BM924998
ACCESSION BM924998
VERSION BM924998.1
KEYWORDS GI:19375377
SOURCE human.
ORGANISM Homo sapiens

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REFERENCE Homo sapiens
AUTHORS Mammaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Mammaryota; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo.
COMMENT NIH-MGC http://mhc.ncl.nih.gov/.
    Unpublished (1999)
    Contact: Robert Strausberg, Ph.D.
    Email: c9apbs-femail.nih.gov
    Tissue Procurement: Life Technologies, Inc.
    CDNA Library Preparation: Life Technologies, Inc.
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
    DNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LNL at:
    http://image.llnl.gov
    Plate: LHAM12812 row: d column: 14
    High quality sequence start: 8
    High quality sequence stop: 689.
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            /db_xref="taxon:9606"
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            /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
            site:1: NotI; site:2: EcoRV (destroyed); RNA source
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            spleen, and 20-22 week male spleens. Library is oligo-dT
            primed and directionally cloned (EcoRV site is destroyed
            upon cloning). Average insert size 1.4 kb, insert size
            range 1-3 kb. Library is normalized and enriched for
            full-length clones and was constructed by C. Gruber
            (Invitrogen). Research Genetics tracking code 026. Note:
            this is a NIH-MGC Library."

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BASE COUNT 180 a 339 c 320 g 219 t

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ORIGIN

Query Match 23.5%; Score 410.8; DB 14; Length 1058;
Best Local Similarity 68.9%; Pred. No. 3.5e-70;
Matches 601; Conservative 0; Mismatches 252; Indels 19; Gaps 2;

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DB 19 GCTGGGCGACCCAGCGCGCGCGCTTCTACGACGACGCGCGCGAGTATTCTT 78
OY 517 CGACGCGACCGCGCGCGCTTCTACGACGACGCGCGCGAGTATTCTT 576
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DB 79 CGACGCGACCGCGCGCGCTTCTACGACGACGCGCGCGAGTATTCTT 138
OY 577 GGGGCGCGCGCGCGCTTCTACGACGACGCGCGCGAGTATTCTT 636
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DB 139 CGCGCGCGCGCGCGCTTCTACGACGACGCGCGCGAGTATTCTT 198
OY 637 GGGGCGCGCGCGCGCTTCTACGACGACGCGCGCGAGTATTCTT 696
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DB 199 GGGGCGCGCGCGCGCTTCTACGACGACGCGCGCGAGTATTCTT 258
OY 697 CCCCCGCGCGCGCGCTTCTACGACGACGCGCGCGAGTATTCTT 756
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DB 259 GCGCGTGGCGCGCGCGCTTCTACGACGACGCGCGCGAGTATTCTT 318
OY 757 CTCTCAGCGCGCGCGCTTCTACGACGACGCGCGCGAGTATTCTT 816
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DB 319 CTCTCAGCGCGCGCGCTTCTACGACGACGCGCGCGAGTATTCTT 378
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DB 601 CTCTGACGCGCGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
OY 1117 GGGGCGCGCGCGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1176
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 661 GGGGCGCGCGCGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
OY 1177 GAGAGTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1236
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 721 GAGAGTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
OY 1237 CCGGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1295
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 781 GGTCTGACGCGCGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
OY 1296 TTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1327
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 841 TCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 872
```

RESULT 3
LOCUS AO939702 443 bp DNA linear GSS 23-AUG-2000
DEFINITION NR5-028R Human NotI clones Homo sapiens genomic, DNA sequence.
ACCESSION AO939702
VERSION AO939702.1 GI:7216080

KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 443)

TITLE Zabarovsky, E.R., Giszatullin, R., Podowski, R.M., Zabarovsky, V.V., Xie
JOURNAL L., Muravenko, O.V., Kozirev, S., Petrenko, L., Skobeleva, N., Li, J.,
MEDLINE Protolopov, A., Kashuba, V., Erberg, I., Winberg, G. and Wahlstedt, C.
COMMENT NotI clones in the analysis of the human genome
20175728
Contact: Podowski RM
Center for Genomics Research
Karolinska Institute
17177 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-337983
Email: Raf.Podowski@cgr.ki.se
Class: NotI site.

FEATURES

source

1..443
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human NotI clones"
/note="Organ: Lung; DNA was isolated from A549 cells after
sodium arsenite exposure for 4 weeks. This fragment was
differentially methylated relative to untreated controls
and was identified using methylation sensitive Ap-Pcr and
sequenced."

Location/Qualifiers

BASE COUNT 43 a 167 c 152 g 80 t 1 others
ORIGIN

Query Match 22.9%; Score 399.4; DB 17; Length 443;
Best Local Similarity 99.1%; Pred. No. 5.2e-68;
Matches 422; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

```
OY 477 GCGGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 536
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 GCGGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
OY 537 TCGACGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 596
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 TCGACGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
OY 597 CGCTCGACGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 656
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 CGCTCGACGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
OY 657 GCGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 716
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 GCGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
OY 717 TCGCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 776
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 TCGCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
OY 777 TCGCCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 836
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 TCGCCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 359
OY 837 TGCCTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 895
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 360 TGCCTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 419
OY 896 CCGGTG 901
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 420 CCGGTG 425
```

RESULT 4
LOCUS CDS02RD3/ 900 bp DNA linear GSS 14-MAY-2000
DEFINITION CDS02RD3/

DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 159H12 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL210432

VERSION AL210432.1 GI:7869251

KEYWORDS GSS: genome survey sequence.

SOURCE Tetraodon nigroviridis.

ORGANISM Tetraodon nigroviridis.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

AUTHORS 1 (bases 1 to 900)

TITLE Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F., Saurin,W. and Weissenbach,J.

JOURNAL Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

REFERENCE 2 (bases 1 to 900)

AUTHORS Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 900)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000)

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source 1..900

1..900 /organism="Tetraodon nigroviridis" /db_xref="taxon:99883" /clone="159H12" /clone_lib="G" /note="Genoscope sequence ID : COAG159D06LPI-end : T7"

BASE COUNT 206 a 242 c 283 g 166 t 3 others

ORIGIN

Query Match 21.1%; Score 368.2; DB 17; Length 900; Best Local Similarity 68.4%; Pred. No. 6.9e-62; Matches 589; Conservative 1; Mismatches 224; Indels 47; Gaps 4;

QY 712 CGCCTTCGCGCCGCGCAGCTGCTGCTTCGATTCGCCGAGAGCTCTCAGCGCGCG 771

Db 899 CGAKTTCAAGCGGCGAGATGCTGCTTCGATGATCCGAGAGCTCCAGCCCGCGAG 840

QY 772 CGTGTCTGCGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 831

Db 839 GGGCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

QY 832 GACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 891

Db 779 GACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 733

QY 892 CGGCGCGGCTTCCCGCTCCGCTGATGGCTCAGCCAAATGCTGGAATTCACCCCG 951

Db 732 GCAACTCCACCGCAGCGCAGCGATTTAC-----702

QY 952 CCTGCCCTTCAATGACCGCTTCTCGTGTGAGAGAGCTGATTTGTTGGTTCTGCTT 1011

Db 701 ---GCCCTTCAAGCAGCCCTTTTTCATCGTGTGAGAGAGCGTCTGCTATCTGCTT 645

QY 1012 TGAGCTGTGTAGCGCTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1071

Db 644 TGAGATATATAGTTCGCTTCTTCCGACGCCAGCAACCGGCTTCTTAAACATCAT 585

QY 1072 GAACCTCATGATTTTGTGCTATCTTCCCTACTTGTGTGCTGGGACCGAGCTGGC 1131

Db 584 GAACCTCATGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 525

QY 1132 CCGGACGAGGCGGCTGCGGCGCAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1191

Db 524 CCAGCAGCAGGCGCAGCGGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCG 466

QY 1192 GGTGCGTGTCTTCCGATCTTCAAGCTGTCCCGGACTCAAGGCGCTGCAATCTTGGG 1251

Db 465 GGTCCGCGGTGTTCGGCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 406

QY 1252 CCAAGCCTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1311

Db 405 CCATACCTCTGGCGCCGACGAGAGAGCTGCGCTCTCAATTTCTTCTGCTGCTGCTG 346

QY 1312 TGTGCTGCTGCTTTCGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1371

Db 345 CGTATCTCTTCTTCCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 286

QY 1372 CACTAGCATCCCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1431

Db 285 CACGAGCATCCCGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 226

QY 1432 AGACATGCGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1491

Db 225 CGATATGAGCGCTATCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 166

QY 1492 CGTCTGCTGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1551

Db 165 CGTATATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 107

QY 1552 CCGGAGACAGAGGCGGAGAGA 1572

Db 106 CCGGAGACGAGATTAAGAGA 86

RESULT 5

CNS03DKC/LOCUS 839 bp DNA linear GSS 15-MAY-2000

DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 017A20 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL238205

VERSION AL238205.1 GI:7898340

KEYWORDS GSS: genome survey sequence.

SOURCE Tetraodon nigroviridis.

ORGANISM Tetraodon nigroviridis.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

AUTHORS 1 (bases 1 to 839)

TITLE Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F., Saurin,W. and Weissenbach,J.

JOURNAL Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

REFERENCE 2 (bases 1 to 839)

AUTHORS Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 839)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000)

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES	Location/Qualifiers
source	1. 839
	/organism="Tetradon nigriviridis"
	/db_xref="taxon:99883"
	/clone="017A20"
	/clone_1lb="G"
	/note="Genoscope sequence ID : C0B6017BA10LPI-end : 77"
BASE COUNT	157 a 246 c 281 g 155 t
ORIGIN	
Query Match	19.6%; Score 342.8; DB 17; Length 839;
Best Local Similarity	65.0%; Pred. No. 6.1e-57;
Matches 571; Conservative	0; Mismatches 24; Indels 60; Gaps 2;
QY	388 GGTGCTCAACGTGGCGGGGCTGCGCTTGAGAGCGCGGGCGCGACAGCTGGCGCTTCCC 447
Db	839 GGTCAATCAACATCTCAGGCGCTGCTTGAAACCAGCTGAAGACCTTGCGCCAGTCCC 780
QY	448 GGACACTGTGCTAGGGGAGCCAGCGCGCGCGCGCTTCTACGACAGCGCGCGCGCA 507
Db	779 GGAGACCTCTCCGGGGGAACCCCGAGAGAGATGCGCTACTCTGACCCGCTCGAACA 720
QY	508 GTATTCTTTCGACCGGACCGGCGCAGGCTTGACGCCGCTCTACTACTACAGTCGG 567
Db	719 GTACTCTTTCGACCGGGAACCGGCGCAGCTTGACGCCACTCTCTACTACTACATCGG 660
QY	568 TGGGCGCTGGCGCGCGCGCGCGACGTCGCGCTGACGTCCTCTGAAAGAGTGGCTT 627
Db	659 CGGCGGCTGAGAGCGCGCGCTCAACGTCGCGCTGACATGTTCTCGAGAGATCAAA 600
QY	628 CTACGGGCTGGGCGCGCGCGCGCTGGCACGCTGCGCGAGAGAGGCTGCGCGTCC 687
Db	599 CTACGAGCTGGGCATGAGAGGCGCATGAGAAAGTTCGCGAGAGAGAGGCGCTCATCGGA 540
QY	688 GCCCGAGCGCCCGCGCGCGCGCGCGCTTGGCGCGCGAGCTGGGCTTGGAGTT 747
Db	539 GGAGAGCGCGCGCGCTGCGCGAGAACGACTTCCAGCGGAGAGTCTCTTTCGAGCA 480
QY	748 TCCCGAGAGCTCTCAGGCGCGCGCGCGCTGCGCGCTAGCTTCCGTCGTCATCCTGT 807
Db	479 CCCGAGAGCTGGGCTCGCGCGCGCGCGCGCGATCGCATGCTGTGATGTCATCTCAT 420
QY	808 CTCAATGCTGCTTCTCTGCTTGAGAGCGCTGCTGACTTCCGCGAGACCGCGAGCGCAC 867
Db	419 CTCATGCTCATCTTCTCTGCTTGAGAGCGCTGCGGAGCTGAAGAGAGACCTGACGAGCG 360
QY	868 GGGGCTTCTGCTGAGCGCGAGCGCGCGCGGCTGTTCGCCGCTGCAATGGCTCCAG 927
Db	359 CGTGCAGGTGTGCGCGCGCAACCCACCATCTTCTACAA----- 321
QY	928 CCAATGCTGGAAATCCACCCCGCTGCCCTTCATATACCGCTTCTTGCTGGAGAC 987
Db	320 -----GCCCTACATCTGACGAGACCCCTTCTTCATGCTGGAGAC 282
QY	988 GCTGTGTAATTTGTTGGTCTCTCTTGAAGCTGCTGCTGACGCTCTGCTGTGCAAGCA 1047
Db	281 GCTGTGCAATCTGTTGTTGTTCTCTCTTGCAGCTCATCTGCGGCTTCTTGCGCTCCAGCA 222
QY	1048 GGTATCTTCTTTCAGAGACGTCATGAACTCATGATTTTGGGCTATCTTCCCTACTT 1107
Db	221 GGGCGCTTCTTTCAGAGAACATGATTAACACCATGACATCTGGGCAATCATCTCCCTACTT 162
QY	1108 TGTGCACTGGGACACGAGCTGGGC-----CGGACAGAGGGGGTGGG 1149
Db	161 CATCACTGTTGGGAGACGAGAGCTGGCGGAGAGGCAACAAGAGGGGCAAGGGCGGCGTGG 102
QY	1150 CCAGCAGGCGCATGTCAGTGGCCATCTGAGATCAATCCGATTTGTCGCTTCCGAT 1209
Db	101 CGAGCAGGCGCACTGTCGGCCATCTCTCAGGCTCATCCGCGTGGGCTTCCGAT 42
QY	1210 CTTCAAGCTGTGCCGAGCACTCAAGGGGCTGCAATCT 1247
Db	41 CTTCAAGCTGTGCCGCACTCAAGGGGCTTCCAGCTTT 4

[illegible]

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LNCM826 row: d column: 21
 High quality sequence stop: 830.

FEATURES

source

Location/Qualifiers

1..876

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5016164"

/clone_lib="NH_MGC_7"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/note="Organ: lung; Vector: pORF7; Site_1: XhoI; Site_2:"

EcoRI; cDNA made by oligo-dr priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 179 a 264 c 233 g 200 t

ORIGIN

Query Match 18.6% Score 325.4; DB 13; Length 876;
 Best Local Similarity 66.0%; Pred. No. 1.5e-53;

Matches 603; Conservative 0; Mismatches 256; Indels 54; Gaps 7;

510 ATTTCCTGACGCGGACCGCCGAGCTTGGAGCCGCTGCTACTACTACCACTCCGAG 569
 2 ACTTCTTGACCGCAACGCGCCAGCTTGAGCCCATCTCTACTACTACCACTCCGAG 61
 570 GCGGCTGCGGCG 629
 62 GCGGCTGCGGCG 121
 630 ACGGCTGCGGCG 669
 122 ACGAGTGGGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 181
 690 CCGAGCGCCCG 749
 182 ACGAGCGCCCG 241
 750 CCGAGCGCTGACG 809
 242 CCGAGCGCTGCGGCG 301
 810 CCATGCTGCTTCTGCTGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 869
 302 CCATGCTGCTTCTTCTGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
 870 GCGTGTGCTGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 929
 362 GCACGCTCCACG 404
 930 AATGCTGCTGAATCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 989
 405 -----CAACATCTTCAACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 442
 990 TGTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1049
 443 TGTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 502
 1050 TGTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1109
 503 CGGACTTCTTCAAAAACATCATGAACTCATGACATGTGGGCGCATCTCTATTTC 562
 1110 TGGCACTGGGCGACGAGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1162
 563 TCACGCTGGGCGACCGAGATAGCTGAGCGAAGAAACGAGGCGGCGCGCGCGCGCG 622

OY 1163 TCACGCGCATCTCGAGAGTATCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1221
 DB 623 TCCTGCGCATCTCTGAGCTCATCTCCGCTTGTAAGGTTTGTGAATCTTTCAAGCTCTC 682
 OY 1222 CCGGCACTCAAGAGCGCTGCAATCTTGGCGCAGAGCGCTTGGGCGCTCCATGCGTGA 1279
 DB 683 CCGGCACTCAAGAGCGCTGCAATCTTGGCGCAGAGCGCTTGGGCGCTCCATGCGTGA 742
 OY 1280 -CTGGGCTCTCATCTTTTCTCTTCA--TCGCTGTGCTCTCTTTTCAGCGCGCT- 1335
 DB 743 CTGAGGCTGCTCATCTTTTCTCTTCAATCCGCGGCTCATCTGTTTCTAGTGCAGTG 802
 OY 1336 CTACTTGGCGAGTTGACCGGCGGTGACGCTCCATTTTCACG-ACGATCCCTGAGTCTCT 1394
 DB 803 GTACTTTGCGGAGCGGAGAGACGTGAGTGCACATCTACATCTATCCCGATGTTCT 862
 OY 1395 GGTGGCGGTGAGT 1407
 DB 863 GGTGGCGGTGAGT 875

RESULT 9

AZ339279/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

636 bp DNA linear GSS 29-SEP-2000
 1M0070M07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0070M07 R, DNA sequence.
 AZ339279
 AZ339279.1 GI:10413383
 GSS.
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (bases 1 to 636)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Relilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.,
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plates: 0070 row: M column: 07
 Seq primer: CACACAGAAACACGATATAC
 Class: plasmid ends
 High quality sequence stop: 636.
 Location/Qualifiers
 1..636
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0070M07"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD29v; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114/b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

Query Match 18.5%; Score 323.8; DB 17; Length 636;
Best Local Similarity 72.0%; Pred. No. 3e-53;
Matches 450; Conservative 0; Mismatches 172; Indels 3; Gaps 2;

QY 977 GTGGTGGAGACGCTGTATTTGTTGTTCTCTTCTGAGCTGCTGAGCTCTCTGTC 1036
DB 636 GTGGTGGAGACGCTGTATTTGTTGTTCTCTTCTGAGCTGCTGAGCTCTCTGTC 577
QY 1037 TGTCCAGCAAGGCTATCTTCTTCAAGACGTGATGAACCTCATGATTTTGGCTATC 1096
DB 576 TGTCCAGCAAGGCTATCTTCTTCAAGACGTGATGAACCTCATGATTTTGGCTATC 517
QY 1097 CTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1156
DB 516 ATTCCTTATTTTATCATCTGAGGACGCTGAGCTGAGCAAGCAAGTAATGGCAGCAG 457
QY 1157 GGCATGCTACCTGCGCATCTGAGAGATGATGATGCTGCTGCTTCTTCTTCTTCTT 1216
DB 456 GGCATGCTGCTGAGCAAGGCTGAGAGATGATGATGCTGCTGCTTCTTCTTCTTCTT 397
QY 1217 CTGCTCCGCGCACTCAAGAGGCTGCAATCTTGGGCGCAGAGCTTCCGCTCCATGCGT 1276
DB 396 CTGCTCCGCGCACTTCAAGAGGCTGCAATCTTGGGCGCAGAGCTTCCGCTCCATGCG 337
QY 1277 GAGCTGGGCTCTCTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1336
DB 336 GAGCTGGGCTCTCTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 277
QY 1337 TACTTTCCCAAGTGTACCGGGGTGAGCTCCCATTTCTACATCCCTGACTCTTCTGG 1386
DB 276 TACTTTCCCAAGTGTACCGGGGTGAGCTCCCATTTCTACATCCCTGACTCTTCTGG 217
QY 1397 TGGCGGTGATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1456
DB 216 TGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 157
QY 1457 GGCAGATAGTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1515
DB 156 GGCAGATAGTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 97
QY 1516 GCGCGTATGCTCTCA -ATTTCAGTACTTTTATCAGCGGAGACAGAGGCGAAGAG 1573
DB 96 TCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 37
QY 1574 GCTGGATGTTCAAGCCTGTGAGCA 1598
DB 36 CTAGCCAGTACATGACGCTGGCA 12

RESULT 10
LOCUS BM963332
DEFINITION UT-M-EG0-bm-1-05-0-UT-11 NIH-BMAP_E00 Mus musculus cDNA clone
IMAGE:5697484 5', mRNA sequence.
ACCESSION BM963332
VERSION BM963332.1 GI:19546752
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS NIH-MGC
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-f@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES
source

location/Qualifiers

1. 745
/organism="Mus musculus"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:5697484"

/clone_1b="NIH-BMAP_E00"

/tissue_type="whole brain"

/dev_stage="embryo 15.5 dpc"

/lab_host="DH10B (71 phage resistant)"

/note="Organ: brain; Vector: pX-Asc; Site: 1; Ecot I; Site: 2; Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 18 agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then sequenced directionally into pX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCAGCAGC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

BASE COUNT 139 a 216 c 202 g 188 t

Query Match 18.5%; Score 322.4; DB 14; Length 745;
Best Local Similarity 71.5%; Pred. No. 5.7e-53;
Matches 453; Conservative 0; Mismatches 151; Indels 30; Gaps 1;

QY 990 TGTGATTTGTTGCTCTTCTGAGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 1049
DB 1 TGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
QY 1050 CTATCTTCTTCAAGAGTATGAACTCATGATTTTGTGCTATCTTCTTCTTCTTCT 1109
DB 61 CGGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 120
QY 1110 TGGCAGTGGGCGAGCTGCGCGGAGCGAGCGAGCGGCTG----- 1147
DB 121 TCACCTTGGGCGAGCGAGCTGCGCGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 180
QY 1148 -----GGCCAGCAGCGAGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1199
DB 181 GTCAAGATGGGCGAGCGAGCGAGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 240
QY 1200 TCTTCCGATCTTAAAGCTGCGCGGAGCTGAAAGGCGCTGCAATCTTGGGCGAGAGC 1259
DB 241 TGTTCGCAATCTTCAAGCTTCCCGGAGCTGCAAGGCGGCTGCAATCTTGGGTAAGCT 300
QY 1260 TTGGGCGCTCATGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1319
DB 301 TACAGGCGCTCATGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 360

obtaining a clone please contact: Juliana Brown
(brownjefas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
High quality sequence stop: 429.

FEATURES

source

1. 575

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="5676446"

/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"

/sex="Both"

/tissue_type="Islets of Langerhans"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;

Site_2: Sal 1; Starting library constructed using

Superscript Plasmid Library kit (Life Technologies). cDNA

made by oligo-dT priming. Size-selected by column

fractionation; average insert size 1.08 kb. Library was

amplified once on solid support and plasmid DNA from

library was prepared. The library DNA was normalized by

method #4 from Bonaldo, Lennon, and Soares 1996 Genome

Research 6:791-806; 0.5 microgram single-stranded library

plasmid DNA was mixed with 5 micrograms PCR product

representing library inserts and hybridized to an EcoT of

20. Single-stranded (unhybridized) plasmids were isolated

by hydroxyapatite chromatography and used to make this

library."

BASE COUNT 118 a 164 c 156 g 137 t

ORIGIN

Query Match

Best Local Similarity 17.5%; Score 305.8; DB 13; Length 575;

Matches 382; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 1087 TGTGGCTATCTTCCCTTCTTGTGGCAGTCGGCAGCGAGTGGCCCGCGCAGCGGGT 1146
 DB 1 TGTGGCATATCTCTTATTTATCTCTGGTATCCAGAGTGGCCAGCAGAGGCAA 60
 QY 1147 GGGCCAGAGCCATGTCACATGCGCATCTGAGAGTCATCGATTGGCTGCTTCCG 1206
 DB 61 TGGACACAGAGCCATGTCCTGCGCATCTGAGAGTATCCGCTGGTAAAGGCTTCCG 120
 QY 1207 CATCTTCAAGCTGTCCGGCAGTCGAAAGGCGCTGCAAAATCTTGGGCGAGAGCGCTTGGGGC 1266
 DB 121 CATCTTCAAGCTGTCCGGCAGTCGAAAGGCGCTGCAAAATCTTGGGCGAGAGCGCTTGGGGC 1266
 QY 1267 CTGCGATCGAGTGGGCGCTCTCTCATCTTCTTCTCATGCGTGGTCCCTCTTTC 1326
 DB 181 GTCCATCGAGAGTGGGATGCTCATCTTCTCTTATTTGGGTCATCCCTTTTCTC 240
 QY 1327 CAGGCGCGTACTTCTCCGAAAGTTGACCGGGTGGATCCCATCTTCCATCCCTGA 1386
 DB 241 CAGGCGCGTACTTCTCCGAAAGTTGACCGGGTGGATCCCATCTTCCATCCCTGA 300
 QY 1387 GTCTTCTGTGGGCGGTAGTACCATGACTACAGTTGGCTATGAGACATGACCGGT 1446
 DB 301 TGCCTTCTGTGGGCGGTAGTACCATGACTACAGTTGGCTATGAGACATGACCGGT 360
 QY 1447 CAGTGGGAGGAGATAGGGGCTCTGTGTCATGCGGGCGCTGCGATATTTTC 1506
 DB 361 GACCATAGGGGAGAGATTTGGGATCTCTGTGTCATGCGGGCGCTGCGATATTTTC 420
 QY 1507 CCTGCCAGTCCCGTCAATTTGTCATTTTACGCTACTTTTACCGGGAGAGAGAGG 1566
 DB 421 ATTGCCAGTCCCGTCAATTTGTCATTTTACGCTACTTTTACCGGGAGAGAGAGG 480
 QY 1567 CGAAGAGGCTGGGATGTTACGAGCATGTGG 1595
 DB 481 GGAAGAGCATCCAGTACATGACGTGG 509

RESULT 13

BM128211

LOCUS

DEFINITION

BM128211 593 bp mRNA linear EST 12-MAR-2002
 i110n09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
 cDNA clone IMAGE:56764160 5' similar to SW:CI3_HUMAN P22001
 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE
 JOURNAL
 COMMENT

Endocrine Pancreas Consortium
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Harvard University, Howard Hughes Medical Institute
 Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center for information on
 obtaining a clone please contact: Juliana Brown
 (brownjefas.harvard.edu) This sequence now available from the IMAGE
 consortium, for clone orders contact: info@image.llnl.gov
 High quality sequence stop: 438.

FEATURES

source

1. 593

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="56764160"

/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"

/sex="Both"

/tissue_type="Islets of Langerhans"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;

Site_2: Sal 1; Starting library constructed using

Superscript Plasmid Library kit (Life Technologies). cDNA

made by oligo-dT priming. Size-selected by column

fractionation; average insert size 1.08 kb. Library was

amplified once on solid support and plasmid DNA from

library was prepared. The library DNA was normalized by

method #4 from Bonaldo, Lennon, and Soares 1996 Genome

Research 6:791-806; 0.5 microgram single-stranded library

plasmid DNA was mixed with 5 micrograms PCR product

representing library inserts and hybridized to an EcoT of

20. Single-stranded (unhybridized) plasmids were isolated

by hydroxyapatite chromatography and used to make this

library."

BASE COUNT 125 a 164 c 162 g 142 t

ORIGIN

Query Match

Best Local Similarity 17.3%; Score 302.6; DB 13; Length 593;

Matches 380; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY 1087 TGTGGCTATCTTCCCTTCTTGTGGCAGTCGGCAGCGAGTGGCCCGCGCAGCGGGT 1146
 DB 1 TGTGGCATATCTCTTATTTATCTCTGGTATCCAGAGTGGCCAGCAGAGGCAA 60
 QY 1147 GGGCCAGAGCCATGTCACATGCGCATCTGAGAGTCATCGATTGGTGGCTTCCG 1206
 DB 61 TGGACACAGAGCCATGTCCTGCGCATCTGAGAGTATCCGCTGGTAAAGGCTTCCG 120

QY 1207 CATCTTCAAGCTGTCCCGGCACTCAAGGCGCTGCAAAATCTTGCGCCAGACGCTTCGGGC 1266
|||||
Db 121 CATCTTCAAGCTGTCCCGGCACTCAAGGCGCTGCAAAATCTTGCGCCAGACGCTTCGGGC 180
QY 1267 CTCATGCGTGAAGTGGGCTCTCTATCTTTTCCCTTCATCGGTGGTCTCTTTTC 1326
|||||
Db 181 GTCACAGCGGAGGTGGGATGTCATCTTCTCTATCTTTTGGGGGATCCCTTTTTC 240
QY 1327 CAGCGCGCTCTACTTGGCGAAGTTGACGGGGTGAGCTCCATTCATGACATCCCTTA 1386
|||||
Db 241 CAGCGCGCTCTACTTGGCGAAGTTGACGGGGTGAGCTCCATTCATGACATCCCTTA 300
QY 1387 GTCTTCTGTGGTGGGCGGTAGTACACATGACTGACTGCTATGAGACATGACACCCGT 1446
|||||
Db 301 TGCCTTCTGTGGGCGGTAGTACACATGACTGACTGCTATGAGACATGACACCCGT 360
QY 1447 CACTGTGGGTGGCGAAGTATGTTGGGCTCTGTGTGCTGCTATGCGGGGCTGCTATTTTC 1506
|||||
Db 361 GACCATAGGGGGGCAAGATTTGTGGGATCTCTGTGCTGCTGCGGGGCTGCTGACATTCG 420
QY 1507 CCGTCCAGTCCCGCTATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566
|||||
Db 421 ATTGCCAGTTCCTCGGATGTTGTCACATTCATTCATTCATTCATTCATTCATTCATTCATTC 480
QY 1567 CGAAGAGCTGGGATGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1595
|||||
Db 481 GGAAGAGCAATCCCATGATGACATGCTGG 509

RESULT 14
B0807519 628 bp mRNA linear EST 31-JUL-2002
LOCUS B0807519
DEFINITION NISC_k050c10.y2 NCI_CGAP_Brn72 Macaca mulatta cDNA clone
IMAGE:5330682.5', mRNA sequence.
ACCESSION B0807519
VERSION B0807519.1 GI:22031728
KEYWORDS EST.
SOURCE rhesus monkey.
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
1 (bases 1 to 628)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-ri@mail.nih.gov
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
inf@image.llnl.gov
Plate: LLM1839 row: E column: 19
Seq primer: M13RP1 reverse primer (ABT).
Location/Qualifiers
1..628

FEATURES
source
/organism="Macaca mulatta"
/db_xref="taxon:9544"
/clone="IMAGE:5330682"
/clone_11b="NCI_CGAP_Brn72"
/tissue_type="hypothalamus"
/lab_host="PH10B (phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6 ccdB. Site: 1:
NotI; Site: 2: EcoRV; Cloned unidirectionally. Primer:
Oligo dt. Average insert size 2.2 kb. Constructed by
Invitrogen. Note: this is a NCI_CGAP library."
BASE COUNT 105 a 212 c 181 g 130 t

ORIGIN
105 a 212 c 181 g 130 t

Query Match 17.3%; Score 302; DB 14; Length 628;
Best Local Similarity 68.5%; Pred. No. 5, 3e-49;
Matches 441; Conservative 0; Mismatches 185; Indels 18; Gaps 1;

QY 525 ACCGCGCCAGCTTGCAGCGCGCTGCTACTACTACAGTCCGCTGGCGCGCGCG 584
|||||
Db 3 ACCGCGCCAGCTTGCAGCGCGCTGCTACTACTACAGTCCGCTGGCGCGCGCG 62
QY 585 CCGCGGACGCTGCGCGCTGCGAGCTTCTGTAAGAGTGGCGCTTCTGCGCGCG 644
|||||
Db 63 CCGTCAACGCTGCGCGCTGCGAGATCTTCTGAGGAGATCCGCTTCAACAGCTGGGAG 122
QY 645 CCGCGCTGCGAGCTGCGCGGAGAGAGGCGCGCGCTGCGCGCGCGCGCGCG 704
|||||
Db 123 AGGCGATGAGAGAGTTCGCGGAGAGAGAGGCGCTTCTGCGGAGAGAGAGCGCG 182
QY 705 CCGCGCGCGCTTGCAGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 764
|||||
Db 183 CCGCGCGCGCTTGCAGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242
QY 765 CCGCGCGCGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
|||||
Db 243 CAGCGCGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
QY 825 GCGTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 884
|||||
Db 303 GCGTCAAGAGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 362
QY 885 CCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 944
|||||
Db 363 ACTCATGATGAGCGCGCGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
QY 945 CAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1004
|||||
Db 418 -----CTTCTGCGAGTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
QY 1005 TCTCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1064
|||||
Db 465 TCTCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 524
QY 1065 ACCTGATGAACTCATGATTTTGTGGCTATTCCTTCTGCTGCTGCTGCTGCTGCTGCT 1124
|||||
Db 525 ACATCATGAACTCATGATTTTGTGGCTATTCCTTCTGCTGCTGCTGCTGCTGCTGCT 584
QY 1125 AGCTGCGCGCGCGAGCGAGGCTGCGCGAGCGCGCTGCTGCTGCTGCTGCTGCT 1168
|||||
Db 585 AGCTGCGCGCGAGCGAGGCTGCGCGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 628

RESULT 15
CNS058RO 1060 bp DNA linear GSS 26-MAY-2000
LOCUS CNS058RO
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
020119 of library A from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL326301
VERSION AL326301.1 GI:8219890
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 1060)
Roest-Crollius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
2 (bases 1 to 1060)
JOURNAL
REFERENCE

FEATURES	source
AUTHORS	Roest-Crolius,H., Jallion,O., Dasilva,C., Fitzmes,C., Fisher,C., Bonneau,L., Billault,A., Quetler,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 1060)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000)
COMMENT	This sequence is a single read and was generated as part of a large scale clone-and sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon .
FEATURES	location/Qualifiers
source	1. 1060
	/organism="Tetraodon nigroviridis"
	/db_xref="taxon:99883"
	/clone="020119"
	/clone_1lb="A"
	/note="Genoscope sequence ID : C0A020CF10C1-end : T7"
BASE COUNT	238 a 239 c 231 g 309 t 43 others
ORIGIN	
Query Match	17.0%; Score 296.6; DB 17; Length 1060;
Best Local Similarity	68.4%; Pred. No. 6.4e-48;
Matches 437; Conservative 0; Mismatches 198; Indels 4; Gaps 2;	
Oy 937	TGGAAATCCACCCGCCCTTCATATGACCCCTTCTTGGTGGAGAGCGCTGTAT 996
Db 8	TGCACACCATCTCCNNGAAGCCATCTCCNATCCCTTCTCATCTGGAGACCGCTTGAT 67
Oy 997	TGTGTGTTCTCTCTTGGAGCTGCTGTGACGCTCCTCGTCTGTCCACGAAGGCTATCTT 1056
Db 68	TGCTTGTTCTTTTGGAGCTGTGTGACGATTTGGGTCTGTCTTACGAAGAAGATT 127
Oy 1057	CTTCAAGAAGCTGATGAACCTCATCTGATTTTGTGGCTATCCTTCCCTACTTTGGGCACT 1116
Db 128	CTTCCACACCTCATGAACAATTTGATATGATATCATCTCATCTCTTATTTGTATACGT 187
Oy 1117	GGGACCCGAGCGGGCGCGGACGAGGGGTGGGC--CAGAGGCCATGTCACGCGCAT 1173
Db 188	GGTTACAGAATTTCTCACACACCGGAGAGAGCTCAGACAGAAATGTCTTGGCCAT 247
Oy 1174	CCTGAGACTCATCCGATTGTGTGCTGTCTCCGACTTCTTCAAGCTGTCCGGCACTCAA 1233
Db 248	TCTGCGCATCTTGGCGTGTAGATTCGCTATTTTCAAACTCAGCAGATTTCAA 307
Oy 1234	GGGCTCGAAATCTTGGGCGACAGCGCTTCCGCTCCATGCGTGAAGCTGGGCTCTCAT 1293
Db 308	GGGTTCGAGATCCCTCGACAGACCCCTGAAGGAAGCATGGGTGA-NTTGGTTGGCTCAT 366
Oy 1294	CTTTTCTCTTCATCGGTGTGGTCCCTTTTTCAGCCGCGCTCATCTTGGCGAAGTTGA 1353
Db 367	TTTTTTCTCTTCATCGGGGCTCATCTCTTCTCCAGTCTATCTACTTTGCCAGAGTTGA 426
Oy 1354	CCGGGTGAGCTCCATTCTACATAGCATCCCTGAGTCTCTTGTGGGGGCGGTAGTCACCAT 1413
Db 427	CGAGCCAAACACGCGAGTTGTTAGATACCCGATGCGATGGTCTTGTGGGCGCTGTTACAT 486
Oy 1414	GACTACACTTGGGCTATGGAGACATGGACCCGCTCACTGTGGTGGCAAGATAGTGGCTC 1473
Db 487	GACTACTGTGGTTATGGGACATGTGTCCCATCACTTGGGAGGCAAAATGGTGGGCGAC 546
Oy 1474	TCTGTGTCACATTTGGGCGGTGTGATATTTCCCTCGGACATGGCCGATTTGTCTCCAA 1533
Db 547	GCTGTGGCCCATCGCTGGAGTGTACCATTTGTCTGTGCTTCCCGCTCATTTGTTCCAA 606
Oy 1534	TTTCAGCTACTTTTATATCACGCGGAGACAGAGGCGGAGAA 1572
Db 607	CTTTAACTACTTTTACACAGAGAGACGAGAGCTGAGGA 645

FEATURES	source
DB	1621 GCGCCTGTGAGGGCAAGGCGCATTTGGGGGGCTGTGTGACGCGGGAGAGTACTAGATCCAC 1633
DB	1621 GCGCCTGTGAGGGCAAGGCGCATTTGGGGGGCTGTGTGACGCGGGAGAGTACTAGATCCAC 1680
DB	1634 CTTCCACTCTGGGCGACCCCGCCAGGAACACTGTGTACCCGAATGTGA 1680
DB	1681 CTTCCACTCTGGGCGACCCCGCCAGGAACACTGTGTACCCGAATGTGA 1727
RESULT 3	
AF315818	1447 bp mRNA linear PRI 19-JUN-2001
LOCUS	
DEFINITION	Homo sapiens voltage-gated potassium channel KCNA7 mRNA, complete cds.
ACCESSION	AF315818
VERSION	AF315818.1
KEYWORDS	GI:14485554
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Bardien-Kruger, S., Wulff, H., Arieff, Z., Brink, P., Chandy, K.G. and Corfield, V.
TITLE	Characterization of the human voltage-gated potassium channel gene, KCNA7, a candidate gene for inherited cardiac disorders, and its exclusion as cause of progressive familial heart block I (PFHBI) unpublished
JOURNAL	2 (bases 1 to 1447)
REFERENCE	Bardien-Kruger, S., Wulff, H., Arieff, Z., Brink, P., Chandy, K.G. and Corfield, V.
AUTHORS	Submitted
TITLE	Direct Submission
JOURNAL	Submitted (23-OCT-2000) SANBI, University of Western Cape, Modderdam Road, Cape Town 7533, South Africa
FEATURES	location/Qualifiers
source	1. 1447
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	/map="19q13.3"
	38. 1408
	/note="hk1.7"
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	LARLEDGCGVPERPLPRAPAROLMLTEPPSSGAAVLAIVSLVLSIVE
	CLTELPDFDRDROGTGLAAAPAPPLNGSSOMGNRLPNDPEFVETLCIG
	WSEELLVRLVLCPSKALFEFNWNMLDFAVILYPAALGELAROKRYGOAMSLAI
	LVRILRVRIETKLSRHSKQLILGOTLRASMKELGLITFLTGYLVFESSAYFAP
	VDRYDSHTSLIPESFMAVVMITVVGDMAPVTVGGKIVSICAIAGVLISLPVPV
	IVSNFSYFHREHTEGEERAGMSHVDMOPCGPLEKANGILVDGVEPLPRLMAPPGK
	HLVTEV"
BASE COUNT	204 a 480 c 451 g 312 t
ORIGIN	
Query Match	82.0%, Score 1378.2; DB 9; Length 1447;
Best Local Similarity	99.4%; Pred. No. 3, 1e-179;
Matches 1405; Conservative	0; Mismatches 3; Indels 5; Gaps 2;
DB	1 ACACGTCTGGTTCGCGGGTCCGGGGCGCGCCATGTGAGCGCGGTGCCCGCG-- 58
DB	1 ACACGTCTGGTTCGCGGGTCCGGGGCGCGCCATGTGAGCGCGGTGCCCGCGCG-- 58
DB	328 CCGTCCGCGCTGCTGCGACGCGCTGTGCTCAACGTGCGCGGCGTTCGAGACGCG 387
DB	59 CCGTCCGCGCTGCTGCGACGCGCTGTGCTCAACGTGCGCGGCGTTCGAGACGCGG 118
DB	388 GCGGCGACGCTTGCGCGCTTCCCGGACACATCTGTAGGAGGACCAAGCGCGCGCGCGC 447

D	b	119	GC	CGCAGACGCTGGGGCCGCTTCCGGAGACACTCTGTAAGGGAGACCCAGCGGGCCGGCCGC	178
O	y	448	TT	TACGACGACGCGCGCCGCGAGATTTCTTCGACCGGCAACCGGCCACGTTTCAGACGC	507
D	b	179	TT	TTCATGACGACGCGCGCCGCGAGATTTTCTTGACCGGACCGCGGCCAGTTTCACGCGC	238
O	y	508	GT	GCTACTACTACTACAGTCCGGTGGGGCGCTCGGGCCGGCCGACGACGTGGCGCTGCAC	567
D	b	239	GT	GCTACTACTACTACAGTCCGGTGGGGCGCTCGGGCCGGCCGACGACGTGGCGCTGCAC	298
O	y	568	GT	CTTCCTCGGAAGAGGAGGCTTCTTACGGGCTGGGGCGCGGGCCCTGTGCACGCTGGC	627
D	b	299	GT	CTTCCTCGGAAGAGGAGGCTTCTTACGGGCTGGGGCGCGGGCCCTGTGCACGCTGGC	358
O	y	628	GAG	ACGAGGGCTGCGCGCGGTCGCGCGGACGCGCCCGCTCGCCCGCCGCTTCGCGCCGC	687
D	b	359	GAG	ACGAGGGCTGCGCGCGGTCGCGCGGACGCGCCCGCTCGCCCGCCGCTTCGCGCGC	418
O	y	748	GT	CTCCGCGGGGTCATCCATCGTCTCCATGTCTTTCGCTCGAGACGCTGCTGAC	807
D	b	479	GT	CTCCGCGGGGTCATCCATCGTCTCCATGTCTTTCGCTCGAGACGCTGCTGAC	538
O	y	808	TT	TTCGCGACGACCGCGACGGCGACGGGGCTTGCTGTGACGCGACCGCGCCGGGTGTT	867
D	b	539	TT	TTCGCGACGACCGCGACGGCGACGGGGCTTGCTGTGACGCGACCGCGCCGGGTGTT	595
O	y	868	CC	CGCTCCGCTGAATGGCTCTCAGCCAAATGCTGGAATTCACCCGCTGCTTCAT	927
D	b	596	CC	CGCTCCGCTGAATGGCTCTCAGCCAAATGCTGGAATTCACCCGCTGCTTCAT	655
O	y	928	GAC	CGCTTCCTCGGGGAGAGCGCTGTATTTGGTTCCTTCCTTACGCTGCTGGA	987
D	b	656	GAC	CGCTTCCTCGGGGAGAGCGCTGTATTTGGTTCCTTCCTTACGCTGCTGGA	715
O	y	988	CG	CTTCCTCGGGGAGAGCGCTGTATTTGGTTCCTTCCTTACGCTGCTGGA	1047
D	b	716	CG	CTTCCTCGGGGAGAGCGCTGTATTTGGTTCCTTCCTTACGCTGCTGGA	775
O	y	1048	TT	TGCGCTATCTTCCCTACTTGTGTGACACTGGGACCGAGCTGGCCCGGACGAGGG	1107
D	b	776	TT	TGCGCTATCTTCCCTACTTGTGTGACACTGGGACCGAGCTGGCCCGGACGAGGG	835
O	y	1108	GT	GGGGGCCGACGGCAGTACGTACGGCCATCCGTAGAGTCAATCGATGGTGGTCTCTC	1167
D	b	836	GT	GGGGGCCGACGGCAGTACGTACGGCCATCCGTAGAGTCAATCGATGGTGGTCTCTC	895
O	y	1168	CG	ATCTTCAAGCTGTCCCGGACATCAAGAGGGCTCAATCTTGGGCGACAGCTTGG	1227
D	b	896	CG	ATCTTCAAGCTGTGTCCCGGACATCAAGAGGGCTCAATCTTGGGCGACAGCTTGG	955
O	y	1228	GC	CTCAGCTGTGAGCTTGAGGCTCTCATCTTTTCTCTTCATCGGTGGTCTCTT	1287
D	b	956	GC	CTCAGCTGTGAGCTGTGAGGCTCTCATCTTTTCTCTTCATCGGTGGTCTCTT	1015
O	y	1288	TC	CACGCGCGCTACTTGTCCGGAAGTTGACCGGGTGGATCCCATTTTCACTAGCATCC	1344
D	b	1016	TC	CACGCGCGCGCTACTTGTCCGGAAGTTGACCGGGTGGATCCCATTTTCACTAGCATCC	1075
O	y	1348	GAG	TCCTTGTGGGGGAGTACACATGACATACAGTTGGCATGAGACATGGACACC	1407
D	b	1076	GAG	TCCTTGTGGGGGAGTACACATGACATACAGTTGGCATGAGACATGGACACC	1135
O	y	1408	GT	CACTGTGGGTGCGACAGATAGTGGGCTCTGTGTGTCATTTGCGGGGTGCTGCTATT	1467
D	b	1136	GT	CACTGTGGGTGCGACAGATAGTGGGCTCTGTGTGTCATTTGCGGGGTGCTGCTATT	1195
O	y	1468	TC	CTCCGCAAGTGCCTCATTTGCTCCAAATTTACGTAATTTATCACCGGACGACAG	1527
D	b	1196	TC	CTCCGCAAGTGCCTCATTTGCTCCAAATTTACGTAATTTATCACCGGACGACAG	1255

1528 GGGAGAGGCTGGATGTTACAGCATGTGAGATGCAGCTTGTGGCCACTGAGAGG 1587
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1588 AAGGCAATGGGGGGCTGTGTGAGAGGGAGATCACTGAGCTACACCTCCTACTGTGGCA 1647
1316 AAGGCAATGGGGGGCTGTGTGAGAGGGAGATCACTGAGCTACACCTCCTACTGTGGCA 1375
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1376 CCCCCAGGAGAACCTGTGTACACCGAAGTGTGA 1408

RESULT 4
AX352535
LOCUS AX352535 1341 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 7 from Patent WO0194390.
ACCESSION AX352535
VERSION AX352535.1 GI:18617765
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1
AUTHORS Curtis, R.A.
TITLE 52906, 33408, and 12189, potassium channel family members and uses
thereof
Patent: WO 0194390-A 7 13-DEC-2001;
JOURNAL Millennium Pharmaceuticals, Inc. (US)
FEATURES
source 1.1341
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RIFKLSRHSKGLQILISQTLRASKRELGLIFELFISVLPSSAVFAEDRDSHTS
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BASE COUNT 190 a 443 c 411 g 297 t
ORIGIN

Query Match 78.7%; Score 1321.6; DB 6; Length 1341;
Best Local Similarity 99.5%; Pred. No. 1.7e-171;
Matches 1337; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

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1 TGGTGGAGGGGCTGGTGCACAGTGGCCGGCTGGCTTCAGACGCGGGCGGACG 60

397 CTGGGGCGCTTCCCGACACTGTCTAGAGGACCCAGCGCGCGCTTCTAGAC 456
1 TGGTGGAGGGGCTGGTGCACAGTGGCCGGCTGGCTTCAGACGCGGGCGGACG 120

61 CTGGGGCGCTTCCCGACACTGTCTAGAGGACCCAGCGCGCGCTTCTAGAC 120

457 GACGCGCGCGGAGATATTTCTTGACCGGACCGCGCGCTTCTAGAC 516
1 TGGTGGAGGGGCTGGTGCACAGTGGCCGGCTGGCTTCAGACGCGGGCGGACG 180

121 GACGCGCGCGGAGATATTTCTTGACCGGACCGCGCGCTTCTAGAC 180

517 TACTACAGTCCGGTGGCGGGCTGGCGCGCGCGCGCTTCTAGAC 576
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577 GAACAGCTGACCTTCTACGGGCTGGCGCGCGCGCTTCTAGACGCGCGAGAGAGAG 636
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241 GAAGAGGTGGCTTCTACAGGGCTGGGGCGGCGGCCCTTGACACGCTTGGCGGAGACGAG 300
637 GGGTGGCGGGTGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 696
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RESULT 5
LOCUS 126643 1599 bp DNA linear PAT 07-OCR-1996
DEFINITION Sequence 9 from patent US 5559009.
ACCESSION 126643
VERSION 126643.1 GI:1606513
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1599)
Chandy, K.G., Kaiman, K., Chandy, G. and Gutman, G.A.
Voltage-gated potassium channel gene, Kv1.7, vectors and host cells
comprising the same, and recombinant methods of making potassium
channel proteins
JOURNAL Patent: US 5559009-A 9 24-SEP-1996;
FEATURES
Location/Qualifiers
source 1. 1599
BASE COUNT 233 a 521 c 502 g 343 t
ORIGIN
Query Match 63.6%; Score 1069; DB 6; Length 1599;
Best Local Similarity 81.5%; Pred. No. 5.2e-137;
Matches 1289; Conservative 0; Mismatches 280; Indels 12; Gaps 4;
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RESULT 6
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LOCUS AF032099
DEFINITION Mus musculus voltage-gated potassium channel Kv1.7 (Kcnc7) mRNA,
complete cds.
ACCESSION AF032099
VERSION AF032099.1 GI:3004906
KEYWORDS
SOURCE Mus musculus.

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1599)
 REFERENCE
 AUTHORS Kalman, K., Nguyen, A., Tseng-Crank, J., Dukes, I. D., Chandy, G.,
 Hustad, C. M., Copeland, N. G., Jenkins, N. A., Mohrenweiser, H. M.,
 Brandriff, B., Cahalan, M. D., Gutman, G. A. and Chandy, K. G.
 TITLE Genomic organization, chromosomal localization, tissue
 distribution, and biophysical characterization of a novel mammalian
 Shaker-related voltage-gated potassium channel, Kv1.7
 JOURNAL J. Biol. Chem. 273 (10), 5851-5857 (1998)
 MEDLINE 98157988
 PUBMED 94887722
 REFERENCE 2 (bases 1 to 1599)
 AUTHORS Kalman, K., Nguyen, A., Tseng-Crank, J., Dukes, I. D., Chandy, G.,
 Hustad, C. M., Copeland, N. G., Jenkins, N. A., Mohrenweiser, H. M.,
 Brandriff, B., Cahalan, M. D., Gutman, G. A. and Chandy, K. G.
 TITLE Direct Submission
 JOURNAL Submitted (30-OCT-1997) Physiology and Biophysics, University of
 California at Irvine, Irvine, CA 92697, USA
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 BASE COUNT 234 a 520 c 502 g 343 t
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 Query Match 63.4%; Score 1065.8; DB 10; Length 1599;
 Best Local Similarity 82.8%; Pred. No. 1.4e-136;
 Matches 1269; Conservative 0; Mismatches 252; Indels 12; Gaps 4;

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 Db 607 CAGCTGTGCTGCTTTTTCGAGTTTCCGAGAGCTTCAGGCGCGCGCGCGCGCGCGCGCG 666
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 Db 727 TTCCGCGACAGCG 786
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 Db 787 CTCGCCCGAGCTGAATGCTCCAGCTCCAGCTCCAGCGAGCGCGCGCGCGCGCGCGCG 846
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 Db 847 GATCCATCTTTTGGTGGAGACCGCTGTATGCTGTTGTTGTTGTTGTTGTTGTTGTTG 906
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 Db 907 CATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 966
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 Db 967 TTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1026
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LOCUS AC008687 Homo sapiens chromosome 19 clone CTB-60B18, complete sequence.
AC008687.5 GI:15887249
VERSION HTG.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 157633)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
2 (bases 1 to 157633)
REFERENCE 2 (bases 1 to 157633)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 157633)
REFERENCE 3 (bases 1 to 157633)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 157633)
REFERENCE 4 (bases 1 to 157633)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Oct 3, 2001 this sequence version replaced gi:10312243.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
SRS Content:
SHGC-15869 G15229
SHGC-15864 G13225
SHGC-5822 G14090
SHGC-58615 G42524.

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Location/Qualifiers
1..157633

BASE COUNT 33926 a 43885 c 42816 g 37006 t
ORIGIN

Query Match 48.5%; Score 814.2; DB 9; Length 157633;
Best Local Similarity 99.0%; Pred. No. 1.5e-102;
Matches 819; Conservative 0; Mismatches 8; Indels 0; Caps 0;

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Db 81417 CTCACCTGTGGGACCCCGGAGGAGACCTGTGTGTACCGAAGTGTGA 81371

RESULT 8
OCU38240 1551 bp DNA linear MAM 30-JUN-1998
LOCUS OCU38240
DEFINITION Oryctolagus cuniculus glibenclamide-sensitive voltage-gated
potassium channel (Kv1.3-glib) gene, complete cds.
ACCESSION U38240
VERSION U38240.1 GI:3264840
KEYWORDS Oryctolagus cuniculus.
SOURCE Oryctolagus cuniculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 1551)
AUTHORS Yao, X., Chang, A.Y., Boulpaep, E.L., Segal, A.S. and Desir, G.V.
TITLE Molecular cloning of a glibenclamide-sensitive, voltage-gated
potassium channel expressed in rabbit kidney
J. Clin. Invest. 97 (11), 2525-2533 (1996)
JOURNAL MEDLINE 96249424
PUBMED 8647945
REFERENCE 2 (bases 1 to 1551)
AUTHORS Desir, G.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-1995) Gary Desir, Medicine, Yale, 2074 LMP 333
Cedar Street, New Haven, CT 06510, USA
On Jun 29, 1998 this sequence version replaced gi:1033191.

[illegible][illegible]

Db	2438	TCTTGCATCGCATTTGCAGTTCCTCCCGATTTGTTTCCAACTTCAATTACTTCTACACAC	2497
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RESULT 10	AL365361/c	AL365361	155343 bp DNA linear PRI 23-FEB-2001
LOCUS	LOCUS	Human DNA sequence from clone Rpl1-284N8 on chromosome 1, complete sequence.	
DEFINITION	DEFINITION	AL365361 AC025151	
ACCESSION	ACCESSION	AL365361.11 GI:13160295	
VERSION	VERSION	HTG.	
KEYWORDS	KEYWORDS	human.	
SOURCE	SOURCE	Homo sapiens	
ORGANISM	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	REFERENCE	1 (bases 1 to 155343)	
AUTHORS	AUTHORS	Mashreghi-Mohammadi,M.	
TITLE	TITLE	Direct Submission	
JOURNAL	JOURNAL	Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk	
COMMENT	COMMENT	On or before May 15, 2001 this sequence version replaced	

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QY 1517 GGGAGACAGGGCGAAGAGGCTGGGATTTCAAGCCATTTGG 1558

Db 120214 GGGAGACAGAGGGAAGAGCAATCCCATGATGACATGCTGG 120173

RESULT 11

HUMKCN 2397 bp DNA linear PRI 26-FEB-2002

LOCUS Homo sapiens voltage-gated potassium channel (HGK5) gene, complete cds.

DEFINITION M38217 X57342

ACCESSION M38217.1 GI:186670

VERSION

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS Cal,Y.C., Osborne,P.B., North,R.A., Dooley,D.C. and Douglass,J.

TITLE Characterization and functional expression of genomic DNA encoding the human lymphocyte type n potassium channel

JOURNAL DNA Cell Biol. 11 (2), 163-172 (1992)

MEDLINE 92189730

PUBMED 1547020

COMMENT On Feb 26, 2002 this sequence version replaced gi:2648038. Draft entry and computer-readable sequence for [Unpublished (1990)] kindly submitted by Y.-C.Cai, 30-AUG-1990. Oregon Health Sciences University Vollum Institute Mail Code: L474 3181 S.W. Sam Jackson Park Road Portland, OR 97201-3098 USA.

FEATURES

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BASE COUNT 532 a 675 c 603 g 587 t

ORIGIN

Query Match 38.1%; Score 640.6; DB 9; Length 2397;

Best Local Similarity 70.5%; Pred. No.1,6e-78;

Matches 878; Conservative 0; Mismatches 349; Indels 18; Gaps 1;

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Db 203 GCTTCGAGACGACAGCTGAAGACCTTTGCCAGTTCCCGAGACGCTGTGGGACCCCA 262

QY 434 CGGCGCGGCGGCTTTCAGAGCAGCGCGCGCGAGTATTTCTTGACCGGACCGCG 493

Db 263 AGCGGCGCATGAGTACTTACCGCGCTGCGCAAGAGTACTTTCGACCGGACCGG 322

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Db 323 CCACTTTCGACCGCATCTCTACTACTATACAGTCCGGGGCCGATCGCGCGGCTCA 382

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Db 383 ACGTGGCCATTCGACATTTTCTCCGAGAGATCCGCTTCTACAGCTGGGCGAGAGGCA 442

QY 614 TGGCAGCGCTGCGGAGAGAGAGAGGCTGCCGCGGCGCGCGGCGCGGCTGCGCG 673

Db 443 TGGAGAGATTCGCGAGAGAGAGAGGCTTCTGCGGGAGAGAGGCGGCTTCCCGG 502

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QY 974 TTGAGCTGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1033

Db 785 TCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 844

QY 1034 TGAACCTCATGATTTGTGCTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1093

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RESULT 12

HUMPOCH

LOCUS Homo sapiens voltage-gated potassium channel (KCNA3) mRNA, complete cds. 1836 bp mRNA linear PRI 14-AUG-1998
 DEFINITION Homo sapiens voltage-gated potassium channel (KCNA3) mRNA, complete cds.

ACCESSION

L23499

VERSION

L23499.1 GI:385222

KEYWORDS

KCNA3 gene; potassium channel; voltage-gated potassium channel.

SOURCE

Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

Polander, K., Lin, S., Koo, G. and Swanson, R.

AUTHORS

Assignment of the gene encoding Kv1.3, a voltage gated potassium channel, to human chromosome 1

TITLE

Unpublished (1993)

JOURNAL

Location/Qualifiers

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 Best Local Similarity 70.4%; Pred. No. 2.8e-78;
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DEFINITION	H.sapiens K+ channel protein (HLK3) mRNA, complete cds.
ACCESSION	M85217
VERSION	M85217.1
KEYWORDS	K ⁺ channel protein; voltage dependent potassium channel.
SOURCE	Homo sapiens Homo sapiens cDNA to mRNA.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 3004)
AUTHORS	Altai,B., Romey,G., Honore,E., Schmid>Alliana,A., Mattei,M.G., Lecage,F., Ricard,P., Barnhard,J. et Lazdunski,M. Cloning, functional expression, and regulation of two K ⁺ channels in human T lymphocytes <i>J. Biol. Chem.</i> 267 (12), 8650-8657 (1992)
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Db	1030	TGGTAAAGGTCTTCCGCAATCTTCAAGCTGTGGCGCATCTCAAGAGGGCTGCGAGATCTCG	1089							
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Db	1090	GSCAAACGCTGAAGCGTCCATGCGGGAGCTGGGATGTGCTATCTTCTTCTCTTATTTG	1149							
OY	1274	GTTGGTCTCTTTCACAGCGCGCTTACTTTCGCGAAGTTGACCGGGTGCATCCCATTT	1333							
Db	1150	GGGTATCTCTTTCACAGCGCGCTTACTTTCGCGAAGGACAGACCCCATCTTCAGGTT	1209							
OY	1334	TCATCAGCATCCCTTAGTCTTCTGTGTGGGCGGTATGTCACATGACTACAGTGGCTATG	1393							
Db	1210	TCAGAGCATCCCGGATCCCTTTCGTGTGGGAGTGTATCAACATGCAACACGGGGTATTCG	1269							

QY	1394	GAGACATGGCA	CCCGTCTGCTGGGTGGCAGATGTGTGGGCTCTGTGGTGCATTTGGG	1453
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QY	1454	GCCTGCTACTATTTT	CCCTCGCAGTGGCCGCATTTGTCTCAATTTACATTTATTC	1513
Db	1330	GTGTCTTGACCAT	TGCAATTTGCAGATTTCCCGATTTGTTTCCAACTTCAATTAATTA	1389
QY	1514	ACCGGGAGACAGAG	GGCGGAGGCTGGGATGTTCCAGCCATGTGG	1558
Db	1390	ACCGGGAGACAGAG	GGGGAGAGCAATCCAGTACATGCACGTGG	1434
RESULT 14				
HUMPCD	LOCUS	HUMPCD	1820 bp	DNA linear PRI 27-APR-1993
DEFINITION	Human potassium channel protein (HPCN3) gene, complete cds.			
ACCESSION	M55515			
VERSION	M55515.1	GI:189672		
KEYWORDS	potassium channel protein.			
SOURCE	Human DNA.			
ORGANISM	Homo sapiens			
REFERENCE	Enkayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
AUTHORS	Phillipson,L.H., Lamendola,J., Bell,G.I. and Steiner,D.F.			
TITLE	Genomic sequence of a human potassium channel related to RCK3			
JOURNAL	Unpublished (1990)			
REFERENCE	2 (bases 1 to 1820)			
AUTHORS	Phillipson,L.H., Hice,R.E., Schaefer,K., Lamendola,J., Bell,G.I., Nelson,D.J. and Steiner,D.F.			
TITLE	Sequence and functional expression in Xenopus oocytes of a human			
JOURNAL	Insulinoma and islet potassium channel			
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 88 (1), 53-57 (1991)			
PUBMED	91095456			
FEATURES	1986382			
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Best Local Similarity	70.3%;	Pred. No. 7.6e-78;		
Matches 875;	Conservative 0;	Mismatches 352;	Indels 18;	Gaps 1;
QY	314	CGGTCCCGCCGCC	CCCGTGCCTGCTGAGACGGCTGTGCTCAACGTGCGCGGCTGC	373
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QY	374	GCTTGAGAGACGGG	CGGCACAGCTGGGCGCTTCCCGGACACTCTGCTAGGGACCCAG	433

D	b	310	GCTTTCGAGACGACGACGTGAAGACCTTTGGCAGTTCCCGAGACGCTGCTGGGACACCCA	369
O	y	434	CGCGCCCGGGCCGCTTCTACGACGACGCGCCCGGAGTATTTCTTCGACCGGACCGGC	493
D	b	370	AGCGGGCCATGAGAGGTACTTTCGACCCCGTCGCGACGAGTACTTCTTCGACCGGACGGC	429
O	y	494	CCACCTTCGAGCGCGGCTCTACTTACCAAGCCGGTGGGGGCTGGGGGGGGCGGCGC	553
D	b	430	CCACCTTCGAGCGCATCTCTACTACTATACGTCCGGGGGGCGGACATCCGCGCGCGGCA	489
O	y	554	ACGTCGCCGCTGACGATCTTCTGGAAGAGTGGCCCTTTCACGGGCTGGGCGCGCGCCG	613
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O	y	614	TGCGACGCTTCGCGGAGAGAGAGGAGCTCCCGGTGCGCGGACGCGCCCTGCCCGGC	673
D	b	550	TGGAGAGATTTCGCGGAGAGAGAGGAGCTTCTCGGGAGAGAGAGCGCCCTTGGCCCGC	609
O	y	674	GCGGCTTGGCGCGGACAGCTGTGGCTCTTTCGAGTTTCCGAGAGCTTCAGGCGCGGC	733
D	b	610	GCGACTTCGACGCGCGCAGAGTGTGGCTCTTTCGAGTACCCCGAGAGCTCGCGGCGGCGC	669
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D	b	952	TGAACCTGATCGACATGTGGCCATCTTCTATTTATCACTCTGGGATACCGAGCTGG	1011
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D	b	1012	CGGAACGACAGGGCAATGACACACGAGGCCATCTCTGTGGCAATCTGAGGGTCATCGCC	1071
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D	b	1072	TGTGTAAGGTCTTCGATCTTCAACCTGTCCGGCCACATCCAAAGGGGCTCGAGATCTCG	1131
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O	y	1394	GAGACATGGAACCCGTCATCTGTGGGTGGCAAGATAGTGGGCTCTGTGTGCATTGGG	1453
D	b	1312	GCGATATGACACCCAGTACCATAGAGGGGGAAGATGTGGGATCTCTGTGTGCATCGCG	1371
O	y	1454	GCGGCTGACATTTTCCCTGCGCGAGTGGCGGTATGTCTCCAAATTTACAGATCTTTAT	1513
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QY 1514 ACCGGAGACAGAGCGGAGAGAGCTGGATGTTCAACCCATGCG 1558
Db 1432 ACCGGAGACAGAGAGAGAGCAATCCAGTACATGACATGCG 1476

RESULT 15
CFU08596 1780 bp mRNA linear MAY 21-DEC-1994
LOCUS Canis familiaris delayed rectifier K+ channel mRNA, partial cds.
DEFINITION U08596
ACCESSION U08596
VERSION U08596.1 GI:475721
KEYWORDS
SOURCE Canis familiaris.
ORGANISM Canis familiaris.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 1780)
AUTHORS Hume, J.R., Sanders, K.M. and Horowitz, B.
TITLE Cloning and characterization of a Kv1.5 delayed rectifier K+
channel from vascular and visceral smooth muscles
JOURNAL Am. J. Physiol. 267 (5 Pt 1), C1231-C1238 (1994)
MEDLINE 95068303
PUBMED 7977686
REFERENCE 2 (bases 1 to 1780)
AUTHORS Overturf, K.E.
TITLE Direct Submission
JOURNAL Submitted (08-APR-1994) Overturf K. E., University of Nevada at
Reno, Department of Physiology, North Virginia St., Reno, NV 89557,
USA

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source Location/Qualifiers
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BASE COUNT 293 a 608 c 577 g 302 t
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Query Match 37.1%; Score 624; DB 4; Length 1780;
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Matches 988; Conservative 0; Mismatches 500; Indels 34; Gaps 3;

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QY 342 CGAGCGGCTGCTCAACGTGGCCGGGCTGCGCTTCAGAGCGCGGCGACAGCTGGG 401
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QY 402 CGCGTCCCGGACACCTGTAGGAGCCAGCGCGCGCGCGCGCTTCAGAGCGAGCG 461
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QY 462 GCCCGGAGTATATTTCTTCACCGGACCGCGCCAGCTTCGAGAGCGCGTCTACTACTA 521
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XX 20-SEP-2001.
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XX 12-MAR-2001; 2001WO-US07735.
PF
XX 10-MAR-2000; 2000US-0188277.
PR 10-MAR-2000; 2000US-0188316.
PR 14-MAR-2000; 2000US-0189139.
PR 14-MAR-2000; 2000US-0189140.
PR 17-MAR-2000; 2000US-0190231.
PR 17-MAR-2000; 2000US-0190401.
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PA (CURA-) CURAGEN CORP.
PI Padigaru M, Vernet CAM, Fernandes E, Shinkets RA, Spaderna SK;
PI mjunider K, Li L;
XX
XX WPI; 2001-570869/64.
DR P-PSDB; AAU08660.
XX
XX Novel polypeptides and nucleic acids homologous to members of collagen,
PT potassium channel, tufellin family of proteins for diagnosing, treating
PT cancer, atherosclerosis, neurological, skin and enamel defect disorders
PT
XX
XX
PS Claim 9; Page 15-16; 128bp; English.
XX
XX The invention relates to isolated NOVX (NOVX1-11) polypeptides and
CC the polynucleotides that encode them. NOVX polypeptides, polynucleotides
CC and anti-NOVX antibodies are useful for treating or preventing a
CC pathology associated with NOVX polypeptide in humans and for treating a
CC syndrome associated with human disease e.g. disorders characterised by
CC altered cell motility, proliferation and migration e.g. cancer,
CC angiogenesis and wound healing (NOVX-3), neurological disorders, e.g.
CC episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's
CC disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,
CC asthma, hypertension and seizure (NOV4), enamel defects, such as
CC amelogenesis imperfecta and disorders involving enamel defects,
CC including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic
CC neurological disorders, e.g. paraneoplastic limbic of brain-stem
CC encephalitis occurring during testicular cancer, diabetes, reproductive
CC health, metabolic and autoimmune disorders, gastrointestinal disorders,
CC immune disorders and autoimmune diseases, respiratory disorders, bone
CC disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell
CC growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and
CC atherosclerosis, abdominal aortic aneurysm and neurological disorders
CC (NOV11). NOVX polypeptide is also useful for identifying an agent that
CC binds to it and a cell expressing NOVX polypeptide is useful for
CC identifying a therapeutic agent for use in treatment of a NOVX related
CC pathology. The antibodies and a polypeptide having 95% sequence identity
CC to NOVX polypeptide are useful for treating a pathological state in a
CC mammal. The present sequence encodes NOV4, a possible voltage gated
CC potassium channel.
XX
XX
SQ Sequence 1747 BP; 255 A; 582 C; 575 G; 335 T; 0 other;
Query Match 100.0%; Score 1680; DB 22; Length 1747;
Best Local Similarity 100.0%; Pred. No. 2, 4e-301;
Matches 1680; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 GTGGCCGGGCTGGCGCTTCGAGACGGCGGGCGGACGCTGGGGCTCCCGGACACTG 420
Db 398 GTGGCCGGGCTGGCGCTTCGAGACGGCGGGCGGACGCTGGGGCTCCCGGACACTG 457
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 DT 13-FEB-2002 (first entry)
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 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
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 PN W0200175067-A2.
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 PD 11-OCT-2001.
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 XX

PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
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 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 XX P-PSDB; ABG14353.
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 1; SEQ ID No 14344; 103bp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations in
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp.wipo.int/pub/published_pcl_sequences](http://wipo.int/pub/published_pcl_sequences).
 XX
 SQ Sequence 1686 BP; 236 A; 545 C; 562 G; 343 T; 0 other;
 Query Match 79.48; Score 1333.6; DB 23; Length 1686;
 Best Local Similarity 99.38; Pred. No. 2.2e-237;
 Matches 1361; Conservative 0; Mismatches 4; Indels 5; Gaps 2;
 Qy 248 CTGGGGCGCGGCTGGGGCGCACAGCTGGTTCGCGGCTCGCGGGGCTGCGCGCCATG 307
 Db 322 CGGGGCGCGGCTGGGGCGCACAGCTGGTTCGCGGCTCGCGGGGCTGCGCGCCATG 381
 Qy 308 GAGCGCGGCTCGCGCGCGCGCTGCGGCTGCGAGCGGCTGCTCAAGCTGGCGG 367
 Db 382 GAGCGCGGCTCGCGCGCGCGCTGCGGCTGCGAGCGGCTGCTCAAGCTGGCGG 439
 Qy 368 GCGTGGCTTGAAGACGCGGGGCGGCAACGCTGGGCGGCTTCCGAGACATGTGTAAGG 427
 Db 440 GCGTGGCTTGAAGACGCGGGGCGGCAACGCTGGGCGGCTTCCGAGACATGTGTAAGG 499
 Qy 428 ACCGAGCGCGCGGCGGCTTCTACGACAGCGCGCGCGAGTATTTCTTCACCGGCG 487
 Db 500 ACCGAGCGCGCGGCGGCGGCTTCTACGACAGCGCGCGCGAGTATTTCTTCACCGGCG 559
 Qy 488 ACCGAGCGCGGCTTGAAGCGCGCTGCTACTACTACCACTCCGGTGGGCGCTGGCGGCG 547
 Db 560 ACCGAGCGCGGCTTGAAGCGCGCTGCTACTACTACCACTCCGGTGGGCGCTGGCGGCG 619
 Qy 548 CGGGCGACGTGGCGCTTGAAGCTTCCCTGGAAGAGGTGGCGCTTACGGGCTGGGCGG 607
 Db 620 CGGGCGACGTGGCGCTTCCCTGGAAGAGGTGGCGCTTACGGGCTGGGCGGCGG 679
 Qy 608 CGGCGCTGACAGCGCTGCGAGAGAGAGGCTCCCGGTGCGCCCGAGCGCCCGCTGCG 667
 Db 680 CGGCGCTGACAGCGCTGCGAGAGAGAGGCTCCCGGTGCGCCCGAGCGCCCGCTGCG 739

QY 668 CCCGCCGCGCTTCCGCCGCCAGCTGTGCTCTTTTCAGATTTCCCGAGAGCTCTCAGG 727
 Db 740 CCCGCCGCGCTTCCGCCGCCAGCTGTGCTCTTTTCAGATTTCCCGAGAGCTCTCAGG 799
 QY 728 CCGCGCGCGTGTCCGCCGAGTCTCGTGTCTGTCATCTCGTCTTCATCTGCTCTTCT 787
 Db 800 CCGCGCGCGTGTCCGCCGAGTCTCGTGTCTGTCATCTCGTCTTCATCTGCTCTTCT 859
 QY 788 GCCTGAGAGAGCGTGTGCTCTTCCGCCGAGAGCGGAGCGGAGCGGCGTGTGCTGTGAG 847
 Db 860 GCCTGAGAGAGCGTGTGCTCTTCCGCCGAGAGCGGAGCGGAGCGGCGTGTGCTGTGAG 919
 QY 848 CCGCAGCGCGCGCGGTGTTCGCCGCTCCGCTGATGATGCTTCACGCCAAATGCCGTGAATC 907
 Db 920 CCGCAGCGCGCGCGCGGTGTTCGCCGCTCCGCTGATGATGCTTCACGCCAAATGCCGTGAATC 976
 QY 908 CACCGCGCGCTGTCTTCATGACCGCTGTCTGTGTGTGAGAGAGCGTGTATTTGTGGT 967
 Db 977 CACCGCGCGCTGTCTTCATGACCGCTGTCTGTGTGTGAGAGAGCGTGTATTTGTGGT 1036
 QY 968 TCTCCCTTGAAGTGTGCTGAGCGCTCTGCTGTCTGTCAGAGCAAGGCTATCTTCTCAAGA 1027
 Db 1037 TCTCCCTTGAAGTGTGCTGAGCGCTCTGCTGTCTGTCAGAGCAAGGCTATCTTCTCAAGA 1096
 QY 1028 AGCTGATGAGACCTCATGATTTTGTGCTATCTCTTCTTGTGTGAGCACTGGCAGCG 1087
 Db 1097 AGCTGATGAGACCTCATGATTTTGTGCTATCTCTTCTTGTGTGAGCACTGGCAGCG 1156
 QY 1088 AGCTGCGCGCGCAGCGAGGGGTGGGCGCAGAGGCCATGTACTGCGCATCTGAGAGTCA 1147
 Db 1157 AGCTGCGCGCGCAGCGAGGGGTGGGCGCAGAGGCCATGTACTGCGCATCTGAGAGTCA 1216
 QY 1148 TCCGATTTGGTGTCTTCCGATTTTCCGATTTTCCGATTTTCCGATTTTCCGATTTTCCGAT 1207
 Db 1217 TCCGATTTGGTGTCTTCCGATTTTCCGATTTTCCGATTTTCCGATTTTCCGATTTTCCGAT 1276
 QY 1208 TCTTGGCGCAGAGCGTTCGGGCTCCATCTGAGCTGAGCGGCGCTCATCTTTTCTCTCT 1267
 Db 1277 TCTTGGCGCAGAGCGTTCGGGCTCCATCTGAGCTGAGCGGCGCTCATCTTTTCTCTCT 1336
 QY 1268 TCATGCGTGTGCTCTCTTTTCCAGCGCGTCTACTTTGCCGAAGTTGACCGGGTGGACT 1327
 Db 1337 TCATGCGTGTGCTCTCTTTTCCAGCGCGCTCTACTTTGCCGAAGTTGACCGGGTGGACT 1396
 QY 1328 CCCATTTTCACTAGCATCCCTGAGTCTCTTGTGAGGGCGGTAGTACCATGACTACAGTTG 1387
 Db 1397 CCCATTTTCACTAGCATCCCTGAGTCTCTTGTGAGGGCGGTAGTACCATGACTACAGTTG 1456
 QY 1388 GCTATGAGACATGAGCACCCTGACCTGTGGGTGGCAAGATAGTGGGCTCTCTGTGCGCA 1447
 Db 1457 GCTATGAGACATGAGCACCCTGACCTGTGGGTGGCAAGATAGTGGGCTCTCTGTGCGCA 1516
 QY 1448 TTGCGGGCGTGTGCTATTTTCCCTGCGAGTGCCTCATTTGTCTCAATTTCACTACT 1507
 Db 1517 TTGCGGGCGTGTGCTATTTTCCCTGCGAGTGCCTCATTTGTCTCAATTTCACTACT 1576
 QY 1508 TTATATACCGGGAGACAGAGGGGGAAGAGAGCGATGTTTCAACCCATGTGAGCATGAGC 1567
 Db 1577 TTATATACCGGGAGACAGAGGGGGAAGAGCGATGTTTCAACCCATGTGAGCATGAGC 1636
 QY 1568 CTTTGTGGCGCTGTGAGGAGGCAAGGCAATGTGGGCGCTGTGTGAGCGGGAG 1617
 Db 1637 CTTTGTGGCGCTGTGAGGAGGCAAGGCAATGTGGGCGCTGTGTGAGCGGGAG 1686

RESULT 4
 ABL57038
 ID ABL57038 standard: cDNA: 1341 BP.

XX ABL57038;
 AC
 XX
 DT 22-JUL-2002 (first entry)
 XX

DE Human potassium channel 12189 partial cDNA.
 XX
 KW potassium channel; ion transport; 12189; nootropic; anticonvulsant;
 KW neuroprotective; antiparkinsonian; hypotensive; neuroleptic;
 KW antidepressant; antimanic; tranquilizer; anorectic; antimigraine;
 KW antiarteriosclerotic; vasotropic; vulnerary; antiarrhythmic;
 KW cardiatic; antiinflammatory; cyostatic; osteopathic; hepatotropic;
 KW antidiabetic; immunosuppressive; antiarthritic; antirheumatic;
 KW antipsoriatic; antihypoid; antilucer; dermatological; antianaemic;
 KW antistatic; antiallergic; ophthalmological; immunomodulator;
 KW analgesic; virucide; human; gene therapy; gene; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT 1..1341
 FT CDS
 FT /tag="a
 FT /product="12189"
 FT /partial
 FT /note="The CDS does not include a start codon"
 XX
 PN WO200194390-A2.
 XX
 PD 13-DEC-2001.
 PD 06-JUN-2001; 2001MO-US18340.
 PF 06-JUN-2000; 2000US-209845P.
 PR 06-JUN-2000; 2000US-209845P.
 XX
 PA (MIL-) MILLENNIUM PHARM INC.
 PI
 PI Curtis RAJ;
 XX
 DR WPI: 2002-401589/43.
 DR P-PSDB: ABB76166.
 DR
 PT New potassium channel family member polypeptide and polynucleotide,
 PT useful for diagnosing, treating viral diseases, neurological, cardiac,
 PT cellular proliferative or differentiative, bone, immune, liver and
 PT metabolic disorders.
 PT
 PS
 PS Claim 1: Page 135-136; 158pp; English.
 XX
 CC The present sequence is that of a partial cDNA for human 12189
 CC (see ABB76166), a novel potassium channel family member. 12189
 CC contains a potassium channel tetramerisation domain, an ion
 CC transport protein domain and a core membrane region including 6
 CC transmembrane domains. The invention provides human potassium
 CC channel 52906, 33408 and 12189 nucleic acids and proteins, as well
 CC as antisense nucleic acid molecules, recombinant expression vectors,
 CC host cells, transgenic animals, fusion proteins, antigenic peptides
 CC and antibodies. Also claimed are: a method for detecting the
 CC presence of a 52906, 33408 or 12189 nucleic acid; a method for
 CC modulating the activity of a 52906, 33408 or 12189 polypeptide using
 CC a compound that binds the polypeptide; a method for identifying a
 CC compound which modulates the activity of the polypeptide; a method
 CC of treating or preventing an ion flux-related disorder using an
 CC agent that modulates the activity or expression of a 52906 or
 CC 12189 polypeptide or nucleic acid, especially a peptide,
 CC phosphopeptide, small molecule, antibody, antisense molecule,
 CC ribozyme, a triple helix molecule, or a 52906 or 12189 nucleic
 CC acid. The ion flux-related disorders include: potassium channel
 CC associated disorders, such as neurological disorders and central
 CC nervous system disorders such as cognitive and neurodegenerative
 CC disorders e.g. Alzheimer's disease, Parkinson's disease, senile
 CC dementia, Huntington's disease, Gilles de la Tourette's syndrome,
 CC multiple sclerosis, progressive supranuclear palsy, epilepsy,
 CC Jacob-Creutzfeldt disease, autonomic function disorders such as
 CC hypertension and sleep disorders, neuropsychiatric disorders such
 CC as depression, schizophrenia, mania, anxiety disorders or phobic
 CC disorders, learning or memory disorders, amnesia or age-related
 CC memory loss, attention deficit disorder, obsessive-compulsive
 CC disorder, migraine or obesity; cardiac-related disorders such as

CC arteriosclerosis, ischaemia reperfusion injury, restenosis, arterial
 CC inflammation, tachycardia, congestive heart failure, myocardial
 CC infection and arrhythmia. The polypeptides and nucleic acids are
 CC also useful as diagnostic targets and therapeutic agents for:
 CC controlling cellular proliferative and/or differentiative disorders
 CC e.g. haematopoietic neoplastic disorders, carcinoma and sarcoma;
 CC disorders associated with bone metabolism such as osteoporosis,
 CC rickets, osteopenia, cirrhosis, hyperparathyroidism, idiopathic
 CC hypercalcaemia; immune disorders such as autoimmune disorders,
 CC diabetes mellitus, arthritis, including rheumatoid arthritis,
 CC osteoarthritis and psoriatic arthritis, multiple sclerosis,
 CC myasthenia gravis, autoimmune thyroiditis, ulcerative colitis,
 CC psoriasis, Sjogren's syndrome, dermatitis, Crohn's disease, asthma,
 CC allergic asthma, conjunctivitis, aplastic anaemia, Grave's disease,
 CC chronic active hepatitis, autoimmune uveitis, scleroderma; liver
 CC disorders including storage disorders such as Gaucher's disease,
 CC glycogen storage disease, haemochromatosis and peroxisomal
 CC disorders; viral diseases; pain; or metabolic disorders such as
 CC obesity, anorexia nervosa, cachexia, lipid disorders and diabetes.

XX Sequence 1341 BP; 190 A; 443 C; 411 G; 297 T; 0 other;

Query Match 78.7%; Score 1321.6; DB 24; Length 1341;

Best Local Similarity 99.5%; Pred. No. 3.5e-235; Mismatches 1337; Conservative 0; Indels 3; Gaps 1;

DB 1 TGGTCGAGAGGCGGTGTGTCTCAACGTGCGCGGCTGCGCTTCGAGACGCGGGCGGACG 60
 QY 337 TGGTCGAGAGGCGGTGTGTCTCAACGTGCGCGGCTGCGCTTCGAGACGCGGGCGGACG 396
 QY 397 CTGGGCGGCTTCCCGGACACTCTGTAGGGACCCAGCGCGCGCGGCTTCTTACGAC 456
 DB 61 CTGGGCGGCTTCCCGGACACTCTGTAGGGACCCAGCGCGCGGCTTCTTACGAC 120
 QY 457 GACGCGCGCGGACAGTATTTCTTCGACCGGACCGGCCAGCTTCGAGCGCGCTCTAC 516
 DB 121 GACGCGCGCGGACAGTATTTCTTCGACCGGACCGGCCAGCTTCGAGCGCGCTCTAC 180
 QY 517 TACTACAGTCCGTGGGCGGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 576
 DB 181 TACTACAGTCCGTGGGCGGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
 QY 577 GAAGAGTGGCTTCTACGGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 636
 DB 241 GAAGAGTGGCTTCTACGGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 QY 637 GCGTGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 696
 DB 301 GCGTGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
 QY 697 CTGCTTTTGAAGTTTCCGAGAGCTCTAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 756
 DB 361 CTGCTTTTGAAGTTTCCGAGAGCTCTAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 QY 757 CTGCTATCTCTCTCTCATCGTCTTCTTGGCTGAGACGCTGCTGACTTCCGGAC 816
 DB 421 CTGCTATCTCTCTCTCATCGTCTTCTTGGCTGAGACGCTGCTGACTTCCGGAC 480
 QY 817 GACCGGAGGCGAGGGGCTTGTGCTGCGACGCGGACGCGGCGGCGGCTTCCCGGCTCGG 876
 DB 481 GACCGGAGGCGAGGGGCTTGTGCTGCGACGCGGACGCGGCGGCGGCGGCGGCGGCGG 537
 QY 877 CTGAATGGCTCAAGCCAAATGCTGGAATCAACCCGCGCTTCAATGACCCGTTG 936
 DB 538 CTGAATGGCTCAAGCCAAATGCTGGAATCAACCCGCGCTTCAATGACCCGTTG 597
 QY 937 TTGCTGGTGAAGAGCTGTATTTGTGTTCTCTTGAAGCTGTGTAAGCGCTCTG 996
 DB 598 TTGCTGGTGAAGAGCTGTATTTGTGTTCTCTTGAAGCTGTGTAAGCGCTCTG 657
 QY 997 GTCTGTCAAGCAAGGCTATCTTCAAGAAGTGATGAACCTATCATGATTTTGTGCT 1056
 DB 658 GTCTGTCAAGCAAGGCTATCTTCAAGAAGTGATGAACCTATCATGATTTTGTGCT 717

QY 1057 ATCTTCCCTACTTTTGGGCACTGGGACCGAGCTGGCCCGGACGAGGGGTGGCCAG 1116
 DB 718 ATCTTCCCTACTTTTGGGCACTGGGACCGAGCTGGCCCGGACGAGGGGTGGCCAG 777
 QY 1117 CAGCCATGTCTACCTGGGCTCTAGAGTATCCGATTTGGTGGCTGTCTTCCGATCTTC 1176
 DB 778 CAGCCATGTCTACCTGGGCTCTAGAGTATCCGATTTGGTGGCTGTCTTCCGATCTTC 837
 QY 1177 AAGCTGCCGCGGCACTCAAGAGGCTGCAATTTTGGGCGAGAGCTTGGGCGCTCCATG 1236
 DB 838 AAGCTGCCGCGGCACTCAAGAGGCTGCAATTTTGGGCGAGAGCTTGGGCGCTCCATG 897
 QY 1237 CGTAGAGTGGGCTCTCTCATCTTTTCTCTTCATTCGCTGTGCTCTTTTCCAGCGCC 1296
 DB 898 CGTAGAGTGGGCTCTCTCATCTTTTCTCTTCATTCGCTGTGCTCTTTTCCAGCGCC 957
 QY 1297 GTCTACTTTGGCGAAGTTGACCGGGGTGACTCCCATTTCACTACATCCCTGATCTTC 1356
 DB 958 GTCTACTTTGGCGAAGTTGACCGGGGTGACTCCCATTTCACTACATCCCTGATCTTC 1017
 QY 1357 TGTGGGCGGTAGTACCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1416
 DB 1018 TGTGGGCGGTAGTACCATGATGATGATGATGATGATGATGATGATGATGATGATG 1077
 QY 1417 GGTGGCAAGATAGTGGGCTCTCTGTGTGTCATTTGGGCGGCGGCTGTGACTATTTCCCTGCA 1476
 DB 1078 GGTGGCAAGATAGTGGGCTCTCTGTGTGTCATTTGGGCGGCGGCTGTGACTATTTCCCTGCA 1137
 QY 1477 GTGCCGCTCATTTCTCTCAATTTAGCTACTTTTATACCGGGGAGACAGAGGGGAGAG 1536
 DB 1138 GTGCCGCTCATTTCTCTCAATTTAGCTACTTTTATACCGGGGAGACAGAGGGGAGAG 1197
 QY 1537 GCTGGATGTTTCAAGCATGTGAGATGATGATGATGATGATGATGATGATGATGATGAT 1596
 DB 1198 GCTGGATGTTTCAAGCATGTGAGATGATGATGATGATGATGATGATGATGATGATGAT 1257
 QY 1597 GGGGGCTGTGTGAGCGGAGAGTACGTGAGCTTACCTCCACTCTTGGGACCCCGCAG 1656
 DB 1258 GGGGGCTGTGTGAGCGGAGAGTACGTGAGCTTACCTCCACTCTTGGGACCCCGCAG 1317
 QY 1657 GAACACCTGTGTACCGGAAGTGTGA 1680
 DB 1318 AAACACCTGTGTACCGGAAGTGTGA 1341

RESULT 5

AAAT04953 standard; cDNA; 1598 BP.

AAAT04953;

11-APR-1996 (first entry)

Mouse Kv1.7 voltage-gated potassium channel coding sequence.

Mouse Kv1.7 voltage-gated potassium channel; insulin antagonist drug screening;

non-insulin-dependent diabetes mellitus; ds.

Mus musculus.

Location/Qualifiers

Key 1..1598

FT CDS /+tag= a

FT /note="specification states sequence is 1599.

PN MO9523858-A1.

PD 08-SEP-1995.

PF 23-FEB-1995; 95WO-0502221.

XX 10-AUG-1994: 94US-0288405.
PR 04-MAR-1994: 94US-0207401.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Chandy G, Chandy KG, Gutman GA, Kalman K;
XX
DR WPI: 1995-320573/41.
P-PSDB: AAR82937.
XX
XX New voltage-gated potassium channel gene - used to identify
PT material(s) which can increase insulin release e.g. for treating
XX non-insulin dependent diabetes mellitus.
PS Claim 1: Page 22-23; 38pp; English.
XX
XX The DNA encodes a mouse Kv1.7, which is a Shaker-related voltage-
CC gated potassium channel. It may be used in drug screening for
CC identification of therapeutics which modulate the channel and,
CC therefore, modulate insulin secretion. Selective antagonists
CC increase insulin release and thereby reduce hyperglycaemia
CC associated with non-insulin-dependent diabetes mellitus.
SQ Sequence 1598 BP: 232 A; 521 C; 502 G; 343 T; 0 other:

Query Match 63.6%; Score 1068; DB 16; Length 1598;
Best Local Similarity 81.5%; Pred. No. 2.4e-188;
Matches 1288; Conservative 0; Mismatches 280; Indels 12; Gaps 4;

QY 100 CGGGGAGGCGAGGCGGGGCGTCCGCGAGAGGCGGCGGTCGCGCCCTGCGCCCTCCG 159
DB 31 CGGAAAGGCGCGGCGGCGAGTGTTCACAGGTGTGGAACGCGAAGGCGCGCCCTAGC 90
QY 160 CCGCGCGGGGTACAGTGCCTCCCTGCGCGCCCTAGCGCCCTCGGGGTATTTTAC 219
DB 91 CCGCGGGGGTAAACCGGCGCCCTCCCGCGCGCTGCGGCGACTTTCATGCTATTTT 150
QY 220 GGGCGGACACCGGACACCGGAGTGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 219
DB 151 ACCCGCGGACCGGACACCGGAGTGGGGTGGTGGCGGCGCGCGCGCGCGCGCGCG 210
QY 280 GCGGGGCGCGGGGCG 339
DB 211 ACCGGCG 267
QY 340 TCGGAGCGCGGTGCTCAACGTGGCGGGGTGGCTTGAAGCGCGCGCGCGCGCGCG 399
DB 268 TCGGAGCGCGGTGCTCAACGTGGCGGGGTGGCTTGAAGCGCGCGCGCGCGCGCG 327
QY 400 GCGCGGTCGCGGACACCTGTGCTAGGGGACCGGCGCGCGCGCGCGCGCGCGCGCG 459
DB 328 GCGCGGTCGCGGACACCTGTGCTAGGGGACCGGCGCGCGCGCGCGCGCGCGCGCG 387
QY 460 GCGCGCGGAGTATTTTTCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 519
DB 388 GCGCGCGGAGTATTTTTCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 447
QY 520 TACCACTGCGGTGGCGGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 579
DB 448 TACCACTGCGGTGGCGGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 507
QY 580 GAGGTGGCGGTTCGAGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 639
DB 508 GAGGTGGCGGTTCGAGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 564
QY 640 TCGCGCGGTGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 699
DB 565 TCGCGCGT---GCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 618
QY 700 CTTTTCGAGTTCGCGAGAGCTCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 759
DB 619 CTTTTCGAGTTCCTGAGAGCTCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 678

QY 760 GTGATCGTCTCCATCGTGTCTTCTGCGCGAGCGCGCGCGCGCGCGCGCGCGCG 819
DB 679 GTGATCGTCTCCATCGTGTCTTCTGCGCGAGCGCGCGCGCGCGCGCGCGCG 738
QY 820 CGGAGCGGCGGCGGTGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 879
DB 739 CGGAGCGGCGGCGGTGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 798
QY 880 AATGCTCCAGCGCAATGCTGGAATCCAGCGCGCGCGCGCGCGCGCGCGCGCG 939
DB 799 AATGCTCCAGCGCGCAATGCTGGAATCCAGCGCGCGCGCGCGCGCGCGCGCG 858
QY 940 GTGCTGAGAGCGGTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 999
DB 859 GTGCTGAGAGCGGTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 918
QY 1000 TGTCCAGCGAGCGTATCTTCTCAAGAAAGTATGATGATGATGATGATGATG 1059
DB 919 TGTCCAGCGAGCGTATCTTCTCAAGAAAGTATGATGATGATGATGATGATG 978
QY 1060 CTTCCCTACTTGTGCGACTGGCGACCGAGCTGGCGCGCGCGCGCGCGCGCG 1119
DB 979 CTTCCCTACTTGTGCGACTGGCGACCGAGTGTAGCCGCGCGCGCGCGCGCGCG 1038
QY 1120 GCGATGTCAGTGGCGCATCCGATGATGATGATGATGATGATGATGATGATG 1179
DB 1039 GCGATGTCAGTGGCGCATCCGATGATGATGATGATGATGATGATGATGATG 1098
QY 1180 CTTCCCGGCGACGCAAGGCGCTGCAAAATCTTGGCGCGAGCGCGCGCGCGCG 1239
DB 1099 CTTCCCGGCGACGCAAGGCGCTGCAAAATCTTGGCGCGAGCGCGCGCGCGCG 1158
QY 1240 GAGCTGGCGCTCTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1299
DB 1159 GAGCTGGCGCTCTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1218
QY 1300 TACTTGGCGAGTGGCGCGGCGGAGCTCCATTTGATGATGATGATGATGATG 1359
DB 1219 TACTTGGCGAGTGGCGCGGCGGAGCTCCATTTGATGATGATGATGATGATG 1278
QY 1360 TGGCGGTAAGTACATGATGATGATGATGATGATGATGATGATGATGATGAT 1419
DB 1279 TGGCGGTAAGTACATGATGATGATGATGATGATGATGATGATGATGATGAT 1338
QY 1420 GCGAAGTATGCGGTCTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1479
DB 1339 GCGAAGTATGCGGTCTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1398
QY 1480 CCGGTATGTCGCAATTTGATGATGATGATGATGATGATGATGATGATGATG 1539
DB 1399 CCGGTATGTCGCAATTTGATGATGATGATGATGATGATGATGATGATGATG 1458
QY 1540 GGGATGTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 1599
DB 1459 GGGATGTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 1518
QY 1600 GGGCTGTGAGGAGGAGTACTGAGTACCACTTCCACTTGGCGACCGCGAGGAA 1659
DB 1519 GGGCTGTGAGGAGTACTGAGTACCACTTCCACTTGGCGACCGCGAGGAA 1578
QY 1660 CACCTGGTACCGAGGTG 1679
DB 1579 CACCTGGTACTGAGGTG 1598

RESULT 6
AAD28734
ID AAD28734 standard; DNA: 691 BP.
XX
XX AAD28734;
XX
DT 07-MAY-2002 (first entry)

XX Human ion channel gene, ion-166.
 DE
 XX
 KW Human: ion channel; neurological disorder; psychiatric disorder;
 KW Schizophrenia; attention deficit hyperactivity disorder; depression;
 KW Proliferation disease; migraine; ischemia; neurodegenerative disease;
 KW macular degeneration; Alzheimer's disease; congestive heart failure;
 KW glaucoma; Parkinson's disease; cardiovascular disease; arrhythmia;
 KW high blood pressure; restenosis; metabolic disease; neuroprotective;
 KW obesity; hormonal disorder; polycystic ovarian syndrome; gene therapy;
 KW alopecia; anxiety; stroke; neuroleptic; nootropic; cancer; diabetes; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 566..658
 FT /tag= a
 FT /product= "Human ion channel ion-166"
 FT /note= "CDS does not include start and stop codon"
 FT /partial
 XX
 XX MO200192303-A2.
 XX
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US16967.
 XX
 XX 26-MAY-2000; 2000US-207119P.
 PR 26-MAY-2000; 2000US-207152P.
 PR 26-MAY-2000; 2000US-207257P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Benjamin CW, Roberts SL, Karnovsky AM, Ruble CL, Gotow LF;
 XX
 XX WPI: 2002-147617/19.
 DR P-SDB: AAEL8034.
 XX
 PT New human ion channel polypeptides and nucleic acids, useful for
 PT treating or diagnosing neurological, psychiatric or neurodegenerative
 PT diseases, e.g. depression, anxiety, stroke, ischemia, or Alzheimer's or
 PT Parkinson's disease
 XX
 XX Claim 1; Page 76; 126pp; English.
 PS
 XX
 XX The invention relates to ion channel polypeptides designated as ion-x
 CC (where x is 157-175) and their corresponding nucleic acids. The ion-x
 CC sequences and their modulators are useful for the treatment of human
 CC diseases and conditions such as neurological or psychiatric disorders.
 CC These compounds are useful for treating schizophrenia, attention deficit
 CC hyperactivity disorder, depression, anxiety, stroke, migraine, ischemia
 CC or neurodegenerative disease (e.g. macular degeneration, Alzheimer's
 CC disease, glaucoma, or Parkinson's disease). The compounds that modulate
 CC ion channels can be used for treating of cardiovascular diseases (e.g.
 CC congestive heart failure, arrhythmia, high blood pressure or restenosis),
 CC metabolic diseases and disorders (e.g. diabetes or obesity), hormonal
 CC disorders (e.g. polycystic ovarian syndrome or alopecia) and
 CC proliferation diseases and cancers. The ion channels are also useful as
 CC targets for discovering ligands or drugs to treat many diverse disorders
 CC and defects. The ion-x sequences and their modulators may also be used
 CC in diagnostic assays for such diseases or conditions. Ion-x nucleic
 CC acids are used in gene therapy. The present sequence is a DNA encoding
 CC human ion channel designated as ion-166.
 XX
 XX Sequence 691 BP; 113 A; 207 C; 185 G; 186 T; 0 other;
 SQ
 Query Match 35.8%; Score 601.4; DB 24; Length 691;
 Best Local Similarity 99.0%; Pred. No. 3..2e-102;
 Matches 605; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 854 CGGGCCGGTTCCTCCGCTGATGATGCTCCAGCCAAATGCTCGGAATCCACCC 913
 DB 81 CTTCCCTGAGTTCCTCCGCTGATGATGCTCCAGCCAAATGCTCGGAATCCACCC 140

QY 914 GCTGCTCCCTTCATGACCCGTTCTTCTGTGTGAGACGCTGTGATTTGTGTTCTCT 973
 DB 141 GCTGCTCCCTTCATGACCCGTTCTTCTGTGTGAGACGCTGTGATTTGTGTTCTCT 200
 QY 974 TTGAGCTGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1033
 DB 201 TTGAGCTGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 260
 QY 1034 TGAACCTCATGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1093
 DB 261 TGAACCTCATGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 320
 QY 1094 CCCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1153
 DB 321 CCCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 380
 QY 1154 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1213
 DB 381 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 440
 QY 1214 GCCAGAGCTTCGAGGCTTCATGAGCTGAGCTGAGGCTGCTGATTTTCTCTTCATCG 1273
 DB 441 GCCAGAGCTTCGAGGCTTCATGAGCTGAGCTGAGGCTGCTGATTTTCTCTTCATCG 500
 QY 1274 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1333
 DB 501 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 560
 QY 1334 TCACTAGATCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1393
 DB 561 TCACTAGATCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 620
 QY 1394 GAGACATGGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1453
 DB 621 GAGACATGGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 680
 QY 1454 GCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1464
 DB 681 GCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 691
 RESULT 7
 ABN95856 standard; DNA; 2867 BP.
 ID
 XX
 XX ABN95856;
 AC
 XX
 DT 13-AUG-2002 (first entry)
 XX
 XX Gene #2354 used to diagnose liver cancer.
 DE
 XX
 KW Gene: liver cancer; ds: hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.
 XX
 OS Homo sapiens.
 XX
 PN WO200229103-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 02-OCT-2001; 2001WO-US30589.
 XX
 PR 02-OCT-2000; 2000US-237054P.
 XX
 PA (GENE-) GENE LOGIC INC.
 PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
 DR WPI: 2002-426119/45.
 PT Diagnosing and detecting the progression of liver cancer,


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QY 1348 GAGTCTTCGTGGGCGGTATGTCACCAATGACTAAGTTGGCTATGGAACAATGGCACCC 1407
Db 1633 GAGCCTTCCTGTGGGCGAGTGCTACCATTGACCACTGTGGGCTACGGGACATGAAGCCC 1692
QY 1408 GTCACTGTGGGTGCAGAAATAGTGGGCTCTCTGTGTGCATTTGCCGGGCTGTGTAATT 1467
Db 1693 ATCACTGTGGGGGGCAAAATCGTGGGCTGCGTGTGGCATATGGCGGGGTCTCTACACATT 1752
QY 1468 TCCCTGCCAGTGGCCGCTGATTTGTCTCCAAATTTTCAGCTACTTTTATCAGCGGAGACAGAG 1527
Db 1753 GCCCTGCTGTGCCCGTATGCTCTCAACTTCAACTACTTCTACACCCGGGAAACGAT 1812
QY 1528 GGCGAAGAGGCTG 1540
Db 1813 CACGAGAGCCGG 1825

RESULT 9
AAH21452
ID AAH21452 standard; DNA; 1836 BP.
XX AAH21452;
AC
XX
XX 18-SEP-2001 (first entry)
DE Human Kvl.5 DNA.
XX
XX Inhibitor; eukaryotic; potassium channel; TRK1; TRK2; TOK1;
KW activator; ds.
OS Homo sapiens.
XX
XX WO200151519-A2.
PD 19-JUL-2001.
PE 05-JAN-2001; 2001WO-EP00055.
PR 11-JAN-2000; 2000DE-1000651.
PA (AVET ) AVENTIS PHARMA DEUT GMBH.
PI Leberger E, Leeuw T, Ritscher A;
DR WPI: 2001-442137/47.
XX
XX This sequence represents a novel method for identifying inhibitors or
XX activators (A) of a eukaryotic potassium channel (KC) by applying a test
XX compound to a mutant Saccharomyces cerevisiae cell in which: (I) the
XX three endogenous KC (TRK1, TRK2 and TOK1) are not expressed; but (II) a
XX eukaryotic KC is expressed heterologously, where the effect of the
XX compound on the eukaryotic KC is then determined. The method is used to
XX identify inhibitors or activators (A) of a eukaryotic potassium channel.
XX (A) are potentially useful as pharmaceuticals. The method is easily
XX automated for parallel processing of many samples, using either different
XX concentrations of test compounds and/or different levels of heterologous
XX gene expression. It allows identification of compounds that inhibit human
XX KC selectively. This sequence represents the human Kvl.5 encoding DNA
XX described in the method of the invention.
XX
XX Sequence 1836 BP: 323 A; 614 C; 580 G; 319 T; 0 other:
XX
Query Match 35.0%; Score 588.2; DB 22; Length 1836;
Best Local Similarity 68.7%; Pred.No. 9,3e-100;
Matches 875; Conservative 0; Mismatches 353; Indels 45; Gaps 3

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Db	322	GACCAGGCTCTGGGACAGGGGCTCCCTGACACACAGGCGGTCCACATCAATCTCCGG	381
Qy	370	CTGCGCTTTCGAGAGACGGGGGCGGCACGCTGGGCGGCTTCCGAGACTCTGCTAGGGAC	429
Db	382	CTGGCGTTTGGAGACGAGCTGGGCGACCTCGGCGAGTTCCCAACACTCTCTGGGGAC	441
Qy	430	CCAGCGGGCGGGCGGCTTCTACAGACGACGGCGCGGAGATATTTCTTGACCGGAC	489
Db	442	CCCCCAAGGGCGCTGCGTACTTCGACCCCTGAGGAAAGAACTACTTCTTCACGCGCAAC	501
Qy	490	CGGGCCAGCTTCGACGCGCGTCTCTACTACACATCCGCTGGGGGCGCTGGGCGGCG	549
Db	502	CGGGCCAGCTTCGACGCTATCTCTACTACCACTCCGGGGCGGCTCTGGAGG---G	558
Qy	550	GGCGGCTGGCGGCTCGACGCTTCTCTGGAAGAGTGGGCTTCTACGGGCTGGGCGGCG	609
Db	559	GTCACAGCTTCCGAGACGTTGGGGGACAGATACGCTTCTACAGCTGGGGGACGAG	618
Qy	610	GCCCTGGACGCTCGGGCGAGGACGAGGGCTGGCCGCGCCCGAGGCGCCCTCTGGCC	669
Db	619	GCCATGAGAGGCTTCCCGCGAGATGAGGGCTTCATTAAAGAGAGAGAGGCGCTGGCC	678
Qy	670	CGCGGCGCTTCGGCGCGGCGGAGCTGTGAGTGCCTTTTGAGTTTCCGAGAGCTCTAGGCG	729
Db	679	CGCACACAGTTTCAGGGCGCACGGGTGTGGCTTATTTTGAATATCCGAGAGCTCTGGTCC	738
Qy	730	GGCGGCGTGTGCGCGGCTAGTACTCCGCTGGTGCATCCCTGCTCCATCGTCTCTTCGC	789
Db	739	GGCGGGGCGATCGGCATCGTCTGGTCTGGTTATCTCATCTCATATCACTTCTGCG	798
Qy	790	CTGACAGAGCTGCTGACTTCCCGGACGACCGCGACGGCGAGGGGCTGCTCTCAGCC	849
Db	799	TTCGAGACCCCTGCTGAGTTTCAGGAGATGAACGTAAGCTCTCGCCACCTCCGGCGGCC	858
Qy	850	GCACGCGGCGCGGTTCGCCGCGCGCTGAATGG-----CTCC	888
Db	859	CACCAAGCTCCCGCGGCCCTCTGGGGCCACGGAGCGGGGTATGGCCCCCGCTCT	918
Qy	889	AGCCAAATGCTTGGAAATCCACCCCGGCTTCCCTTCAATAGACCGTCTTCTGCTGGAG	948
Db	919	GGCCCTACGGTGGAGCGGCTCTGCGCCAGAGACCCCTGGCGGACCCCTTCTTCAATCGTAGG	978
Qy	949	ACGCTGTGATTTGTGGTCTCTCTTTGAGCTGGTGTACGGCTCTGTGCTGTCCAAAG	1008
Db	979	ACCAAGTGGATCTGTTCACCTTCCTGACCTCTCTGTCGGCTTCTTCGCTGCCCGACG	1038
Qy	1009	AAGGCTATCTTCTTCAAGAACGTAATGAACTCATGATTCGATTTGTGGCTATCTTCCCTAC	1068
Db	1039	AAGGCAAGGTTCTCCGGAACATCATGAATCATGATGTGTGGCCATCTTCCCTAC	1098
Qy	1069	TTTGTGGACATGGGACACGAGCTGGCGCGGACGAGGGGTGGG-----	1113
Db	1099	TTTCATCACCTCGGGACACCGAATCTGGACAGACAGCAAGGGGCGCGAGGGCGGAC	1158
Qy	1114	-----CAGCAGGCGCATGTCATCTGGCCATCTCTGAGAGTCATCCGATGGCTGCTCTTC	1167
Db	1159	AATGGGACGAGGCGCATGCTCCCTGGGCGATCTCCGAGTCATCCGCTGGCTGGGGTGTTC	1218
Qy	1168	CGCATTTTCAAGCTGTCCCGGCACTAAAGGGCTTCAAAATCTTGGGCGCAAGCGTTTGG	1227
Db	1219	CGCATCTTCAAGGCTTCCCGCACTCCAAAGGGGCTCAAGATCCTGGGCAAGACTTTTGA	1278
Qy	1228	GGCTTCAAGCGTGGGCGCTCTCTCATTTTCTTCTTCATCGGTTGGTCTCTCTT	1287
Db	1279	GGCTTCAAGGAGGAGCTGGGGGCTGTCTATCTTCTCTTCTTATCGGGGTCACTCTCTTC	1338
Qy	1288	TCCAGCGCGCTTACTTTGCCGAGATTGACCGGGGTGAGCTCCCATTTTCACTAGATCCCT	1347
Db	1339	TCCAGTGGCTGTACTTCCGAGAGGGGTACAAACAGGAACCATTTCTGTGATCTCT	1398
Qy	1348	GAGTCTTCTTGGTGGGCGGTATGACCACTACTTACAGTTGGCTATGGAGACATGGCACCC	1407

DB 2578 ATACGCTGACATCTTACCTGTCACATTTGAGAGCAAGATCGTGCGTCTGTCGCAT 2637
1449 TCGGGCGCTGCTACTATTTTCCCTGCCAGTGCCTGCATATGTCATTTCCAAATTTACACTT 1508
DB 2638 CGTGTGTGTGTACATTTGCGCTGCCGCTACCTGTCATTTGTCCATTTCAACTATTTT 2697
QY 1509 TTATCAACCGGAGACAGAGCGGAGAGGCTGGGATGTCAGCATGT 1556
DB 2698 CTACCCACCGAAGCTGAGGGGAGAGGAGCGCTCAGTTCCTCATGT 2745
RESULT 11
AB019704
ID AB019704 standard; DNA; 994 BP.
XX
AC AB019704;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 6295.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
XX
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guelty D;
XX
DR WPI: 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC AB013410-AB013412 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
XX Sequence 994 BP; 131 A; 152 C; 380 G; 331 T; 0 other;

Query Match 28.9%; Score 485; DB 24; Length 994;
Best Local Similarity 74.2%; Pred. No. 1e-80;
Matches 676; Conservative 0; Mismatches 185; Indels 50; Gaps 3;
QY 2 TGAGAGACCCAGACAGATCCCGGCGGACAGAGGACGAGAAAGGAGACCCGGG 61
DB 71 TGAGAGACCTAGATAGATTTTGGGCGTAGAAGACGAGAGAAAGGAGATTTGGGA 130
QY 62 CGGAAAGCGGACAGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 121
DB 131 CGGAAAGCGGAGTAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 190
QY 122 CCGGCGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 181
DB 191 TTTTTCGCGCTTTTATGCTTTTGTGCGGCTTTTATTTTATGCGCGGATATCGGA 250
QY 182 CTCCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
DB 251 TTTTTCGCGCTTTTATGCTTTTGTGCGGCTTTTATTTTATGCGCGGATATCGGA 310
QY 241 CACGCGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 258
DB 311 TATCGGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 370
QY 259 -GTGCGGCGCACAGCTGCGGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 313
DB 371 CGGCGCTGGGCGGCTTATACGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGG 430
QY 314 CGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 373
DB 431 CGGTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 488
QY 374 GCTTCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 433
DB 489 GTTTCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 548
QY 434 CGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 493
DB 549 CGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 608
QY 494 CCAAGCTTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 553
DB 609 TTAGCTTCGACGCTGCTTTTATTTATTTATTTATTTATTTATTTATTTATTTAT 668
QY 554 ACCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 613
DB 669 ACCTGCTGCTTCGACGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 728
QY 614 TGGCAGCGCTTGGCGGAGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 673
DB 729 TGTACGCTTGGCGGAGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 788
QY 674 GCGCCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 733
DB 789 GCGCTTTCGCTGCTTGTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTT 848
QY 734 GCGTTCGCGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 793
DB 849 GCGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 908
QY 794 AGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 853
DB 909 AGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 968
QY 854 CCGGCGGCGGCGG 864
DB 969 TCGGTTCCGGG 979
RESULT 12
AB019705/c
ID AB019705 standard; DNA; 994 BP.
XX

AC	ABQ19705;
XX	
DT	12-JUL-2002 (first entry)
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 6296.
XX	
KM	Human: cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW	drug; side effect; cancer; central nervous system; cardiovascular;
KM	gastrointestinal; respiratory system; single nucleotide polymorphism;
XX	SNP; cell differentiation; ds.
OS	Homo sapiens.
XX	
PN	WO200218632-A2.
PD	
XX	
PF	01-SEP-2001; 2001MO-EPI0074.
PR	
XX	01-SEP-2000; 2000DE-1043826.
PR	05-SEP-2000; 2000DE-1044543.
PA	(EPig-) EPIGENOMICS AG.
PI	
DR	Olek A, Piepenbrock C, Berlin K, Guetig D;
PT	WPI: 2002-371829/40.
XX	
PS	Determining the degree of cytosine methylation in genomic DNA, useful
XX	for diagnosis and prognosis, comprises selective hybridization of
XX	amplicons from chemically treated DNA -
XX	
FL	Claim 12; 56pp + Sequence Listing; 56pp; German.
CC	This invention describes a novel method for determining the degree of
CC	methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC	genomic sample of DNA. The sample is treated chemically to convert in a
CC	cytosine (C) but not methylated C, to uracil, then part of the genomic
CC	DNA that contains the target C is amplified to form a labeled amplicon.
CC	The amplicon is hybridised to two classes, each with at least one
CC	member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC	and the degree of hybridisation to both classes is determined from the
CC	label on the amplicon. From the ratio of labels hybridised to the two
CC	classes of oligomers, the degree of methylation is calculated. The method
CC	is used: (i) for diagnosis and/or prognosis of side effects of
CC	therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC	of the central nervous, cardiovascular, gastrointestinal and respiratory
CC	systems etc., particularly by detecting mutations or single nucleotide
CC	polymorphisms (SNP's), and (ii) for differentiation of cell or tissue
CC	types and for investigating cell differentiation. The method allows the
CC	methylation status of many C residues to be determined simultaneously.
CC	ABQ13410-ABQ51121 represent genomic DNA sequences used to illustrate the
CC	method for determining the degree of cytosine methylation described in
CC	the disclosure of the invention.
SQ	
XX	Sequence 994 BP; 331 A; 380 C; 152 G; 131 T; 0 other;
Query Match	28.9%; Score 485; DB 24; Length 994;
Best Local Similarity	74.2%; Pred. No. 1e-80;
Matches	676; Conservative 0; Mismatches 185; Indels 50; Gaps 3
OY	2 TGGAGAGACGCAGACAGATCCCGCGCGCAGAGAAGCGAAGAAAGCGACC CGCGGA 61
Db	924 TGGAGAGACGTAGTAGTATTTCGCGCGGTAGAAAGACGAGAGAAAGCGGATTTCGGGA 865
OY	62 CGGGAAAAGCGCGAGAGACAGGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 121
Db	864 CGGGAAAAGCGGTAGAGTAGCGCGCGCGCGCGCGCGCGCGCGCGGTAGAGGCGCGCGCT 805
OY	122 CCCGGCAGAGGCGCGCGCGGTGCGCGGTGTCGCGCCCTCCGCCCGCGCGCGGTACAGTGCCCC 181
Db	804 TTCGGTAGAGGGCGCGCGGTCTTTTGTCTTTTCTTTTCTTTTCTTTTCTTTTATATAGTCTTTT 745

OY	182	CTCCTCGGCGCCACACCGCCCTCCGGGCA-TTTTACGCGGACACGCGACCGCA	240
Db	744	TTTTTTCGCTTAAAGTCGTTTTTTCGCGATTATTTTACGCGGAGATCGATATCGGA	685
OY	241	CACCGGCGCTGGGGGCGC-----	258
Db	684	TATCGGGTTTGGGCGCGCGCGCGCTCGAGCGGTCGAGCGGGGTCTATCGGGT	625
OY	259	----GTGGGGGCCACACACTGCGTTTCGGGGTTCGCGGGGCTGCGCGCCATGAGCCG	313
Db	624	CGGGGCTGGGGTTATACGTCGTTTCGCGGGTCTCGGGGGTTCGCGCGTTATGAGATCG	565
OY	314	CGGTCCCGCCCGCCCGCTCGCGGCTGTCGACGCGGCGTGTCAACTGTGGCGGGCTGC	373
Db	554	CGGTTCCTGGTGC--TCGTGCGGTTGTTCCGACGCGGTGTGTTAAAGTGTGCGGTTGC	507
OY	374	GCTTGAGACACGCGGGCGCGCACGCTGGGACCTTCCCGGACACTCTGAGGGACACAG	433
Db	506	GTTTTCGAAACCGCGGGCGCGTACGTTGGGTGCTTTTTCGGATATTTTGTAGGGGATTTAG	447
OY	434	CGCGCGCGCGCGCTTCTACAGACAGCGCGCGCGAGTATTTCTTCGACCGGACACGC	493
Db	446	CGCGTGGCGGTGCTTTTACAGACAGCGCGGCTCGCAGTATTTTTCGATCGGATACGCT	387
OY	494	CCAGCTTGCAGCGCGCTGCTACTACTACACAGTCCGGTGGGCGCGTCCGCGCGCGCC	553
Db	386	TTAGTTTTCGACGTCGCTGTTTATTATTAATTAAGTTTCGGTGGGCGGTTGCGGCT	327
OY	554	ACGTCGCCCTCGACGCTCTCTCCGAAAGAGTGCCTCTTACGGGCTGGCGCGCGCC	613
Db	326	ACGTCGCTTTCGACGCTTTTTCGAAAGAGTGTCTTTTACGGGTTGGGCGCGGCTT	267
OY	614	TGGCACGCTTCGCGAGAGACGAGGGCTGCCGCTGCCCGCCGACGCGCCCTGCCCGCC	673
Db	266	TGGTACGTTTCGCGAGAGACGAGGGTGTCTCGGTCTCGACCGCTTTTGTTCGTC	207
OY	674	GCGCTTTCGCCCGCCAGCTGTGGCTGCTTTTCAGATTTCCCGAGAGCTCCAGCGCGCC	733
Db	206	GCGTTTTCGTTTCGTTAGTTGGGTTGTTTTCGAGTTTTCGAGATTTTAAAGTTCGCGC	147
OY	734	GCGTCTCGCGGTAGTCCCTGCTGGTGGTACATCTCCATCGTCCGCTTCTGCTCG	793
Db	146	GCGTTCGCTGCTAGTTCGTTGCTGTTGGTATTTTCGTTTATCGTCGTTTTCGTTTCG	87
OY	794	AGACGCTCCGACCTTCGCGACGACCGGACGCGAGCGGCGCTTCTGCTGACGCGCAG	853
Db	86	AGACGCTGTTGATTTTTCGACGACATCGCGACGCGGTACGGGATTTGTTGTGATGCTAG	27
OY	854	CCGCGCCCGGTG 864	
Db	26	TCGGTTTCGCTG 16	
RESULT 13			
ABQ19702/c			
ID	ABQ19702 standard; DNA; 994 BP.		
AC	ABQ19702;		
XX	12-JUL-2002 (first entry)		
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 6293.		
XX			
KW	Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;		
KM	drug; side effect; cancer; central nervous system; cardiovascular;		
KX	gastrointestinal; respiratory system; single nucleotide polymorphism;		
XX	SNP; cell differentiation; ds.		
OS	Homo sapiens.		
PN	WO200218632-A2.		
PD	07-MAR-2002		

XX	01-SEP-2001; 2001WO-EP10074.
PF	
XX	01-SEP-2000; 2000DE-1043826.
PR	05-SEP-2000; 2000DE-1044543.
XX	
PA	(EPiG-) EPiGENOMICS AG.
XX	
PI	Olek A, Plepenbrock C, Berlin K, Guetig D;
DR	WPI; 2002-371829/40.
XX	
PT	Determining the degree of cytosine methylation in genomic DNA, useful
PT	for diagnosis and prognosis, comprises selective hybridization of
PT	amplicons from chemically treated DNA -
PS	Claim 12; 56pp + Sequence Listing; 56pp; German.
XX	
CC	This invention describes a novel method for determining the degree of
CC	methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC	genomic sample of DNA. The sample is treated chemically to convert
CC	cytosine (C) but not methylated C, to uracil, then part of the genomic
CC	DNA that contains the target C is amplified to form a labeled amplicon.
CC	The amplicon is hybridised to two classes, each with at least one
CC	member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC	and the degree of hybridisation to both classes is determined from the
CC	label on the amplicon. From the ratio of labels hybridised to the two
CC	classes of oligomers, the degree of methylation is calculated. The method
CC	is used: (i) for diagnosis and/or prognosis of side effects of
CC	therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC	of the central nervous, cardiovascular, gastrointestinal and respiratory
CC	systems etc., particularly by detecting mutations or single nucleotide
CC	polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC	types and for investigating cell differentiation. The method allows the
CC	methylation status of many C residues to be determined simultaneously.
CC	AB013410-AB054121 represent genomic DNA sequences used to illustrate the
CC	method for determining the degree of cytosine methylation described in
CC	the disclosure of the invention.
XX	
XX	Sequence 99ABP; 129 A; 152 C; 354 G; 359 T; 0 other;

	Query Match	28.4%	Score 477.8	DB 24	Length 994
	Best Local Similarity	73.9%	Pred. No.2.e-79		
	Matches 670	Conservative 0	Mismatches 187	Indels 50	Gaps 3
QY	5 AGAGACGCAGACAGAGATCCCGCGCGGACAGAAAGACGAGAGAAAGGGAGCCCGGACGG 64				
Db	921 AAAAAACGAAAAACAATATCCGACGACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGCA 862				
QY	65 GAAAGCGCGAGACGAGCGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGTCC 124				
Db	861 AAAAAACGCAAAACCAAAACGCGCAACGACGACGAGAAACAAACCAAAACCAACGACGTCC 802				
QY	125 GGCAGGGGCGCGCGGTGGCCCTGTGCGCCCTCCGCGCGCGCGGGGTCAAGTGGCCCTTC 184				
Db	801 GACAAAAAACCGCGCATGTGGCCCTATCGCCCTTCGCGCCGCGCAATTCACAAATATCCCTTC 742				
QY	185 CCTCGCGCCCTTAGCGGCCCTGCGCGGCTA-TTTTACGCGCGGACACCGGACACCGGACAC 243				
Db	741 CCTCGCGCCCTTAACCGCCCTACCGAACTATTTTACGGCGCAACACCGAAACCGGAACAC 682				
QY	244 CGGCGTGGGGGGCGGCG----- 258				
Db	681 CGAACTAAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 622				
QY	259 --GTTGGGGGACACAGTGGTTCGCGGGGTGCGCGGGGCTGCGCGGCGGCGGCGGCGGCGGCGGCGG 316				
Db	621 ACGTGAACACACAGTGGATTCGCGGAATTCGCGGAATTCGCGGAATTCGCGCGGCCCTTAACACCGGCA 562				
QY	317 TGCCCGCGCCCGGTGCGGCTGTCTCGAGCGGGCTGTGTCTAACGTTGCGCGGCTGTGCGCT 376				
Db	561 TACCGCGCGG--CCGTACACACTACTACGAACGACTATATACGCTTAACGCTAACCAATACGCT 504				

QY	377	TCGAGACGGGGGCGGACGCTGGGGCCGCTTCCCGGACACTCTCTAGGGAGCCACGACGC	436
Db	503	TCGAAACCGGAACCGCGACGCTAAACCGCTTCCCGGAACACTCTCTAAAAAACCACACGC	444
QY	437	GCCGGGCGCGCTTCTACAGACGACGCGCGCCGCGAGTATTTCTTGAGCCGGACCGGCCA	496
Db	443	GCCCGGACCGCTTCTACGACGACGCGCGCCGCGAGTATTTCTTGAGCCGACCGGACCA	384
QY	497	GCTTGGACGCGCGTGTCTACTACTACTACAGTCAGTCCGGTGGGCGGCTGGCGCGCGGACG	556
Db	383	ACTTGGACGCGGCTACTACTACTACTACTACCAATCCGATTAAAGCACTACGACGACGCGACG	324
QY	557	TGCGCGCTGACGCTCTCTCTGGAAGAGTGGCTTCTACAGGGCTGGCGCGCGGCTCTGG	618
Db	323	TACCGCTTGAGCGTCTTCTCTAAAAAAAATTAACCTTCTACGAACCTAAACGCGACGACCTAA	264
QY	617	CACGCTGCGGGAGAGAGAGGGCGGCCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	676
Db	263	CACGCTGACGGGAAAGCAAAACACTACACCGGATACCGCGCGCGCGCGCGCGCGCGCGCG	204
QY	677	CCTTGGCGCCGCGCAGCTGTGGCTGTGGCTTTTTCAGATTCCCGAGAGCTCTCAGGCGCGCGG	738
Db	203	CCTTGGCGCCGCGCAGCTATTAATCTACTTTTTCGAAATTTCCCGAATACTCTCAAAACGCGCGG	144
QY	737	TGCTGCGCGGTAGTCTCGGTGCTGATCTGTCTCATCTGCTCATCTGCTCTTCTGCTCGAGA	796
Db	143	TACTTCCGCGTATCTCCGTAATCATCTCGTCTCATCTGCTCTTCTACTCTGAAA	84
QY	797	CGCTGCCCTGACTTCCGCGACGACGCGGACGCGGAGGGGCTTGTCTGTGACGCGCGACCG	856
Db	83	CGCTACCTTAACCTCCGCGACGACCGCGGACGACGAGAACTTACTACTACAAACCGCAACCG	24
QY	857	GCCCGCGT 863	
Db	23	ACCGCAT 17	
RESULT 14			
ABO19703			
ID	ABO19703 standard; DNA; 994 Bp.		
AC	ABO19703;		
XX			
DT	12-JUL-2002 (first entry)		
XX			
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 6294.		
XX			
XX	Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;		
KW	drug; side effect; cancer; central nervous system; cardiovascular;		
KW	gastrointestinal; respiratory system; single nucleotide polymorphism;		
KW	SNP; cell differentiation; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200218632-A2.		
XX			
PD	07-MAR-2002.		
XX			
PF	01-SEP-2001; 2001WO-EPI0074.		
XX			
XX	01-SEP-2000; 2000DE-1043826.		
PR	05-SEP-2000; 2000DE-1045453.		
XX			
PA	(EPIG-) EPIGENOMICS AG.		
XX			
PI	Olek A, Piepenbrock C, Berlin K, Gueltig D;		
XX			
DR	WPI; 2002-371829/40.		
XX			
PT	Determining the degree of cytosine methylation in genomic DNA, useful		
PR	for diagnosis and prognosis, comprises selective hybridization of		
XX	amplicons from chemically treated DNA		
XX			

RESULT 14	
ABQ19703	
ID	ABQ19703 standard; DNA; 994 BP.
XX	
AC	ABQ19703;
XX	
DT	12-JUL-2002 (first entry)
XX	
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 6294.
XX	
KW	Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW	drug; side effect; cancer; central nervous system; cardiovascular;
KW	gastrointestinal; respiratory system; single nucleotide polymorphism;
KW	SNP; cell differentiation; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200218632-A2.
XX	
PD	07-MAR-2002.
XX	
PF	01-SEP-2001; 2001WO-EP10074.
XX	
PR	01-SEP-2000; 2000DE-1043826.
PR	05-SEP-2000; 2000DE-1044543.
XX	
PA	(EPiG-) EPIGENOMICS AG.
XX	
PI	Olek A, Piepenbrock C, Berlin K, Guetig D;
XX	
DR	WPI; 2002-371829/40.
XX	
PT	Determining the degree of cytosine methylation in genomic DNA, useful
XX	for diagnosis and prognosis, comprises selective hybridization of
XX	amplicons from chemically treated DNA -

Query Match 21.9%: Score 367.4; DB 24; Length 7642;
Best Local Similarity 57.8%: Pred No 6e-59;
Matches 684; Conservative 0; Mismatches 481; Indels 18; Gaps 1;

QY 344 AGCGGCTGTGTCTCAACGTCGGCGGGCTGCTTCGAGACGGGGCGCCAGCTGGGCC 403
DB 2401 AAGCGTATTCATCAACATCTCCGAACTACGCTTCGAAACGCACTAAACACCTTTTAC 2442
QY 404 GCTTCCCGACACTGTGCTAGGGGACCCGAGCGCGCGCGCTTCTACAGCAGCCG 463
DB 2341 AATTCGCCCAACGCTACTAAACGACCCCAACGACATAAATCTTCGACCCCTCC 2282
QY 464 GCGGAGATTTCTTCGACCGGACCGGCGGCTTCACGCGCTCTACTACTAC 523
DB 2281 GCAACGAATCTTCTTCGACCGGACCGACCGCACTTCGACGCTCTACTACTATC 2222
QY 524 AGTCGGTGGCGGCTGCGGGCGCGCGGCTGCGCTGACGCTTCTCGAAGAG 583
DB 2221 AATTCGAAACCGCATCCGCGACCGATCAGTACCATTTCTCCGAAAAA 2162
QY 584 TGGCCTTACCGGCTGGGGCGGGCGCGCTGCGACGCTGCGGAGAGAGGCTGCC 643
DB 2161 TCCGCTTACCACTAAACGAAAAACCATAAATAATTCGCGAAAAACAACTTCC 2102
QY 644 CGTGGCGCGCGGCGCGCGCTGCGCGCGCGCTTCGCGCGCGAGCTGGGCTGTT 703
DB 2101 TACGAAAAAAGAACGACCTTACCCGCGCGCTTCACAGCCCAATATTAATCTCT 2042
QY 704 TCGAGTTTCCGAGAGCTCTCAGGCGCGCGGCTGCTCGCGCTAGTCTCGTGTCTCA 763
DB 2041 TCGAATATCCCGAAACCTCCGAAACGACCGGAAACATCGCATGATCCGTAATCA 1982
QY 764 TCGCTCTCCCATCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 823
DB 1981 TCGCTCTCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1922
QY 824 ACGGACGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 883
DB 1921 ACTACCGCGCTGAGCTGCAAACTCATTCGAAACACCGCAACACACGTCGAAAT 1862
QY 884 GCTCAGCCAAATGCTGGAATTCACCCGCGCTGCTGCTGCTGCTGCTGCTGCTG 943
DB 1861 CCGGCGCAAAAA-----CTTCGAACTTCTCGGATCCCTTCTCTGTAA 1820
QY 944 TGGAGAGCGCTGTATTTGTGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1003
DB 1819 TAAAAAGCTATACATCATTAATTCCTGCACTACTAATACGATTCCTGCTATC 1760
QY 1004 CAAGCAAGCTATCTCTCAAGAACGTATGAACTCATGATTTTGGGCTATCTTC 1063
DB 1759 CTAAACAAACCACTTCTCGCGAACAATACATAAACCCTAATCGACATTTATACCATATTC 1700
QY 1064 CCTACTTTGGCACTGGGACCGAGCTGCGCGGAGGAGGAGGAGGAGGAGGAGGCA 1123
DB 1699 CTTATTTTATCACTTAATACGAACTAACGAAACGAAACAAATTAACAAACCA 1640
QY 1124 TGTCACTGGCCATCTCGAAGATCATCGATGCTGCTGCTGCTGCTGCTGCTGCTG 1183
DB 1639 TATCTTAACCATCTTAAATAATCTCGGCTAATAAATCTTCGCACTTCAAACTAT 1580
QY 1184 CCGGACATCAAGGCGCTGCAAAATCTGGGCGAGAGCTGCGGCGCTCATGCTGAGC 1243
DB 1579 CGGCGCATTCGAAAAAATCAAAATCTGAAACAAAGCTAAAAACGTCATAGGAAAC 1520
QY 1244 TGGGCTCTCATCTTTCTCTCTCATCGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1303
DB 1519 TAAATTTACTCATCTTCTCTCTCTTATTAATATCATCTTTCTCAACGCGATCTACT 1460
QY 1304 TTGCGCAATTTGACGGGAGGAGCTCCCATTTCTAGTCAATCCCTGAGTCTTCTGCTGG 1363
DB 1459 TTACGAAACAAACGACCCCATCTTCAAAATTTCAACAAACATCCGAAATACCTTCTAATAA 1400

QY 1364 CGGTACTACCATAGTACAGTTGGCTATGAGACATGCGACCCGTCACCTGTGGTGGCA 1423
DB 1399 CATATATTAACATTAACAAATTAATTAACAGATATTAACCCCAATTAACATTAACAA 1340
QY 1424 AGATAGTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1483
DB 1339 AATTAATAAATCTCTATATACCATGCGGATATCTTAACCATGCGATTAACCAATTC 1280
QY 1484 TCATGTCCTCAATTCAGCTACTTTTATACCGGAGAGAGA 1526
DB 1279 TAATTAATTCCAACTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1237

Search completed: February 20, 2003, 06:32:37
Job time : 439.041 secs

Query Match 63.6%; Score 1069; DB 1; Length 1599;
Best Local Similarity 81.5%; Pred. No. 1,7e-198;
Matches 1289; Conservative 0; Mismatches 280; Indels 12; Gaps 4;

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QY 100 CGGGGCAAGGCGGCGGCGTCCCGGACAGAGGCGGCGGCGTCCCTGTCGCCCTCCG 159
DB 31 CGGAAAAGCCCGGGGTGATTTTCCACAGGTGTGGAACGGACGAGAGGGGCGCCCTAGC 90
QY 160 CCGGCGGCGGTCAACAGTACCGCCCTCCCTCGCGCCCTAGCGCCCTGCGGGCTATTATAC 219
DB 91 CCGGCGGCGGTCAACAGCGGCGCCCTCCCTCGCGCCCTGCGGGCTTCATGCTATTTT 150
QY 220 CCGGCGGCGGTCAACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 279
DB 151 ACCGCGGCGGTCAACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 210
QY 280 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 339
DB 211 ACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 267
QY 340 TGGGAGGCGGTGTGTCAACAGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 399
DB 268 TGGGAGGCGGTGTGTCAACAGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 327
QY 400 GCGGCGGCGGTGTGTCAACAGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 459
DB 328 GCGGCGGCGGTGTGTCAACAGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 387
QY 460 GCGGCGGCGGTGTGTCAACAGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 519
DB 388 GCGGCGGCGGTGTGTCAACAGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 447
QY 520 TACCAAGTCCGCGGTGTGTCAACAGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 579
DB 448 TACCAAGTCCGCGGTGTGTCAACAGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 507
QY 580 GAGGTGCTTCTTCAACAGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 639
DB 508 GAGGTGCTTCTTCAACAGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 564
QY 640 TGGCGGCGGCGGTGTGTCAACAGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 699
DB 565 TGGCGGCGGCGGTGTGTCAACAGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 618
QY 700 CTTTTCAGATTTTCCGAGAGCTCTCAAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 759
DB 619 CTTTTCAGATTTTCCGAGAGCTCTCAAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 678
QY 760 GTATCTCTGTCTCAACAGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 819
DB 679 GTATCTCTGTCTCAACAGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 738
QY 820 CCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 879
DB 739 CCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 798
QY 880 AATGCGTCAAGCAAAATGCGTGAATCAACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 939
DB 799 AATGCGTCAAGCAAAATGCGTGAATCAACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 858
QY 940 GTGCGTCAAGCAAAATGCGTGAATCAACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 999
DB 859 GTGCGTCAAGCAAAATGCGTGAATCAACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 918
QY 1000 TGTCAAGCAAAATGCGTGAATCAACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1059
DB 919 TGTCAAGCAAAATGCGTGAATCAACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 978
QY 1060 CTTCCCTCACTTGTGCGACTGGGCGAGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1119
DB 979 CTTCCCTCACTTGTGCGACTGGGCGAGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1038
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QY 1120 GCCATGTCACTGGCCATCTCTGAGAGTCATCCGATTTGGTGTGCTCTTCCGCACTTCAAG 1179
DB 1039 GCTATGTCCCTGGCCATCTCTTAAAGGATTCGATTTGGTGTGCTCTTCCGCACTTCAAG 1098
QY 1180 CTGTCCCGGCGCAAAAGGCGGCGTCAAACTTGGGCGGAGAGCTTGGGCGGCGTCCATGCT 1239
DB 1099 CTGTCCCGGCGCAAAAGGCGGCGTCAAACTTGGGCGGAGAGCTTGGGCGGCGTCCATGCT 1158
QY 1240 GAGCTGGGCGGCGTCAAACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1299
DB 1159 GAGCTAGGTCTCCATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1218
QY 1300 TACTTTCGCAAGTTCAGCGGCGGAGTCCCATTTTCACTACATCCCTGAGTCTCTG 1359
DB 1219 TACTTTCGCAAGTTCAGCGGCGGAGTCCCATTTTCACTACATCCCTGAGTCTCTG 1278
QY 1360 TGGGCGGCGTACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1419
DB 1279 TGGGCGGCGTACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1338
QY 1420 GGCAGATAGTGGGCTCTGTGTGCGCATTCGCGGCGTGTGATATTTCTTCCGCACTG 1479
DB 1339 GGCAGATAGTGGGCTCTGTGTGCGCATTCGCGGCGTGTGATATTTCTTCCGCACTG 1398
QY 1480 CCGCTCAATGTCTCAATTTTCACTTCTTATTCACCGGAGAGAGAGGCGT 1539
DB 1399 CCGCTCAATGTCTCTTCACTTCTTATTTTACACCGGAGAGAGAGGCGT 1458
QY 1540 GGGATGTTCAGCCATGTGAGCATGACCTTGTGCGGCGGCGGCGGCGGCGGCGGCGGCG 1599
DB 1459 GGGATGTTCAGCCATGTGAGCATGACCTTGTGCGGCGGCGGCGGCGGCGGCGGCGGCG 1518
QY 1600 GGGGTGTGAGCGGAGGAGTACCTGAGCTACCACTTGTGCGGCGGCGGCGGCGGCGGAG 1659
DB 1519 GGGGTGTGAGCGGAGGAGTACCTGAGCTACCACTTGTGCGGCGGCGGCGGCGGCGGAG 1578
QY 1660 CACCTGTCAACCGAGTGTGA 1680
DB 1579 CACATGTGTGAGTGTGTGA 1599
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RESULT 2
US-08-527-152-1
; Sequence 1, Application US/08527152
; Patent No. 5827655
; GENERAL INFORMATION:
; APPLICANT: Chandu, Kanianthara G.
; APPLICANT: Cahalan, Michael D.
; APPLICANT: Grissmer, Stephan
; APPLICANT: Goldin, Alan L.
; APPLICANT: Dehliels, Brent A.
; APPLICANT: Gutman, George A.
; APPLICANT: Masmuth, John J.
; TITLE OF INVENTION: Assay, Methods and Products Based On n
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert,
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/527,152
; FILING DATE: UNKNOWN
; CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/170,418
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/558,568
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dreyer, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-54444-2/MHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1994 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 150..1736
US-08-527-152-1

Query Match 36.6%; Score 614.2; DB 1; Length 1994;
Best Local Similarity 66.1%; Pred. No. 1.6e-110;
Matches 960; Conservative 0; Mismatches 468; Indels 25; Gaps 4;

115 CGGGCGTCCCGGAGAGGCGCGGCTGCGCCCTCCGCCCGCGCGGGGTCACA 174
115 CGGGCGTCCCGGAGAGGCGCGGCTGCGCCCTCCGCCCGCGCGGGGTCACA 174
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175 GTGCCCCCTCCCGGAGAGGCGCGGCTGCGCCCTCCGCCCGCGCGGGGTCACA 234
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235 ACCGAGACCGGAGAGGCGCGGCTGCGCCCTCCGCCCGCGCGGGGTCACA 294
205 GCGGGGAGCGCGGCTGCGCCCTCCGCCCGCGCGGGGTCACA 263
295 TGGCGCGCGGAGAGGCGCGGCTGCGCCCTCCGCCCGCGCGGGGTCACA 348
264 TACGAGCGACGCGGAGAGGCGCGGCTGCGCCCTCCGCCCGCGGGGTCACA 323
349 CTGCGCTCAGCGGAGAGGCGCGGCTGCGCCCTCCGCCCGCGGGGTCACA 408
324 GTGGTATGCAACATGCGGAGAGGCGCGGCTGCGCCCTCCGCCCGGGTTC 383
409 CCGGACACTGCGGAGAGGCGCGGCTGCGCCCTCCGCCCGCGGGGTCACA 468
384 CCGGAGACGCGGAGAGGCGCGGCTGCGCCCTCCGCCCGCGGGTTC 443
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529 GTGGGCGCGGAGAGGCGCGGCTGCGCCCTCCGCCCGGGTTC 588
504 GGGGCGCGGAGAGGCGCGGCTGCGCCCTCCGCCCGGGTTC 563
589 TTCTACGCGGAGAGGCGCGGCTGCGCCCTCCGCCCGGGTTC 648
564 TTCTACGCGGAGAGGCGCGGCTGCGCCCTCCGCCCGGGTTC 623
649 CCGCGGAGCGCGGAGAGGCGCGGCTGCGCCCTCCGCCCGGGTTC 708
624 GAGGAGGAGCGCGGAGAGGCGCGGCTGCGCCCTCCGCCCGGGTTC 683
709 TTTCGCGGAGAGGCGCGGAGAGGCGCGGCTGCGCCCTCCGCCCGGGTTC 768
684 TATTCGAGAGGCGCGGAGAGGCGCGGCTGCGCCCTCCGCCCGGGTTC 743

769 GTCTCATGCTGCTCTTCTGCTGAGAGCGTGCCTGACTTCCGCGAGCGCGGCG 828
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829 ACGGGGCTGCTGCTGAGAGCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTG 888
801 -----TATCCCGCGCTCCCGCTGCGAGAGCGTGTGAGGCTGCGCAACAGCAGC 851
889 AGCCAAATGCTGGAATTCACCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 948
852 TCGGGGCGCGCTGCTGAGAGCGTCCAG-----CTTCTGAGAGCGCTTCTGCTGCTGAG 905
949 ACGCTGATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1008
906 ACGCTGATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 965
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966 AAGCCACTTCTGCAAG 1025
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1086 CTGCGCATCTGAG 1145
1189 CACTCAAG 1248
1146 CATTCTAAG 1205
1249 CTCTCATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1308
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1266 GAGGAG 1325
1326 GTAACATGAT 1385
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1386 GTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1445
1489 GTCTCAATTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1548
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1549 AGCCATGTGACA 1561
1506 ATGACAGCTGGACA 1518

RESULT 3
US-09-178-109-3
Sequence 3, Application US/09178109
Patent No. 6395477
GENERAL INFORMATION:
APPLICANT: Cockett, Mark I.
APPLICANT: Diks, Daniel W.
APPLICANT: Chang Ling, Hual-Ping
APPLICANT: Sokol, Patricia T.
TITLE OF INVENTION: Human Polysium Channel Polynucleotides and
TITLE OF INVENTION: Polypeptides and Uses Therefor
FILE REFERENCE: ahp-98089
CURRENT APPLICATION NUMBER: US/09/178,109
CURRENT FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3
LENGTH: 2064
TYPE: DNA
ORGANISM: human
US-09-178-109-3

Query Match 12.88; Score 215.6; DB 4; Length 2064;
Best Local Similarity 52.88; Pred. No. 1.9e-33;
Matches 622; Conservative 0; Mismatches 499; Indels 57; Gaps 5;

343 GAGGGGCTGGTCTCAACGTGGCCGGCTGGCTGGAGAGGAGGCGGCGGAGCGTGGG 402
190 GAGCTGATTTGCTCAACGTAGTGGGGAGGTTCCAGACTGGAGACCACTGGAG 249
403 CGCTTCCGAGACTCTGTAGGGGACCAGCGCGCGCGCTTCTTACAGAGACG 462
250 CGCTACCGGAGACCTTGTGGGAGACGAGAAAGAGTTCTTCAAGAGAGACAC- 308
463 CGCGCGAGATTTTCTTGGACCGGCGGCGGCGGCTTCAAGCGCGCTTCTACTAC 522
309 --CAAGAGATCTTCTTGGACCGGAGACCGGAGGTTCCCTGCTCAACTTCTAC 366
523 CAGTCCGGTGGGCGGCGGCGGCGGCGGCGGCGGCTGCAAGTCTTCTGAGAGAG 582
367 C--GCAGGGGAGAGCTGCACTACCGGCGCTAGAGTGCATCTGCTTACGAGAGAG 423
583 GTGGCTTCTTACAGGGCTGGGCGGCGGCGGCGGCGGCTGCGCGAGAGAGAGGCTGC 642
424 CTGGCTTCTTACAGGGCTGGGCGGCGGCGGCGGCGGCTGCGCGAGAGAGATACAG 483
643 CGGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTGGCGGCGGAGCTGTGCTCT 702
484 GACCGCAAGAGAGGAGAGAGCGCGGAGC-----GGCTCATG 516
703 TTGAGTTTCCGAGAGCTCTCAGGCGGCGGCGGCGGCGGCTGCGGCTTCTGCTGTC 762
517 GAGCACAACGACTCGGAGAACACAGAGAGTCCATGCTTCTGCTGCTTCCGAGAGCC 576
763 ATCTCTCTTCCATCGTCTGCTTCTGCTGCTGAGAGCGTCTGCTGCTTCCGAGAGCGC 822
577 ATGTGGGGGGCTTGGAGAACCCGACACAGCAGCGTGGGCGGCTTCTTACAGTGTG 636
823 GACGGGAGGGGGCTTGGCTGCTGAGAGCGGAGCGGCGGCGGCTTCCGCTGCTGAT 882
637 ACTGGCTTCTTCAATCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 696
883 GGTCTCAGCCAAATGCTGGAATTCACCCGCGCTGCTGCTGCTGCTGCTGCTGCTG 942
697 ACGGTCCCGGAGCAGAGAGAGCTGCTGCGGGAGCGCTACTGCTGCTGCTGCTGCTG 756
943 GTGGAGAGCGTGTGATTTGTTGTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1002
757 CTGAGCAGGGGGCTGCTGATGATCTTCAACGCTGAGTACCTCGGCGGCTTGGCGGCT 816
1003 CCAAGCAAGGCTATCTTCTTCAAGAGCTGATGAACTCATGATTTTGTGCTATCTT 1062
817 CCCAGCGCTACCGCTTCAATCCGAGCGTCAATGAGCATCATGAGTGTGGCATCATG 876
1063 CCCACTTTGGGAGCGAGGAGCGAGCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAG 1122
877 CCCACTTACATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 915
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916 GTGGCGGGGCTTGGCA---CGCTCGGGGCTTTCGCGCTTTCAGAGATTTTCAAGTTT 972
1183 TCCGCGCATCAAGGCGCTGCAATTTTGGGCGAGAGCTTGGGCGCTTCAGTCAAGT 1242
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1033 CTGGGCTTCT 1092

1303 TTTCGCAAGTTGACCGGGTGGAGTCCCATTTTCACTACATCCCTGAGTCTTGCTGG 1362
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1363 GCGGTAGTCACTATGACTAGTGGTGGTATGAGAGATGAGACCGGCTGCTGCTGGTGG 1422
1153 ACATTTGCACTAGTACACACTGGGATGAGAGATGAGTGTCTTAAAGCATTTGAGGG 1212
1423 AAGATGAGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1482
1213 AAGATCTTGGCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1272
1483 GTCAATGTCTTCAATTTCACTTATATATATATATATATATATATATATATATATAT 1520
1273 GTGATTTGTTCCAACTTAGCCGAGATTACACAGAA 1310

RESULT 4

US-09-142-791A-3
Sequence 3, Application US/09142791A
Patent No. 6368823
GENERAL INFORMATION:
APPLICANT: Antoine Michel Alain Brill
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Faivre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142.791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR FILING DATE: 1997-03-27 97402971.2
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2072
TYPE: DNA
ORGANISM: HOMO SAPIENS
US-09-142-791A-3

Query Match 12.88; Score 215.6; DB 4; Length 2072;
Best Local Similarity 52.88; Pred. No. 1.9e-33;
Matches 622; Conservative 0; Mismatches 499; Indels 57; Gaps 5;

343 GAGGGGCTGGTCTCAACGTGGCCGGCTGGCTGGAGAGGAGGCGGCGGAGCGTGGG 402
118 GAGCTGATTTGCTCAACGTAGTGGGGAGGTTCCAGACTGGAGACCACTGGAG 177
403 CGCTTCCGAGACTCTGTAGGGGACCAGCGCGGCGGCGGCTTCTTACAGAGAGCG 462
178 CGCTACCGGAGACCTTGTGGGAGCAGAGAGAGAGTCTTCTTCAAGAGAGACAC- 236
463 CGCGCGAGATTTTCTTGAACCGGCGGCGGCGGCGGCTTCAAGCGGCTTCTACTAC 522
237 --CAAGAGATCTTCTTGAACCGGAGCCGAGAGTGTTCGCTGCTGCTCAACTTCTAC 294
523 CAGTCCGGTGGGCGGCTGCGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGAGAG 582
295 C--GCAGGGGAGGCTGCACTACCCGCTTACAGTCACTTCTGCTTCAAGAGAGAG 351
583 GTGGCTTCTTACAGGGCTGGGCGGCGGCGGCGGCTGCGGCGGCTGCGGAGAGAGGCTGC 642
352 CTGGCTTCTTACAGGCATCTTCCGAGATATATCGGAGAGTGTCTGCTAGAGAGATACAG 411
643 CGGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCCGCGGCGGAGCTGTGCTGCTT 702

Db 412 GACCGAAGAGGAGAACGCCGAGC-----GGCTCATG 444
QY 703 TTGAGATTCCCGAGAGCTCTCAGGGCGGGGCTGCTGCCCTAGCTCTCCGTGCTG 752
Db 445 GAGGACAAAGCACTCGAGAAACAACAGAGTCCATGCCCCGCTCAGCTTCCCAACACC 504
QY 763 ATCTGCTCTCAGCTGCTCTCTGCTGCTGAGAGCGCTGCTGCTGCTGCTGCTGCTG 822
Db 505 ATGTGGCGGGCTTTCAGAAACCCACACAGACGCTGGCCCTGGCTCTTCTACTACGTG 564
QY 823 GACGAGACGGGGCTTCTGCTGCTGAGCCGACCGCCCGGCTGTTCCCGCTCCGCTGAAT 882
Db 565 ACTGCTTCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 624
QY 883 GGCTCCAGCCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 942
Db 625 ACGGTCCCGGGGAGCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 684
QY 943 GTGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1002
Db 685 CTGGAGACGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744
QY 1003 CCAAGCAAGGCTATCTTCTTCAAGAACTGATGATGATGATGATGATGATGATGATG 1062
Db 745 CCCAGCGCTACCGCTTCAATCCGAGGCTCATGATGATGATGATGATGATGATGATG 804
QY 1063 CCTACTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1122
Db 805 CCTACTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
QY 1123 ATGTCACTGGCCATCTGAGAGTCAATCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1182
Db 844 GTGTCCGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 1183 TCCCGGACTCAAGAGGCTGCAAAATCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1242
Db 901 TCCCGGACTCAAGAGGCTGCAAAATCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 960
QY 1243 CTGGGCT 1302
Db 961 CTGGGCT 1020
QY 1303 TTGAGCAAGTGTGAGCGGGGAGCTCCCATTTCTAGTACATGCTGCTGCTGCTGCTG 1362
Db 1021 TATGCGAGAGAGGCTCTCTGCGGCGAGAGTTCACAAAGCATCTCTGCTGCTGCTG 1080
QY 1363 GCGGTAGTACCATGACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1422
Db 1081 ACCATTTGCTACATGACACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1423 AATATAGTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1482
Db 1141 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1483 GTGATTTGCTCAATTTTCACTACTTTTATCACCGGGA 1520
Db 1201 GTGATTTGCTCACTTTTACCGGATTTTACACAGAA 1238

RESULT 5
US-09-142-791A-1
; Sequence 1: Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Brill
; APPLICANT: Thierry Paul Gerard Calmels
; APPLICANT: Jean-Francois Simon Pierre Faivre
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142, 791A

; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2104
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-142-791A-1

Query Match 12.8%; Score 215.6; DB 4; Length 2104;
Best Local Similarity 52.8%; Pred. No. 1.9e-33;
Matches 622; Conservative 0; Mismatches 499; Indels 57; Gaps 5;

QY 343 GAGCGCTGTGCTCAACGTGGCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 402
Db 118 GAGCTGATTTCTCTCAACGTGAGTGGCGGAGGTTCCAGACTGAGAGCACAGCTGGAG 177
QY 403 CGCTCCCGGACACTGCTGCTGAGGAGACCAAGCGGCGCGCGCTTCTCAAGAGACGCG 462
Db 178 CGCTACCGGACACTGCTGCTGAGGAGACCAAGAGAGATTTCTTTCACAGAGAGAC- 236
QY 463 CGCGCGAGTATTTCTTCAACGTGGCCCGGACCGGCTTCTGAGCGCGCTGCTACTACTAC 522
Db 237 --CAAGAGTACTTCTTCAACGTGGAGACCGGAGGTTCCGCTGCTGCTGCTGCTGCTG 294
QY 523 CAGTCCGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582
Db 295 C---GCAGCGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 351
QY 583 GTGGGCTTCTACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 642
Db 352 CTGGCTTCTACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 411
QY 643 CGGTGCGCGGCGAGCTT 702
Db 412 GACCGCAAGAGGAGGAACGCCGAGC-----GGCTCATG 444
QY 703 TTGAGATTCCCGAGAGCTCTCAGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 762
Db 445 GAGGACAAAGCACTCGAGAAACAACAGAGTCCATGCTGCTGCTGCTGCTGCTGCTGCTG 504
QY 763 ATCTGCTCTCAATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 822
Db 505 ATGTGGCGGGCTTTCAGAAACCCACACAGACGCTGGCCCTGGCTCTTCTACTACGTG 564
QY 823 GACGAGACGGGGCTTCTGCTGCTGAGCCGACCGCGGCTGTTCCCGCTCCGCTGAAT 882
Db 565 ACTGCTTCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 624
QY 883 GGCTCCAGCCAAATGCTGGAATTCACCCCGCTGCTTCAATGACCCGCTTCTGCTG 942
Db 625 ACGGTCCCGGGGAGCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 684
QY 943 GTGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1002
Db 685 CTGGAGACGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744
QY 1003 CCAAGCAAGGCTATCTTCTTCAAGAACTGATGATGATGATGATGATGATGATGATG 1062
Db 745 CCCAGCGCTACCGCTTCAATCCGAGGCTCATGATGATGATGATGATGATGATGATG 804
QY 1063 CCTACTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1122
Db 805 CCTACTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843

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QY 1123 ATGTCACCTGGCATCTCTGAGAGTCATCCGATGTGGCTGCTCTTCCGATCTTCAACCTG 1182
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Db 844 GTGTCCGCGCCTTCCGCA---CGCTCCGGGCTCTTCCGCGCTTCAAGAGCTTCAAGCTT 900
QY 1183 TCCCGGACACTCAAAAGGCGCTGCAAAATCTTGGGCGAGACGGCTTGGGGCTCCATCGTGAG 1242
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 901 TCCCGGACACTTCCAGGCGCTGCGGATCTTGAGCTACACACTGAAAGACTGTGGCTCCGAA 960
QY 1243 CTGGGCTCTCATCTTTTCTCTTCATGATGATGTGGCTCTCTTCTTCCAGGCGCTTAC 1302
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 961 CTGGGCTTCTCTCTCTCTCCCTACCATGAGCATCATCTTGGCACATGATGTT 1020
QY 1303 TTTCGCAAGTTGACCGGGGTGAGCTCCCATTTTCACTAGCATCCCTAGTCTTGTGGTGG 1362
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1021 TATGCCAGAAAGGCGCTCTCTGCGGCGAGCAAGTTCACAAAGCATCCCTGCTGTTTGTAC 1080
QY 1363 GCGGTACTACACATGATACAGTTGCTATGAGACATGACACCGGCTACCTGTTGGGGC 1422
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1081 ACCATTTGTACACATGACACACTGGGATACGAGACATGTCCTTAAGACGATTGACAGG 1140
QY 1423 AAGTATGAGGCTCTCTGTGTCATTTGCGGCGCTGCTGCTATTTTCCCTGCGAGTCCC 1482
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1141 AAGTATGAGGCTCTCTGCTCTGCTGCTGAGTGGCTCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1483 GTCAATGTCTCAATTTTCACTTCTTATTCACCGGGA 1520
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1201 GTGATGTCTTCAACTTTAGCCGGATTTACACACAGAA 1238
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RESULT 6

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US-09-178-109-1
; Sequence 1, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Diks, Daniel W.
; APPLICANT: Chang Ling, Hwai-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/09/178, 109
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2121
; TYPE: DNA
; ORGANISM: human
US-09-178-109-1
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Query Match 12.8%; Score 215.6; DB 4; Length 2121;
Best Local Similarity 52.8%; Pred. No. 2e-33;
Matches 622; Conservative 0; Mismatches 499; Indels 57; Gaps 5;
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QY 343 GAGCGGCTGTCTCAAGTGGCGGGCTGCGCTTCGAGACGGGCGCGCAGCTGAGC 402
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 GAGCTGATTTCTCTCAAGTGGCGGGGAGGTTCCAGACACTGAGAGACACAGCTGAG 249
QY 403 CGCTTCCCGACACTGCTGCTAGGAGACCGAGCGCGCGCGCTTCTACAGACAGCG 462
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 CGCTACCGGAGACCGCTGCGGGGAGAGGAGGATTTCTTCAACGAGGAGAC- 308
QY 463 CGCGGAGATTTCTTCAAGTGGCGCGCGCGCGCTTCAAGCGCGCTTCACTACTAC 522
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 --CAAGSAGTACTTCTTCAAGCGGAGACCGAGGTGTTCCGCTCGCTCACTTCTAC 366
QY 523 CAGTCCGCTGGCGCTGCGCGCGCGCGCGCAGCTGCGCTGCACTGCTTCTGGAAGAG 582
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 367 C--GCAGGGGAGAGCTGCTACACCGCGCTACAGAGTCACTCTGCTTCAAGAGAG 423
QY 583 GTGGCTTCTACAGCTGGGCGCGCGCGCTTCAAGCGCTGCGCGAGAGAGGCTGC 642
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Db 424 CTGGCTTCTACGCGCATCTCCGAGATATCTCGGAGACTGCTCTACGAGAGTACAG 483
QY 643 CGGTTGCGCGCGAGCGCCCTGCTCCCGCGCGCTTTCGCGCGCAGCTGTGGCTCTT 702
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 484 GAGCGCAAGAGGAGAGAGCGCGAGC-----GGCTCATG 516
QY 703 TTGAGATTTCCGAGAGCTCTCAGGCGCGCGCTGCTGCGCTGATGCTCCGTCTGTC 762
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 517 GACGACAAAGACTTGGGAGAACACACAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 576
QY 763 ATCTCTGCTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 822
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 577 ATGTGGGCGGCTTTCGAGAACCCACACAGACAGCTGGGCTGCTGCTTCTTACTACGTC 636
QY 823 GAGGCGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 637 ACTGCTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 696
QY 883 GGTTCACGCAAAATGCTGGAATTCACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 942
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 697 ACGGTCCCGGCGACAGAGAGCTCCGTCGCGGAGCGCTACTGCTGCTGCTGCTGCTGCTGCT 756
QY 943 GTGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1002
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 757 CTGGACACGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 816
QY 1003 CCAAGCAAGGCTATCTTCTTCAAGAGCTGATGACCTCATGATTTTGTGGCTATCTT 1062
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 817 CCCAGCGCTACCGCTTCTCATCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 876
QY 1063 CCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1122
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 877 CCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 915
QY 1123 ATGTCACCTGGCATCTCTGAGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1182
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Db 916 GTGTCCGCGCCTTCCGCA---CGCTCCGGGCTCTTCCGCGCTTCAAGATCTTCAAGTCTT 972
QY 1183 TCCCGGACACTCAAAAGGCGCTGCAAAATCTTGGGCGAGACGCTTGGGCGCTCCATCGTGAG 1242
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Db 973 TCCCGGACACTTCCAGGCGCTGCGGATCTGCGCTACACACTGAAAGACTGTGGCTCCGAA 1032
QY 1243 CTGGGCTCTCTCATCTTTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1033 CTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1092
QY 1303 TTTCGCGAAGTTCACCGGGGTGAGTCCCATTTTCACTGACATCCCTGAGTCTTGTGGTGG 1362
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1093 TATGCCAGAAAGGCTCTCTGCGCGAGCAAGTTCACAAAGCATCCCTGCTGCTGCTGCTGCTGCT 1152
QY 1363 GCGGTACTACACATGATACAGTTGGCTATGAGACATGCGACCGCTGCTGCTGCTGCTGCTGCT 1422
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Db 1153 ACCATTTGTACACATGACACAGCTGAGTACGAGACATGAGTGGCTTAAGAGATTTGACAGGG 1212
QY 1423 AAGTATGAGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1482
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1213 AAGATTTCTGCTCTCATCTGCTTCTGAGTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 1483 GTCAATGTCTTCAATTTCACTACTTTTATCACCGGGA 1520
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Db 1273 GTGATGTCTTCAACTTTAGCGGGATTTACACACAGAA 1310
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RESULT 7

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US-09-336-643A-9
; Sequence 9, Application US/0933643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
```


178 CGCTACCCGAGACACCCCTGTGGGAGACGAGAGAGTTCTTCAACAGAGACAC- 236
463 CGCGCGAGATTTCTTCGACCGGACCGGACCGCTTCGACGCGCGGCTCTACTAC 522
237 - -CAAGAGAGTCTTTCGACCGGACCGGAGGTTCGCTCGCTCACTTCTAC 294
523 CAGTCCGTTGGGGGCTGCGGCGGCGGACGTCGCGCTTCGACGCTTCCTGAGAG 582
295 C---GCACGGGGAAGCTGACACTACAGCGGCTAGACAGTGCATCTGCTAGAGAGAG 351
583 GTGGCTTCTTACAGGGCTGGGCGGCGGCTTCGACGCTTCGCGAGAGAGAGGCTGC 642
352 CTGGCTTCTTACAGGCTACCTCCGAGATCATCGGGAGACTGCTCTACGAGAGTACAG 411
643 CCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 702
412 GACCGAGAGAGAGAGAGAGCGGAGC-----GGCTCATG 444
703 TTGAGATTTCCGAGAGCTCTCAGGCGCGGCGGCTGCTCCGCTCATGCTCGTCTGTC 762
445 GAGGACACAGACTTCGAGAGACACAGAGATCCATGCTCCGCTGCTACGCTTCGCGACAC 504
763 ATCTGCTCTCATGCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 822
505 ATGTGGCGGCGCTTCGAGAGACCGGACGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 564
823 GAGGCGAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 882
565 ACTGGCTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 624
883 GAGTCCAGCCAAATGCTGAGAAATCCACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 942
625 ACGGTCCCGGAG 684
943 GTGAGAGAGCTGTGTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1002
685 CTGAGACAGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 744
1003 CCAAGCAAGGCTATCTTCTTCAAGAGAGTATGAACTGATGCTGCTGCTGCTGCTGCTGCT 1062
745 CCGACGCGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 804
1063 CCGTACTTGTGCGACTGCGGACGAGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 1122
805 CCGTACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
1123 ATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1182
844 GTGTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
1183 TCCGCGGCTCAAGAGGCGCTGCAAAATGCTGCGGAGAGGCTGCGGCGGCTGCTGCTGCTG 1242
901 TCCGCGGCTCAAGAGGCGCTGCGGAGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
1243 CTGGGCGCT 1302
961 CTGGGCGCT 1020
1303 TTTGCGGAATTTGACGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1362
1021 TATGCGGAGAGAGGCTCTCTGCGGAGCAGTTCACAGCAATCTCTGCTGCTGCTGCTGCTG 1080
1363 GCGGTGCTCAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1422
1081 ACCATTGCTCAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
1423 AAGATAGTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1482
1141 AAGATCTTGGGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
1483 GTCAATGCTCAATTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1520

Db 1201 GTGATGTTTCAACTTATAGCGGATTTACCACGAA 1238
RESULT 9
US-08-288-405A-19
Sequence 19, Application US/08288405A
Patent No. 5559009
GENERAL INFORMATION:
APPLICANT: Chandu, Kanianthara G.
APPLICANT: Kalman, Katalin
APPLICANT: Chandu, Gitscha
TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Honbach, Test, Albritton & Herdert,
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,405A
FILING DATE: 10-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,431
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-59844-1/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
US-08-288-405A-19
Query Match 11.3%; Score 189.2; DB 1; Length 271;
Best Local Similarity 93.7%; Pred. No. 1.8e-28;
Matches 208; Conservative 0; Mismatches 7; Indels 7; Gaps 1;
Query 1466 TTTCCCTGCGAGTGGCGGCTGATGCTGCTCAATTTTCACTTATACCGGAGACAG 1525
Db 1 TTTCCCGGCGAGTGGCGGCTGATGCTGCTCAATTTTCACTTATACCGGAGACAG 60
Query 1526 AGGCGGAAGAGGCTGGGATGTTAGCCATGTGACATGACAGCTTGTGGCCCACTGAGG 1585
Db 61 AGGCGGAAGAGGCTGGGATGTTAGCCATGTGACATGACAGCTTGTGGCCCACTGAGG 120
Query 1586 G-----CAAGCGCATTTGGGGGCTGCTGAGAGGAGGAGTACCTGAGTACCACTGCA 1638
Db 121 GNNCANCNANNNCATTTGGGGGCTGCTGAGAGGAGGAGTACCTGAGTACCACTGCA 180
Query 1639 CTCTGGCACCCCGGAGAGAACACTGCTGACCAAGTGTGA 1680
Db 181 CTCTGGCACCCCGGAGAGAACACTGCTGACCAAGTGTGA 222
RESULT 10

US-07-955-916-5
; Sequence 5, Application US/07955916
; Patent No. 5397702
; GENERAL INFORMATION:
; APPLICANT: CAHALAN, Michael D.
; APPLICANT: CHANDY, Kanlanthara G.
; APPLICANT: GRISMER, Stephen
; APPLICANT: GHANSHANI, Sanjiv
; APPLICANT: GUTMAN, George A.
; APPLICANT: DETHEFS, Brent A.
; TITLE OF INVENTION: ASSAY FOR AND TREATMENT OF AUTOIMMUNE
; DISEASES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/955,916
; FILING DATE: 19921002
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-54474-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 696 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-07-955-916-5

Query Match 11.2%; Score 187.4; DB 1; Length 696;
Best Local Similarity 61.8%; Pred. No. 4.7e-28;
Matches 368; Conservative 0; Mismatches 191; Indels 36; Gaps 3;

QY 944 TGGAGAGCGTGTATTTGTTGGTCTTCCTTGAGCGTGGTACGCGCTCCGCTGCTGTC 1003
DB 14 TCGAGGGCGCTGTGTGCTGTGCTTACCTCGAGTTCACATGCGCTGTCTATCTTCTGCC 73
QY 1004 CAAGCAAGGCTATCTTCTTCAGAAAGCTGATGAACCTCATCGATTTTGGTATCTCTTC 1063
DB 74 CCAACAAGGTAGAGTTCATCAAGAACTCGCTCAACATCATGATCTTTGGCCATCTCTGC 133
QY 1064 CCTACTTTGGCAGCTGGGACCGAGCTGCGCCGCGAGCGAGGGGTGGGCCACAGGCCA 1123
DB 134 CCTTCTACCTTGGAGGTGGG-----GCTGAGCGGCTGTCTTCCAAAGCGAGCCAAAGGAGC 187
QY 1124 TGTCACTGGGCATCTGAGAGTATCCGATTTGTTGGTGTGCTTCCGATCTTCAAGCTGT 1183
DB 188 TG---CTGGGCTTCTGCGCGGTGTCGCGCTTGTGCGCATCTTGAACCTGA 244
QY 1184 CCGGAGCACTCAAGGCGCTGCAATCTTGGGCGAGAGCTTCCGGGCTCCATGCGTAGC 1243
DB 245 CCGGACACATTTTGGGCGCTGCGGGGTCTGGGGCCACAAGCTCCAGGACAGACAAGAGT 304
QY 1244 TGGGCTCTCATCTTTTCTTCTTATCATGAGTGTGCTCTTTTTCAGGCGCGCTCTACT 1303
DB 305 TCTGTGCTCATCATCTTCTGCGCTTGGCCCTTGGGCTGTGATCTTCCACACATGATCTACT 364

QY 1304 TTGCCGA-----AGTTGACCGGTGAGCTCCCATTTTCA 1336
DB 365 AGCCCGAGAGATAGGGGGCAGACCCCATGACCCGCGCATGAGACAGACTTTTA 424
QY 1337 CTAGCATCCCTGAGTCTTCTGTGGTGGCGGTATACACATGACTACAGTTGGTATGAG 1396
DB 425 AGAACAATCCCATCGGCTCTGCTGGGCGCTGTCTACACATGACAGACCTGGGCTATGAG 484
QY 1397 ACATGGACCCGTCAGTCGTGGTGGCAAGATAGTGGGCTCTGTGTGCCATTTGGCGGGC 1456
DB 485 ACATGTACCCGACAGAGTGTCTCCGATGCTGTGTGGGCTCTGTGTGCGCTGGCGGCG 544
QY 1457 TGTGACTATTTCTCTGCGAGTCCCGCTCATTTGCTTCATTTACGCTACTTTTA 1511
DB 545 TGTCTACATCGGCATTCGCCGCTCCGTACTATCGTAACATTTCCGAGTATTTA 599

RESULT 11
US-07-955-916-6
; Sequence 6, Application US/07955916
; Patent No. 5397702
; GENERAL INFORMATION:
; APPLICANT: CAHALAN, Michael D.
; APPLICANT: CHANDY, Kanlanthara G.
; APPLICANT: GRISMER, Stephen
; APPLICANT: GHANSHANI, Sanjiv
; APPLICANT: GUTMAN, George A.
; APPLICANT: DETHEFS, Brent A.
; TITLE OF INVENTION: ASSAY FOR AND TREATMENT OF AUTOIMMUNE
; DISEASES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/955,916
; FILING DATE: 19921002
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-54474-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1805 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-07-955-916-6

Query Match 10.3%; Score 173.8; DB 1; Length 1805;
Best Local Similarity 60.9%; Pred. No. 2.3e-25;
Matches 355; Conservative 0; Mismatches 192; Indels 36; Gaps 3;

QY 944 TGGAGAGCGTGTATTTGTTGGTCTTCCTTGAGCGTGGTACGCGCTCCGCTGCTGTC 1003
DB 879 TCGAGGGCGCTGTGTGCTGTGCTTACCTCGAGTTCACATGCGCTGTCTATCTTCTGCC 938
QY 1004 CAAGCAAGGCTATCTTCTTCAGAAAGCTGATGAACCTCATCGATTTTGGTATCTCTTC 1063

Db	939	CCAAACAAGGTGGAAATTCATCAAGAATCCCTCAATATCATTTGTGGCAATTTGCC	998
Qy	1064	CCCTACTTTGTGCGCATGTGGGACACCGAGCTGGCCCGGACGAGAGGGTGGGCCACGACGSCA	1123
Db	999	CCCTTCTACTCCGTGGAGGTGG--CCCTAAGCGGGCTGTCTCTCAAAAGCGGCCAAGACGTT--	1054
Qy	1124	TGTCATCGGCACATCCGAGAGTATCATCCGATTTGGTGGCGTGTCTCCGATCTTCAAGCTGT	1183
Db	1055	-----CTGGGCTTCCTGCGGGCTGTCCGCTGTGGGGCATCCTGGGCATCTTCAAGCTGA	1109
Qy	1184	CCGGGCACTCAAAAGGCGCTGCAAAATTGTGGCCAGACGCTTGGGCGTTCATGCGTGAGC	1243
Db	1110	CCCCCACTCTGAGGCGCTAAGGGTCTCTGGGCAACAACGCTCGTCCGACAGCAACAGCT	1169
Qy	1244	TGGGCTCTCATCTTTCTTTCTTTCATCGGTGTGGTCTCTTTTCCAGCGCCGCTACT	1303
Db	1170	TCTGCTGCTTATCATCTTCTCTGGCCCTGGAGTGTACTCTTTCCACCATGATCTACT	1229
Qy	1304	TTGCGCA-----AGTTGACCGGGTGGACTCCCATTTCA	1336
Db	1230	ACGGCGAGAGGATAGGGGACACGCCCAATGACCCCAAGCGCCGACGAMACACACTTTA	1289
Qy	1337	CTACGATCCGTAAGTCCCTTGTGGTGGGGTGTACCATGATCTACATTTGGCTATGGAG	1396
Db	1290	AAAAATATCCCATATGCGCTTCTGTGGGCTGTGGTACCATGACGACATGGGCTATGGAG	1349
Qy	1397	ACATGGCAACCGTCACTGTTGGGTGGCAAGATAGTGGGCTCTCTGTGTGCCATTGGGGCG	1456
Db	1350	ACATGTATCCCAAGACGTGGTCTGGAATGCTGTGGAGACCTTGTGTCTCTGGCTGGTG	1409
Qy	1457	TGCTGACTATTTCCCTGGCAAGTTCGCCGTCATTTGTCACAAATT	1499
Db	1410	TGCTGACCATTTGCCATATGCGGTGCTGTGATCATGTGACAAATTT	1452

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1      RESULT 12
2      US-08-464-340A-1
3      Sequence 1, Application US/08464340A
4      Patent No. 5710019
5      GENERAL INFORMATION:
6      APPLICANT: LI, ET AL.
7      TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
8      NUMBER OF SEQUENCES: 13
9      CORRESPONDENCE ADDRESS:
10     ADDRESSEE: CARLELLA, BYRNE, BAIN, GILFILLAN,
11     ADDRESSEE: CECCHI, STEWART & OLSTEIN
12     STREET: 6 BECKER FARM ROAD
13     CITY: ROSELAND
14     STATE: NEW JERSEY
15     COUNTRY: USA
16     ZIP: 07068
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: 3.5 INCH DISKETTE
19     COMPUTER: IBM PS/2
20     OPERATING SYSTEM: MS-DOS
21     SOFTWARE: WORD PERFECT 5.1
22     CURRENT APPLICATION DATA:
23     APPLICATION NUMBER: US/08/464,340A
24     FILING DATE: June 5, 1995
25     CLASSIFICATION: 435
26     PRIOR APPLICATION DATA:
27     APPLICATION NUMBER: PCT/US94/08449
28     FILING DATE: 28 JUL 1994
29     ATTORNEY/AGENT INFORMATION:
30     NAME: FERRARO, GREGORY D.
31     REGISTRATION NUMBER: 36,134
32     REFERENCE/DOCKET NUMBER: 325800-415
33     TELECOMMUNICATION INFORMATION:
34     TELEPHONE: 201-994-1700
35     TELEFAX: 201-994-1744
36     INFORMATION FOR SEQ ID NO: 1:
37     SEQUENCE CHARACTERISTICS:
38     LENGTH: 2127 BASE PAIRS

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; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
;
US-08-464-340A-1

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Query Match	161;	Score	161;	DB	1;	length	2127;
Best Local Similarity	48.88;	Pred. No.	7.1e-23;				
Matches	629;	Conservative	0;	Mismatches	630;	Indels	30;
						Gaps	6

QY	286	CGCCGGGGGCTGCGCGGCGCCATGTGAGCGCGCGGTGCTCCCGCGCCCGCGGGCTGTGCGAG	345
Db	438	CGCCAGGGGCTGTCAAGGCGCCGAGGACCGCCCGCTGGCATATCATCAAGCTAAGCGGGCATC	497
QY	346	CGGCTGGTGCCTCAACGTGGCCGGGCTGCGCTTTCGAGACGCGGGCGCGCACGCTGGGCGGC	405
Db	498	AAGTACTGCGTGGCCCTGGACACAGCGTGGAGAGATTCGCGTGCAGCGGCTGGGCCAGGCTC	557
QY	406	TTCCCGGACACTGTGCTAGGGGACCCAGCGCGCCGCGCGCTTCTAGCAGCAGCGCGGC	465
Db	558	AAGCGCTGCACCAACTTCGACGACATCTCAAGTGTGGATGACTACGACCTCACTGAC	617
QY	466	CGGAGATTTTCTTTCGACGCGGACCGGCGCCAGCTGTGAGCGCGTGTCTACTATCAACAG	525
Db	618	AAGCAGTTCTTCTTCGACCGCCAAACCCGGGGGCTTGTGGCATTACTCTGACTTCCCTGGCG	677
QY	526	TCCGGTGGGCGGCTGCGCGCGCCCGGCGCACGTGCGCCCTCGAGGCTTCTCTGGAAAGGTG	585
Db	678	GGGGGCAAGCTGGGGGCTGTGCGCGAGATGTGCGGCTGTC---CTTCCAGGAGAGGTG	734
QY	586	GCCTTCTACGGGCTGGGCGCGGCGCCCTGTGACGCTTCGCGGAGAGCAGAGGGCTGCGCG	645
Db	735	CTGTACTGGGGCATCTCGCGAGGACCACTGTGAGCGGTCTGCAAGGCGCGCTACTGTAG	794
QY	646	GTCGCGCGCCGACGGGCCCCCGCCCGCGCGGCTGTGGCCCGCAGCTGTGGCTCTTTC	705
Db	795	AAGATTAGAGATTTCCGGAGATGTGTGAGACGGGAGAAAGAGACAGCGCTGGACACAC	854
QY	706	GAGTTTCCCGAGAGCTC---TCAAGCGCGCGCGGCTGCTCGCGTATGTCTCCGTGTGTC	762
Db	855	GAGGGCGCGGCACAGCGAGGGCCCCGCGGAGGCGGAGAGGGCGGCTGGGGGCTGTGATGGGG	914
QY	763	ATCTCGTCTTCATCGTCGTCCTTCTGCGCTCGAGACGCTGCTGACTTCCGCGACGACCGC	822
Db	915	CGATCTGCGGCACATGTGTGGAGAGGCGCGCACTCGGGGCTGCTGTGGCAAGGTGTTCCTGTC	974
QY	823	GAGGGCAGGGGGGTGCTGTGTGAGCGGACCGAGCGGCGCGGTGTCCCGCTCGGTGAT	882
Db	975	C---TGTGGGTGCTCTTCGAGCGGTACCGCGCTGAACCTCTCCGTACGACCTTGGCC	1031
QY	883	GGCCTCAGCCAAATGCTGTGAAATTCACCCCGCGCTGACCCTTGAAATGACCCGTTCTTGCG	942
Db	1032	AGCGTAGGGAGGAGGAGGAGGACGAGGGCCACTGTTCACATGTGCGACAAAGCTTTTATTC	1091
QY	943	GTTGAGACGCTGTGTATTATTGTGTCTCTTTGAGCTGCTGTGTACGCTCTGTGCTGT	1002
Db	1092	GTTGAGTGTGCTGTGCGTGGGCTGTTCCTCCGTGGAATTCCTCTCGGGCTCAATTCAGCG	1151
QY	1003	CCAAAGCAAGGCTATCTTTCCTCAGAAAGCGATGAAACCTATGATTTTGTGGCTTATCTT	1065
Db	1152	CCACGACAGTTGCGCTTCTCTCGGAGACCGCGTBAAGCTATGAACTGTGTGCATCTCTG	1211
QY	1063	CCCTACT-----TTGTGGCACTGTGGACCGGACGCACTGGCCGCGAGGAGGGGTG	1110
Db	1212	CCCTACTACTACACGCTGCTGTGTGGAGCGCGCGCGGCGGCGGCTGTGCAAGCGCGGGCGG	1271
QY	1111	GGCCAG-----CAGGCACTGTCACTGGCCATCTCTGAGAGTATCCGATTGTGCTGTCTC	1166
Db	1272	GGCAACAGTACTGTGACCAAGGTGGGGGCTGTGTCTCGCGTCTCGGGCGCTGTGGCATTC	1331
QY	1165	TTCGCGATCTTCAACGTGTGCCGGGACACTAAMAGGCGCTCAATCTTGGGCGACAGCGTT	1222
Db	1332	CTGTACTGTATGTGGCTGTGGGCGCCCACTCCGTGGGGGCTGCACAGCCTGTGGGTCTCGCC	1391

QY 1225 CGGGCTCCATCGTGTAGTGGGCTCTCTCATCTTTTCCTCTTCAATCGGTGTCTC 1284
11
Db 1392 CGCGCTGACCGGAGTTCGGGCTCTGTGCTCTCTCTGCTGCGCATCGGCTC 1451
QY 1285 TTTTCCAGGCGGCTCTACTTTCGCCGAGTTGACCGGGTGA---CTCCATTCTACTAGC 1341
11
Db 1452 TTCGGGCCCCCTCTACTCTACATCGAAGAGATGGCCGACAGCCCCGATTCAACAC 1511
QY 1342 ATCCCTGAGTCTCTGTGGGGGGGAGTACACATGACATGAGTGGCTATGAGACATG 1401
11
Db 1512 ATCCCTGCTCTACTGTGGGCTGTGATCACCATGAGCGGTGAGCTATGGCGCATG 1571
QY 1402 GCACCGCTCACTGTGGGTGGCAAGATAGTGGGCTCTGTGTGCGCATTTGCGGGCTGTG 1461
11
Db 1572 GTCCCGAGAGACACCGCGGCGGAGTGTGGCTGTGAGCAGCATCTGTGAGCGGCTGTG 1631
QY 1462 ACTATTTCCCTCCAGTGGCCGCTCATTTGTCTCAATTTTCAGCTACTTTATCACCGGGAG 1521
11
Db 1632 CTCATGGCTTCCAGTACCTTCATCTTCCACACTTCTCCCGCTCTTACCTGTGAGCTC 1691
QY 1522 ACAGAGGCGAAGGCTGGATGTTCCG 1550
11
Db 1692 AAACAGGAGCAAGAGAGGCTGATGTTCCG 1720

RESULT 13

PCT-US94-08449A-1
Sequence 1, Application PC/TUS9408449A
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Potassium Channel Protein 1 and 2
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08449A
FILING DATE: SUBMITTED HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2127 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
PCT-US94-08449A-1

Query Match 9.6%; Score 161; DB 5; Length 2127;
Best Local Similarity 48.8%; Pred. No. 7,1e-23;
Matches 629; Conservative 0; Mismatches 630; Indels 30; Gaps 6;

QY 286 CGCGGGGCTCGCGCGCATGAGAGCCGCGGTGCCCGCCCGCTGCGGCTGTCGAG 345
11
Db 438 CGCCAGGCGCTGTGAGCCCGGAGACCGCCGCCCTGGATATATCAACGAGGCGGCATC 497
QY 346 CGGCTGTGTCAAGTGTGCGGGCTGCGCTTGTGAACGCGGGCGGACGCTGGGCGG 405
11
Db 498 AATGACTGCTGCGCTGAGACACGCTGTGACGAGTTCCTGCTGAGCGGCGGCGGCTC 557
QY 406 TTCCGGACACCTGCTAGGGGACCCAGCGCGCGGCGGCTTACAGCAGAGGCGGCG 465
11
Db 558 AAGGCTGCACCACTTCGACGACATCTCAAGTGTGCGATGACGACGTACACTGTG 617
QY 466 CGGAGTATTTCTTCGACGCGGACCGCGCCAGCTTGTGACGCGCTGTCTACTACTAC 525
11
Db 618 AAGGATTTCTTTCGACCGGCAACCGGGGCGCTTGGGACATTCCTGACCTTCGCGG 677
QY 526 TTCGGTGGGCGCTGCGGCGGCGGCGACAGTGGCTGTGACGCTTCTGTGAAGAGTG 585
11
Db 678 GCGGCGAAGCTGCGGCTGTGCGCGAGATGTGCGGCTGTG---CTTCCAGAGAGCTG 734
QY 586 GCGCTTACGGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 645
11
Db 735 CTGTACTGGGCGATCGCGGAGACACCTGTGACGCTGTGACAGGCGCGCTACGTGAG 794
QY 646 GTGCGCGCGGAGCTTTC 705
11
Db 795 AAGATTGAGGATGCTCCGAGATGTGTGAGCGGAGAGAGAGACAGCGGCTGTGAGCAG 854
QY 706 GAGTTTCCGAGAGCTC---TCAGGCGGCGGCGGCTGTGCGCTGTCTCTGCTGTGTC 762
11
Db 855 GAGGCGCGGAGACGAGGAGGCGCGGCGGAGGAGGAGGAGGCGCGGCTGTGAGGCGG 914
QY 763 ATCTGTCTCCATGCTGCT 822
11
Db 915 CGACTCGGAGACATGTGTGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 974
QY 823 GAGGCGAGGCGGCTGTGCTGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 882
11
Db 975 C---TGTGCTGTCTTCTGTGAGCTGTACCGGCTGTACCTCTCTCTCTCTCTCTCTCT 1031
QY 883 GCGTCCAGCCAAATGCTGTGAAATTCACCCCGGCTGTCTCTCTCTCTCTCTCTCTCTCT 942
11
Db 1032 AGCGTGAAGGAG 1091
QY 943 GTGGAACGCTGTGTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1002
11
Db 1092 GTGGAGT 1151
QY 1003 CCAAGCAAGGCTATCTTCTCAAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1062
11
Db 1152 CCCAGCAAGTGTGCTTCTGCGGAGCGGCTGTACGCTGTATGACCTGTGCTGTGCTGTG 1211
QY 1063 CCGTACT-----TTGTGGCATGGGACCGAGCTGGCCGCGGACGAGGAGTG 1110
11
Db 1212 CCTTACTATACATCAGCTGT 1271
QY 1111 GGGCAG-----CAGGCAATGTATGCGCATTCCTGTAGAGTCAATCCGATTGTGTGTGT 1164
11
Db 1272 GGGCAACGCTACCTGTGACAAAGGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1331
QY 1165 TTCCGATCTTCAAGCTGT 1224
11
Db 1332 CTGTACTGTATGTGCGCTGTGCGGCGGCTGTGAGAGCGTGTGAGAGCGTGTGAGGCG 1391
QY 1225 CGGCGCTCATGT 1284
11
Db 1392 CGCGCTGTGACCGCGGAGTTCGGGCTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1451
QY 1285 TTTTCCAGGCGGCTGTACTTTCGCCGAGTTGACCGGGTGA---CTCCATTCTACTAGC 1341
11
Db 1452 TTCGGGCCCCCTGTACTCTACATCGAAGAGATGGCCGACAGCCCCGATTCAACAC 1511
QY 1342 ATCCCTGAGTCTCTGTGGGGGGGAGTACACATGACATGAGTGGCTATGAGACATG 1401


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; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; PCT-US94-08449A-3

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Query Match	9.1%;	Score 152.8;	DB 5;	Length 2483;
Best Local Similarity	53.0%;	Pred. No. 2.8e-21;		
Matches 350;	Conservative 0;	Mismatches 307;	Indels 3;	Gaps 1

QY	943	GTGGAGACGGCTGGTATTTTGTGGTCTCTCTTGTAGACCTGCTGTAGCGCTCGTGCTGT	1002
Db	1357	GTGGAGACGGCGTGACATTTGGCTGGTTCCACCCTGGAGTACCTCTCGCCTCTTCTCGTCA	1416
QY	1003	CCAAGCAGGCTATCTTCTTCAAGAACGTGATGAACCTCATCGATTTGTGGCTATCCCTT	1062
Db	1417	CCCAACACGTGACACTTGTCCGGCTGTCTCTTCATGAACATTTGGAGCTGTGGCCATCTTC	1476
QY	1063	CCCTACTTGTGGACACTGGGCAACCGAGCTGGCCCGGCACGAGGGGTGGGCCACGAGGCC	11222
Db	1477	CCCTTCTACGTGACCTCACGCTCACGCAACCTGGGGGCCCGCATATGAGCTGTGACCAAC	1536
QY	1123	ATGTACATGGCCATCCCTGAGAGTCAATCCGATTTGGTGTCTGTCTCCGATCTTCAAGCTG	1182
Db	1537	GTGCAGCAGGCGCGAGAG--GCGCTGGGATGATGATGCGATGCGCGCATCTTCAAGCTG	1593
QY	1183	TCCCGGCACTCAAGGGCCCTGCAATCTTGGGCGAGACGCTTGGGACCTCCATGCGGTAG	1242
Db	1594	GCCCGCCACTCTCGGGGCCCGAGACCCTACCTAAGCCCTCAACGCGAGCTTCAAGGAA	1653
QY	1243	CTGGGCGCTCCATCTTTTCCCTTCATCCGGGTGGTGCCTCTTTCAGAGCGCGCTATAC	1302
Db	1654	CTGGGGCTGCTGCTCATGTACCTGGGAGTGGGTATCTTGTCTTCTTGGCCCTGGGCTTAC	1713
QY	1303	TTTGGCGAAGTTGACCGGGGTGACTCCCATTTCACTAGCATCCCGAGTCTTCTGTGATG	1362
Db	1714	ACCATGGAGCAGAGACCATCCAGAGACCCGTTTAAGAACATCCCCAGACCTCTTGTGGG	1773
QY	1363	GGGCTACTCAACGATGACTACAGTGGCTATGAGAGATGAGGACCCCTGACATGTGGGTGGC	1422
Db	1774	GCACTATCAACCATGACACCCGCTGGCTACGGGAGATCTACCCCAAGACACAGCTGTAGC	1833
QY	1423	AGATTAAGTGGGCTCTCTGTGTGGCATTTGGGGGCGTGGTACTATTTTCCCTGGCAAGTCCC	1482
Db	1834	AAGCTCAAGCGGGCATACAGCTCTTGTGTGGGTGATTTGCCATGCGCTGCGCATCTCAC	1893
QY	1483	GTCATTGTCTCCAAATTTCAAGCTACTTTTATCAACCGGAGAGACAGAGGGCGAAGAGGCTGGG	1542
Db	1894	CCCATCTCAACAACATTTGTCAAGTACTCAACAAAGCAGCGGTCTGTGAGACGCGCGCC	1953
QY	1543	ATGTTCAGCCATGGAGCATGAGAGCGCTTGTGGGCCCACTGGAGAGGAAGGCCAATGGGGGG	1602
Db	1954	AAGCAGCAGCTGGAGCTGATGGTAACTCAACTCCAGCAGCGGGGGGAGAGGCAACGCGGG	2013

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Search completed: February 20, 2003, 06:35:32
Job time : 97.0574 secs
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D	b	584	GAACCTCATTAGACATCGTGTCCATTTTCGCTTAATTTCACTGTCCGCAGACGTGGC	525
O	y	1095	CCGGCAGCGAGGGGTGGGCCACAGACAGCCATGTCACTGGCCATCTGAGAGTCATCCGATT	1154
D	b	534	CCAGCACACGAGGCAACGGGACAGAACGCATCATS--TTCCGCATCTCGAGAAATAAATCCGCT	466
O	y	1135	GGTGGTGTCCTTCGSCATCTTCAAGCTGTCCGGGACATCAAAGGGCCGTGAATCTTGG	1214
D	b	465	GGTCCGCTGTTCGSCATCTTCAATCTGTCCAGACTGTCAAAGGGGCTGCAGATCTTGG	406
O	y	1215	CCAGACGGTTGGGGGCTTCATATGCGTGAAGCTGGGCTCCCTCATCTTTTTCCTTCATCG	1274
D	b	405	CCATACCCTCGCGCGCAGACATGAGGAGACTGGCCCTCTCATTTTCTTGTGGATCGG	346
O	y	1275	TGTGGTCTCTTTTCCAGCGCCGTCTACTTTGCGAGAATTGACCGGGTGACTCCCATTT	1334
D	b	345	CGTATCCTCTTTTCCAGCGGCTACTTGTGCGAGGCGAGACGACCCACTCTCCATTT	286
O	y	1335	CACATAGCATCCCTTAGTCTTCTGTGGGGGTGTAATACATGACTACAGTTGGCTATGG	1394
D	b	285	CACACGACATCCCCGACGGTGTGTGGGCTGTGTAACTATGACGAGGGGTGATACGG	226
O	y	1395	AGACATGTGACCCCGCATCTGTGGGCGGAGAATAGTGGGCTCTGTGTGCTATTCGGG	1454
D	b	225	CGATATGAAAGCTATACAGGTCGTGGGGAAGATCTGTGGGCTCCGTGTCCGCATTCGGG	166
O	y	1455	CGTCTGACATATTTCCCTGCCAGTGGCCCGTCATGTCTCCAAATTTCACTACTTTATCA	1514
D	b	165	CGTGTAAACGATCGCGCTGCG-C-GTCCCGGTATCTGTCCAACTTTAATTTACTTTTACA	107
O	y	1515	CCGGAGACAGAGGGCGGAAGA	1535
D	b	106	CCGGAGACCGATAACGAAGA	86

RESULT 5
Locus CNS03DKC/c

LOCUS DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 017A20 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL239205

VERSION AL239205.1 GI:7898340

KEYWORDS GSS: genome survey sequence.

SOURCE Tetraodon nigroviridis

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphae; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodonidae; Tetraodon.

REFERENCE 1 (bases 1 to 839)
Roest-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Flzames,C., Wincker,P., Broitler,P., Quetier,F., Saurin,W. and Weissensbach,J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

.TITLE Unpublished

JOURNAL 2 (bases 1 to 839)
Roest-Crollius,H., Jalllon,O., Dasilva,C., Flzames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissensbach,J.
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

COMMENT Unpublished
Genoscope.
Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
<http://www.genoscope.cns.fr/tetraodon>.

[illegible]

RESULT 7						
A1322534						
LOCUS	A1322534	522 bp	mrna	linear	EST 23-DEC-1998	
DEFINITION	mh3g06.y1	Scores mouse placenta	4NMPL3.5	14.5 Mus musculus	cdna	

clone IMAGE:457594.5' similar to gb:xl7622_cds1 POTASSIUM CHANNEL PROTEIN KV1.6 (HUMAN);, mRNA sequence.

ACCESSION	A1322534
VERSION	A1322534.1
KEYWORDS	EST.
SOURCE	house mouse.

Euarchyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 522)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

REFERENCE

AUTHORS

TITLE	EST	PROJECT
The Washu-HHMI Mouse	EST	Project
Unpublished (1996)		
CONTACT: Marra M/Mouse	EST	Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:274482
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop:367.

```

FEATURES
SOURCE
Location/Qualifiers
1. .522
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image:457594
/clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT73D-Pac (Pharmacia)

```

with a modified polylinker: Site-1: Not I; Site-2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5].

TGTTACCAATCTGAAGTGGAGCGCGCCGCGAATTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT	58 a	192 c	188 g	84 t
ORIGIN				

Query Match	19.7%	Score 331.4	DB 9	Length 522
Best Local Similarity	81.9%	Pred. No. 3e-54		
Matches 407; Conservative	0	Mismatches 66	Indels 4	Gaps 2

148 GTCGCCCTCCGCCCCGCGGGGTACAGTGCCTCCCTCGCGCCCTAGCGCCCTGCC 207

Db 28 GCGGCCCTAGCCCCGCGGGGTAAACACCGCCCCCTCCCCCGGCCCTGGCCGGACTTTC 87

208 GGGCTATTTTACGCGCGGACACCGGACACCGGGCTGGGGCGGGCTCGGGCC 267

Db 88 CATGCTATTTTACCCCGCCGACACCGGACACCCGACTGGGGTGGCTGGGGCGTGGGGCC 14/

268 ACACGTCGGTTCGCGGGTCGCGCGCCCAAGAGCCCGGTCGCCGCC 327

DB 148 ACACGTCGATCACCGATGCCCCGGCAGTGTGCGGCGATGGAGCCACCGATGCCCCCGCC 207

[illegible][illegible][illegible][illegible][illegible]

005 565

[illegible]

556 ACGCTCTTCCGGAAGAGGTGGCCCTTACACGGCTGGGCGCGGCGCGCCCTGGCCACGCCCTGCC 625

446 CGGTCTTCTGAGGAGGTCTTCTACGGCTGGGCGGCGGCGCTTGGCGGCTGC 505

0v 626 GCGAGGACGAGGCTGC 642

Db 506 GGGAGGACGAGGGCTGC 522

RECEIVED
B117089

DEFINITION .602867882F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:5016164 5',

ACCESSION BILL7089
1117000 1 OF 1457000

KEYWORDS	EST.
CONDUCT	business

ORGANISM	Homo sapiens
Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:	

REFERENCE
1 (bases 1 to 876)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA LIBRARY PREPARATION: LING HONG/KUOLN LABORATORY

QY 1283 TCTTTTCAGAGCCGCTCTACTTTCGCGAAGTTGACCGGGTGAGCTCCATTTCTAGCA 1342
 Db 361 TCTTTTCAGAGCCGCTCTACTTTCGCGAAGTTGAGTGTGACTGCTTCCATGCA 420
 QY 1343 TCCCTAGTCTTCTGTGTGGCGGTAGTACCATCTAGTGTGCTATGAGACATGG 1402
 Db 421 TCCCATATGCTCTGTGTGGCGGTAGTACCATCTAGTGTGCTATGAGACATGT 480
 QY 1403 CACCCCTCATCTGTGGGTGAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1462
 Db 481 ACCCATGACGTAGGGGAGAGATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 1463 CATTTTCCCTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1522
 Db 541 CATTTTCCCTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 QY 1523 CAGAGGCGCAGAGAGCTGGAGTTTCAACCATGT 1556
 Db 601 CGGAGCAGAGAGAGAGCTGGAGTTTCAACCATGT 634

RESULT 11
 B1764377 772 bp mRNA linear EST 25-SEP-2001
 LOCUS 603046295F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186518 5',
 DEFINITION mRNA sequence.
 ACCESSION B1764377
 VERSION B1764377.1 GI:15755955
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 772)
 AUTHORS NIH-MGC Eutheria: Primates; Catarrhini; Hominiidae; Homo.
 TITLE Mammalia: Eutheria: Primates; Catarrhini; Hominiidae; Homo.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgarbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM11465 row: n column: 23
 High quality sequence stop: 772.
 Location/Qualifiers
 1..772

FEATURES
 source
 1..772
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="5186518"
 /clone_lib="NIH_MGC_116"
 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs; 62 yo male and 70 yo female. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb.
 Insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH_MGC Library."

BASE COUNT 150 a 240 c 236 g 146 t
 ORIGIN

Query Match 18.5%; Score 311.4; DB 13; Length 772;
 Best Local Similarity 76.6%; Pred. No. 2.3e-50;
 Matches 416; Conservative 0; Mismatches 106; Indels 21; Gaps 2;

QY 1018 TTCTTCAGAGCGATGATGAACCTCATCAGATTTTGTGGCTATCCCTTACTTTGTGGCA 1077
 Db 19 TTCTTCAGAGCGATGATGAACCTCATCAGATTTTGTGGCTATCCCTTACTTTGTGGCA 78
 QY 1078 CTGGGACCGAGCTGGCCCGGACGAGGGGTG- 66CCAGC 1117
 Db 79 CTGGGACCGAGCTGGCCCGGACGAGGGGTG- 66CCAGC 138
 QY 1118 AGGCGATGCTACGCGCATCTGAGATCATCCGATGTGGTGGCTGCTGCTGCTGCTG 1177
 Db 139 AGGCGATGCTACGCGCATCTGAGATCATCCGATGTGGTGGCTGCTGCTGCTGCTG 198
 QY 1178 AGCTGTCCCGGACCTCAAGAGGCTGAGATCTGGGCGAGAGCTTGGGCGCTCATGC 1237
 Db 199 AGCTGTCCCGGACCTCAAGAGGCTGAGATCTGGGCGAGAGCTTGGGCGCTCATGC 258
 QY 1238 GTGAGCTGGGCTCTCATCTCTTTTCTCTTTTCTCTTTTCTCTTTTCTCTTTTCT 1297
 Db 259 GTGAGCTGGGCTCTCATCTCTTTTCTCTTTTCTCTTTTCTCTTTTCTCTTTTCT 318
 QY 1298 TCTACTTGGCGAAGTTGACCGGGGTGACATCCATTTCTAGTATCCCTGAGTCTTCT 1357
 Db 319 TCTACTTGGCGAAGTTGACCGGGGTGACATCCATTTCTAGTATCCCTGAGTCTTCT 377
 QY 1358 GGTGGGCGGTAGTACCATCTGAGTGTGCTATGAGAGCATGCGACCCGCTCATGTGG 1417
 Db 378 GGTGGGCGGTAGTACCATCTGAGTGTGCTATGAGAGCATGCGACCCGCTCATGTGG 437
 QY 1418 GTGGCAGATATGAGGCTCTGTGTGTCATTTGGGGGCTGTGACTATTTCCCTGGCAG 1477
 Db 438 GTGGCAGATATGAGGCTCTGTGTGTCATTTGGGGGCTGTGACTATTTCCCTGGCAG 497
 QY 1478 TGCCCGCTATGCTCTGCAATTTGAGTCTTTATCACCAGGACAGAGGCGAAGAG 1537
 Db 498 TGCCCGCTATGCTCTGCAATTTGAGTCTTTATCACCAGGACAGAGGCGAAGAG 557
 QY 1538 CTG 1540
 Db 558 CGG 560

RESULT 12
 BML28683 575 bp mRNA linear EST 12-MAR-2002
 LOCUS BML28683
 DEFINITION if14f08.y1 Melton Normalized Human Islet 4 M4-HIS 1 Homo sapiens
 cDNA clone IMAGE:5676446 5' similar to SW:CIK3_HUMAN p22001
 ACCESSION BML28683
 VERSION BML28683.1 GI:17123227
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 575)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 TITLE if14f08.y1 Melton Normalized Human Islet 4 M4-HIS 1 Homo sapiens
 JOURNAL cDNA clone IMAGE:5676446 5' similar to SW:CIK3_HUMAN p22001
 COMMENT VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL3 ; mRNA sequence.

TITLE Endocrine Pancreas Consortium
 JOURNAL Unpublished (2000)
 COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@molbio.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center For information on

OY	1170	CATCTTCAAGCGTCGCCGACATCAAAGGCCTCAAAATCTTTGGCCACAGCCTTCGGGC	1229
Db	121		180
OY	1230	CTCCATGGGTGAAGTAGGGCCCTCATCTCTTTTCTCTTCAATCGGCTGTGCTCTTTTC	1289
Db	181		240
OY	1290	CAGGCGCCTCTACTTGTGCCGAAGTTGACC GGSTGGAGCTCCCATTTTCACTAGATCCCTGA	1349
Db	241		300
OY	1350	GTCCTCTTGAGGGGGGTAGTACACCATGACTACTGATTGAGTATGAGACATGGACCGGT	1409
Db	301		360
OY	1410	CACGTGTGGGTGGCAAGATAGTGGGCTCTGTGTGCCATTGGGGGGCGTGTGACTATTTTC	1469
Db	361	GACCATATGAGGGGACAGATTGTGGGATCTCTGTCTGCCATTCGGCGGGTGTGTGACCATGCG	420
OY	1470	CCTGCACTGGCCCCGATCTTGTCTCCAATTTCAAGTACTTTTATCACCGGGAGACAGAGGG	1529
Db	421		480
OY	1530	ATTGGCACTTCCCCTGATGATGTTTCCCACTTCAATTACTTTCACACCGGAGACAGAAGG	1598
Db	481		509
RESULT 14			
LOCUS	B0807519	628 bp	mRNA linear EST 31-JUL-2002
DEFINITION	NISC_KK05c10.y2_NCI_CGAP_Brn72 Macaca mulatta cDNA clone		
ACCESSION	B0807519		
VERSION	B0807519.1	GI:22031728	
KEYWORDS	EST.		
SOURCE	Rhesus monkey.		
ORGANISM	Macaca mulatta		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
TITLE	Cercopithecinae; Macaca.		
JOURNAL	1 (bases 1 to 628)		
COMMENT	NCI-CGAP http://www.ncbi.nlm.nih.gov/hic/cgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-tr@mail.nih.gov CDNA Library Preparation: CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNLN DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC) Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: info@image.lnl.gov plate: LHAM1839 row: E column: 19 Seq primer: M13RP1 reverse primer (ABI). Location/Qualifiers 1..628 /organism="Macaca mulatta" /db_xref="taxon:9544" /clone="IMAGE:5330682" /clone_lib="NCI_CGAP_Brn72" /tissue_type="hypothalamus" /lab_host="DH10B (phage-resistant)" /note="Organ: brain; Vector: pCMV-SPORT6, ccdb; Site:1; NotI; Site:2; EcoRV; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.2 kb. Constructed by Invitrogen. Note: this is a NCI_CGAP library."		
FEATURES			
SOURCE			
BASE COUNT	105 a	212 c	181 g 130 t
ORIGIN			

Query Match	18.0%	Score 302	DB 14	Length 628
Best Local Similarity	68.5%	Pred. No. 1.5e-48		
Matches 441	Conservative 0	Mismatches 185	Indels 18	Gaps 1
QY	488	ACCGGCCAGCTTGACGCGCGTCTACTACTATACAGTCGCGTGGCGGCGCGC	547	
Db	3	ACCGGCCAGCTTGACGCGCGTCTACTACTATACAGTCGCGTGGCGGCGCGC	62	
QY	548	CGCGGCACGTCGCGCTCGAGCTCTTCTGGAAGAGTGGCTTCTACGCGCTGGCGCGG	607	
Db	63	CGGTCAAGTCCCATCATCATCTCTCTCCGAGAGATCCGCTTACACAGCTGGCGCGAGG	122	
QY	608	CGGCGCTGGCAAGCGCTGGCGGAGACGAGGGGTGCGCGCGCGCGCGCGCGCGC	667	
Db	123	AGCGCATGGAAGATCTCCGACGAGACGAGGGGTTCTCTCGGAGAGGAGCGCGCTTGC	182	
QY	668	CCCGCGCGCGCTTGCGCCCGCAGCGAGTGGAGCTTTTCCGAGAGCTTCACG	727	
Db	183	CCCGCGCGCGCTTGCGCCCGCAGCGAGTGGAGCTTTTCCGAGAGCTTCACG	242	
QY	728	CCGCGCGCGTCTGCGCGCTAGTCTCTCGTGGTGTATCTCTGTCTCATCTGCTTCT	787	
Db	243	CAGCGCGCGCGCTGCGCGCTAGTCTCTCGTGGTGTATCTCTGTCTCATCTGCTTCT	302	
QY	788	GCTCTGAGACGCTGCGCTACTTCCGCGACGACCGCGAGCGGAGCGGCGTGTGTGAG	847	
Db	303	GCTCTGAGACGCTGCGCTACTTCCGCGACGACCGCGAGAGAGACTACCGCGCTGCGAGG	362	
QY	848	CCGAGCGCGCGCGTGTCTCCCGCTCGCGTGAATGAGCTCCAGCCCAATGCTGGAAATC	907	
Db	363	ACTCATCTGATGACAGCGCGCAACAGCACGTCGCGGCGCGCGCGGAGCGCTTCAG	417	
QY	908	CACCGCGCGCTGCTTCAATGACCGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT	967	
Db	418	-----CTTCTCGGATCT	464	
QY	968	TCTCTTGTGAGCTGT	1027	
Db	465	TCTCTTGTGAGCTGT	524	
QY	1028	ACGTGATGACCTCATGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1087	
Db	525	ACATCATGACCTCATGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	584	
QY	1088	AGCTTGGCGCGCGCGAGCGAGGGGTGGCGCAGAGCCATGTCTACTG 1131		
Db	585	AGCTTGGCGCGCGAGCGAGGGGTGGCGCAGAGCCATGTCTACTG 628		
RESULT 15				
CNS058RO				
LOCUS				
DEFINITION				
LOCUS				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
REFERENCE				

Search completed: February 20, 2003, 11:45:25
Job time : 2806.74 secs

AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Fizes, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1060)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
1. 1060
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/db_xref="taxon:99883"
/clone="020119"
/clone_lib="A"
/note="Genoscope sequence ID : C0AA020CF10C1-end : 77"
BASE COUNT 238 a 239 c 231 g 309 t 43 others
ORIGIN
Query Match 17.7%; Score 296.6; DB 17; Length 1060;
Best Local Similarity 68.4%; Pred. No. 1.7e-47;
Matches 437; Conservative 0; Mismatches 198; Indels 4; Gaps 2;
QY 900 TGGAAATCCACCCCGCTGCTTCATGACCGCTTCTGCTGGAGAGCGCTGTAT 959
DB 8 TGCAGCACCATCTCNGNAGCCATCTCCNATCCCTTCTCATCTGAGAGCCGCTTCAT 67
QY 960 TTGTTGTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1019
DB 68 TCGTTGTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
QY 1020 CTTCAAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1079
DB 128 CTTTCACACACCTCATGACATTTATGATATGATATGATATGATATGATATGAT 187
QY 1080 GGGCAGCAGAGCTGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1136
DB 188 GGTACAGAAATCTCACAACACCGAGAGAGCTCAGAGAGAGAGAGAGAGAGAG 247
QY 1137 CTTGAGAGTATCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1196
DB 248 TCTGCGCATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 307
QY 1197 GGGCTGCAATCTGGGCGAGAGCTGGGCGCTGCTGCTGCTGCTGCTGCTGCT 1256
DB 308 GGGCTGCAATCTGGGCGAGAGCTGGGCGAGAGAGAGAGAGAGAGAGAGAGAG 366
QY 1257 CTTTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1316
DB 367 TTTTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
QY 1317 CCGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1376
DB 427 CGAGCCAAACACGAGTGTGAGCATACCGAGAGAGAGAGAGAGAGAGAGAG 486
QY 1377 GACTACAGTGGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1436
DB 487 GACTACAGTGGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546
QY 1437 TCTGTGTCATGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1496
DB 547 GCTGTGTCATGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1556
QY 1497 TTTACAGTCTTTATACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1535
DB 607 CTTTACTACTTCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 645

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 19, 2003, 23:59:06 ; Search time 133.056 Seconds
(without alignments)
9410.374 Million cell updates/sec

Title: US-09-804-014a-7_COPY_970_1525

Perfect score: 556
Sequence: 1 gtctctgctgtgtgagacgc.....ccctgcagtcgcgcattc 556

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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- 24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	100.0	1341	24	ABL57038 Human potassium ch
2	556	100.0	1686	23	AA578540 DNA encoding novel
3	556	100.0	1747	22	AA513338 Human CDNA encodin
4	556	100.0	1792	24	AA537899 Human ion channel
5	532	95.7	691	24	AA528734 Human ion channel
6	436.6	78.5	1598	16	AA504953 Mouse Kv1.7 voltag
7	334.2	60.1	1836	22	AA521452 Human Kv1.5 DNA.
8	334.2	60.1	2867	24	AA595856 Gene #2354 used to
9	334.2	60.1	24	ABL5917	Lung cancer relate

10	311.8	56.1	3147	24	AB199654 Mouse ischaemic co
11	273.4	49.2	2157	22	AA529512 Human endocrine po
12	273.4	49.2	2159	23	ABK43428 DNA encoding novel
13	233.8	42.1	492	22	ABK06356 Human CDNA SEQ ID
14	233.8	42.1	492	22	AA528936 CDNA encoding for
15	233.8	42.1	492	22	AA529636 Human endocrine po
16	233.8	42.1	492	22	AA530165 DNA encoding rena
17	233.8	42.1	492	22	ABK43751 DNA encoding novel
18	211	37.9	7642	24	AB133116 Human immune syste
19	209.2	37.6	2237	23	AB132855 Drosophila melanog
20	195	35.1	7642	24	AB133117 Human immune syste
21	190.2	34.2	8758	24	AB133119 Human immune syste
22	180.2	32.5	7488	24	ABK33112 Human immune syste
23	180.2	32.4	998	22	ABK43164 Human breast cell
24	180.2	32.4	998	22	ABK53583 Human foetal liver
25	180.2	32.4	998	22	ABK23338 Human foetal liver
26	180.2	32.4	998	22	ABK01849 Probe #1804 for ge
27	180.2	32.4	998	22	ABK27308 Human brain expres
28	180.2	32.4	998	22	AA111882 Probe #1815 for ge
29	180.2	32.4	998	22	AA133209 Probe #1895 used t
30	180.2	32.4	998	22	AA101820 Probe #1811 used t
31	180.2	32.4	998	24	ABK01828 Human genome-deriv
32	180.2	32.4	1340	22	ABK50280 Human breast cell
33	180.2	32.4	1340	22	ABK68220 Human foetal liver
34	180.2	32.4	1340	22	ABK35230 Probe #13696 for g
35	180.2	32.4	1340	22	AAK16601 Human brain expres
36	180.2	32.4	1340	22	AAK42356 Human bone marrow
37	180.2	32.4	1340	22	AA123127 Probe #13060 for g
38	180.2	32.4	1340	22	AA148435 Probe #17121 used
39	180.2	32.4	1340	22	AA108782 Probe #8773 used t
40	180.2	32.4	1340	24	ABK16411 Human genome-deriv
41	180.2	32.4	1979	22	ABK54144 Human breast cell
42	180.2	32.4	1979	22	ABK55622 Human foetal liver
43	180.2	32.4	1979	22	ABK25318 Probe #3784 for ge
44	180.2	32.4	1979	22	AAK03850 Human brain expres
45	180.2	32.4	1979	22	AAK29317 Human bone marrow

ALIGNMENTS

RESULT 1	ABL57038 standard; cDNA; 1341 BP.
ID	ABL57038.
AC	ABL57038.
XX	
DT	22-JUL-2002 (first entry)
XX	
DE	Human potassium channel 12189 partial cDNA.
XX	
KW	Potassium channel; ion transport; 12189; noctropic; anticonvulsant;
KW	neuroprotective; antiparkinsonian; hypotensive; neuroleptic;
KW	antidepressant; antianemic; tranquilizer; anorectic; antitachycardic;
KW	antiarteriosclerotic; vasodilator; antidiabetic; antihypertensive;
KW	cardiac; antiinflammatory; cytostatic; osteopathic; hepatotropic;
KW	antidiabetic; immunosuppressive; antitachycardic; antirheumatic;
KW	antipruritic; antihypertensive; antitumor; dermatological; antianemic;
KW	antiallergic; antiallergic; ophthalmological; immunomodulator;
KW	analgesic; virucide; human; gene therapy; gene; ss.
XX	
OS	Homo sapiens.
XX	
PH	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	1..1341
FT	/*tag= a
FT	/product= "12189"
FT	/partial
FT	/note="The CDS does not include a start codon"
PN	W0200194390-A2.
XX	
PD	13-DEC-2001.

PF	06-JUN-2001.	2001WO-US183440.
XX		
PR	06-JUN-2000.	2000US-209845P.
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
XX		
P1	Curtis RAW;	
DR	WPI: 2002-401589/43.	
PT	P-PDB: ABB76166.	
XX		
XX	New potassium channel family member polypeptide and polynucleotide,	
PT	useful for diagnosing, treating viral diseases, neurological, cardiac	
PT	cellular proliferative or differentiative, bone, immune, liver and	
XX	metabolic disorders -	
PS	Claim 1; Page 135-136; 158pp; English.	
XX		
CC	The present sequence is that of a partial cDNA for human 12189	
CC	(see ABB76166), a novel potassium channel family member. 12189	
CC	contains a potassium channel tetramerisation domain, an ion	
CC	transport protein domain and a core membrane region including 6	
CC	transmembrane domains. The invention provides human potassium	
CC	channel 52906, 33408 and 12189 nucleic acids and proteins, as well	
CC	as antisense nucleic acid molecules, recombinant expression vectors,	
CC	host cells, transgenic animals, fusion proteins, antigenic peptides	
CC	and antibodies. Also claimed are: a method for detecting the	
CC	presence of a 52906, 33408 or 12189 nucleic acid; a method for	
CC	modulating the activity of a 52906, 33408 or 12189 polypeptide using	
CC	a compound that binds the polypeptide; a method for identifying a	
CC	compound which modulates the activity of the polypeptide; a method	
CC	of treating or preventing an ion flux-related disorder using an	
CC	agent that modulates the activity or expression of a 52906 or	
CC	12189 polypeptide or nucleic acid, especially a peptide,	
CC	phosphopeptide, small molecule, antibody, antisense molecule,	
CC	rhozyme, a triple helix molecule, or a 52906 or 12189 nucleic	
CC	acid. The ion flux-related disorders include: potassium channel	
CC	associated disorders, such as neurological disorders and central	
CC	nervous system disorders such as cognitive and neurodegenerative	
CC	disorders e.g. Alzheimer's disease, Parkinson's disease, senile	
CC	dementia, Huntington's disease, Gilles de la Tourette's syndrome,	
CC	multiple sclerosis, progressive supranuclear palsy, epilepsy.	
CC	Jacob-Creutzfeldt disease, autonomic function disorders such as	
CC	hypertension and sleep disorders, neuropsychiatric disorders such	
CC	as depression, schizophrenia, mania, anxiety disorders or phobic	
CC	disorders, learning or memory disorders, amnesia or age-related	
CC	memory loss, attention deficit disorder, obsessive-compulsive	
CC	disorder, migraine or obesity; cardiac-related disorders such as	
CC	arteriosclerosis, ischaemia reperfusion injury, restenosis, arterial	
CC	inflammation, tachycardia, congestive heart failure, myocardial	
CC	infarction and arrhythmia. The polypeptides and nucleic acids are	
CC	also useful as diagnostic targets and therapeutic agents for:	
CC	controlling cellular proliferative and/or differentiative disorders	
CC	e.g. haematopoietic neoplastic disorders, carcinoma and sarcoma;	
CC	disorders associated with bone metabolism such as osteoporosis,	
CC	rickets, osteopenia, cirrhosis, hyperparathyroidism, idiopathic	
CC	hypercalcaemia; immune disorders such as autoimmune thyroiditis,	
CC	diabetes mellitus, arthritis, including rheumatoid arthritis,	
CC	osteoarthritis and psoriatic arthritis, multiple sclerosis,	
CC	myasthenia gravis, autoimmune thyroiditis, ulcerative colitis,	
CC	psoriasis, Sjogren's syndrome, dermatitis, Crohn's disease, asthma,	
CC	allergic asthma, conjunctivitis, aplastic anaemia, Grave's disease,	
CC	chronic active hepatitis, autoimmune uveitis, scleroderma; liver	
CC	disorders including storage disorders such as Gaucher's disease,	
CC	glycogen storage disease, haemochromatosis and peroxisomal	
CC	disorders; viral diseases; pain; or metabolic disorders such as	
CC	obesity, anorexia nervosa, cachexia, lipid disorders and diabetes.	
XX		
S0	Sequence 1341 BP: 190 A; 443 C; 411 G; 297 T; 0 other:	
Query Match	100.0%;	Score 556; DB 24; Length 1341;
Best Local Similarity	100.0%;	Pred. No. 4.7e-146;

	Matches	556:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps	0:
QY	1	GTTCCTTCGGTGGAGAGACCGCTGTGATATTTGTTGGTTCCTCTTGGAGCGCTGCTACGCT	60							
Db	594	GTTCCTTCGGTGGAGAGACCGCTGTGATATTTGTTGGTTCCTCTTGGAGCGCTGCTACGCT	653							
QY	61	CTGTGCTGTGTCACAAAGAGGCTATCTTCTTCAAGAACGATGAACCTCATGATTTGT	120							
Db	654	CCTGTGCTGTGTCACAAAGAGGCTATCTTCTTCAAGAACGATGAACCTCATGATTTGT	713							
QY	121	GGCTATCCTTCCCTTACTTTTGGCACACTGGGGACCCGAGCTGGCCGGCAGACGAGGTGGG	180							
Db	714	GGCTATCCTTCCCTTACTTTTGGCACACTGGGGACCCGAGCTGGCCGGCAGACGAGGTGGG	773							
QY	181	CCAGAGAGGCATGTACTAGTGGGCATCCTGTAGAGTCAATCCGATTTGGTGGCGTCTCCGAT	240							
Db	774	CCAGAGAGGCATGTACTAGTGGGCATCCTGTAGAGTCAATCCGATTTGGTGGCGTCTCCGAT	833							
QY	241	CTTTCAGAGCTGTGCCGCGACACTCAAAAGGGCCCTGCMAATCTTGGGCGCAGAGCTTCG	300							
Db	834	CTTTCAGAGCTGTGCCGCGACACTCAAAAGGGCCCTGCMAATCTTGGGCGCAGAGCTTCG	893							
QY	301	CATGGGTAGCTGGGGCTCCTCATCTTTTCTCTTCATCGGTGTGGTCTCTTTCCAG	360							
Db	894	CATGGGTAGCTGGGGCTCCTCATCTTTTCTCTTCATCGGTGTGGTCTCTTTCCAG	953							
QY	361	CGCCCTTACTTTGGCCGAAGTTGACCGGGGTGGACGCCATTTTCACTAGCATCCTGAGTC	420							
Db	954	CGCCCTTACTTTGGCCGAAGTTGACCGGGGTGGACGCCATTTTCACTAGCATCCTGAGTC	1013							
QY	421	CTTCTGTGTGGGGGTAGTACCATGACTACATGTTGGCTATGAGACATGGACCCGTCAC	480							
Db	1014	CTTCTGTGTGGGGGTAGTACCATGACTACATGTTGGCTATGAGACATGGACCCGTCAC	1073							
QY	481	TGTGTGTGGCAAGATAGTGGGCTCTCTGTGTGCATTTGGGGGCGTGTACTATTTCCCT	540							
Db	1074	TGTGTGTGGCAAGATAGTGGGCTCTCTGTGTGCATTTGGGGGCGTGTACTATTTCCCT	1133							
QY	541	GCCAGTGCCCGTCATT	556							
Db	1134	GCCAGTGCCCGTCATT	1149							
RESULT 2										
AK	AA578540									
ID	AA578540	standard; cDNA; 1686 BP.								
XX	AA578540;									
AC	AA578540;									
XX	13-FEB-2002	(first entry)								
DT	13-FEB-2002									
XX	DNA encoding novel human diagnostic protein #14344.									
DE	Human; chromosome mapping; gene mapping; gene therapy; forensic;									
XX	Food supplement; medical imaging; diagnostic; genetic disorder; ss.									
KW	Homo sapiens.									
XX	OS									
XX	PN	WO200175067-A2.								
XX	PD	11-OCT-2001.								
XX	PF	30-MAR-2001; 2001WO-US08631.								
XX	PR	31-MAR-2000; 2000US-0540217.								
XX	PR	23-AUG-2000; 2000US-0649167.								
XX	PA	(HYSE-) HYSEQ INC.								
XX	PI	Drmanac RT, Liu C, Tang YT;								
XX	WP	WPI: 2001-639362/73.								
DR	P-PSDB; ABG14353.									

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

PS Claim 1, SEQ ID No 14344; 103pp; English.

XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent upon human
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 1686 BP; 236 A; 545 C; 562 G; 343 T; 0 other;

Query Match 100.0%; Score 556; DB 23; Length 1686;

Best Local Similarity 100.0%; Pred. No. 5.2e-146;

Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTCTGCTGGAGAGCCCTGTATTTGTTGCTTCCTTTGAGCTGCTGACGCTT 60
DB 1002 GTTCTCTGCTGGAGAGCCCTGTATTTGTTGCTTCCTTTGAGCTGCTGACGCTT 1061
OY 61 CCGGCTCTGCTGGAGAGCCCTGTATTTGTTGCTTCCTTTGAGCTGCTGACGCTT 120
DB 1062 CCGGCTCTGCTGGAGAGCCCTGTATTTGTTGCTTCCTTTGAGCTGCTGACGCTT 1121
OY 121 GGTATCTCTGCTGGAGAGCCCTGTATTTGTTGCTTCCTTTGAGCTGCTGACGCTT 180
DB 1122 GGTATCTCTGCTGGAGAGCCCTGTATTTGTTGCTTCCTTTGAGCTGCTGACGCTT 1181
OY 181 CCAGCAGGCGCATGTCACTGCGCATCTGAGAGTCATCCGATTGGTCCGTCTCCGCAT 240
DB 1182 CCAGCAGGCGCATGTCACTGCGCATCTGAGAGTCATCCGATTGGTCCGTCTCCGCAT 1241
OY 241 GTTCAAGCTGTCCCGCATCTCAAAAGGCGCTGCAAACTTTGGGCGAGACGCTTGGGCTTC 300
DB 1242 GTTCAAGCTGTCCCGCATCTCAAAAGGCGCTGCAAACTTTGGGCGAGACGCTTGGGCTTC 1301
OY 301 CATGCGTGAAGTGGGCGCTCTCATCTTTTCCCTTCATCGGTTGGTCTCTTTCCAG 360
DB 1302 CATGCGTGAAGTGGGCGCTCTCATCTTTTCCCTTCATCGGTTGGTCTCTTTTCCAG 1361
OY 361 CGCGCTTACTTTGGCGAAGTTGACGGGTGACCTCCATTCTACATAGCATCCCTGAGTC 420
DB 1362 CGCGCTTACTTTGGCGAAGTTGACGGGTGACCTCCATTCTACATAGCATCCCTGAGTC 1421
OY 421 GTTCTGCTGGGCGGTAGTACATGATGATGCTGCTATGGAGATGACGACCCGCTCAC 480
DB 1422 GTTCTGCTGGGCGGTAGTACATGATGATGCTGCTATGGAGATGACGACCCGCTCAC 1481
OY 481 TGTGGTGGCAAGATAGTGGGCTCTGTGTGCGCATTTGGGGGCTCTGACATTTTCCCT 540
DB 1482 TGTGGTGGCAAGATAGTGGGCTCTGTGTGCGCATTTGGGGGCTCTGACATTTTCCCT 1541
OY 541 GCCAGTGGCCGTCATT 556

DB 1542 GCCAGTGGCCGTCATT 1557

RESULT 3
ID AAS13338
X X AAS13338 standard; cDNA; 1747 BP.
X X
AC AAS13338;
X X
DT 18-DEC-2001 (first entry)
X X

Human cDNA encoding NOV4 protein.

XX Human; NOV4; ss: cytosolic; neurotrophic; neuroprotective; vulnerrary;
KW cerebroprotective; antiparkinsonian; hypotensive; antisthmatic;
KW antidiabetic; antipsoriatic; antinflammatory; immunosuppressive;
KW antiatherosclerotic; dermatological; cancer; neurological disorder;
KW Parkinson's disease; diabetes mellitus; asthma; enamel defect;
KW immune disorder; autoimmune disease; respiratory disorder;
KW bone disorder; musculoskeletal disorders; leukaemia; lymphoma;
KW cell growth regulation disorder; lesional psoriatic skin;
KW atherosclerosis; abdominal aortic aneurysm.

XX Homo sapiens.

OS Homo sapiens.

Key Location/Qualifiers

FT 5'UTR 1..37

FT CDS 38..1717

FT 3'UTR 1718..1747

FT W0200168851-A2.

20-SEP-2001.

12-MAR-2001: 2001WO-US07735.

10-MAR-2000: 2000US-0188277.

10-MAR-2000: 2000US-0188316.

14-MAR-2000: 2000US-0189139.

14-MAR-2000: 2000US-0189140.

17-MAR-2000: 2000US-0190231.

17-MAR-2000: 2000US-0190401.

(CURA-) CURAGEN CORP.

Padigaru M, Vernet CAM, Fernandes E, Shinkets RA, Spaderna SK;

Majumder K, Li L;

WPI: 2001-570869/64.

P-PSDB; AAU08660.

Novel polypeptides and nucleic acids homologous to members of collagen,

potassium channel, tufelin family of proteins for diagnosing, treating

cancer, atherosclerosis, neurological, skin and enamel defect disorders

Claim 9; Page 15-16; 128pp; English.

The invention relates to isolated NOVX (NOVX1-11) polypeptides and
CC the polynucleotides that encode them. NOVX polypeptides, polynucleotides
CC and anti-NOVX antibodies are useful for treating or preventing a
CC pathology associated with NOVX polypeptide in humans and for treating a
CC syndrome associated with human disease e.g. disorders characterised by
CC altered cell motility, proliferation and migration e.g. cancer,
CC angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.
CC episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's
CC disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,
CC asthma, hypertension and seizure (NOV4), enamel defects, such as

CC amelogenesis imperfecta and disorders involving enamel defects,
CC including hypoplasia and hypominerallisation (NOV5-7), paraneoplastic
CC neurological disorders, e.g. paraneoplastic limbic of brain-stem
CC encephalitis occurring during testicular cancer, diabetes, reproductive
CC health, metabolic and endocrine disorders, gastrointestinal disorders,
CC immune disorders and autoimmune diseases, respiratory disorders, bone
CC disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell
CC growth regulation disorders (NOV8), leisional psoriatic skin (NOV9-10) and
CC atherosclerosis, abdominal aortic aneurysm and neurological disorders
CC (NOV11). NOVX polypeptide is also useful for identifying an agent that
CC binds to it and a cell expressing NOVX polypeptide is useful for
CC identifying a therapeutic agent for use in treatment of a NOVX related
CC pathology. The antibodies and a polypeptide having 95% sequence identity
CC to NOVX polypeptide are useful for treating a pathological state in a
CC mammal. The present sequence encodes NOV4, a possible voltage gated
CC potassium channel.

XX
XQ Sequence 1747 BP; 255 A; 582 C; 575 G; 335 T; 0 other;

OY 121 GGCATATCTTCCCTACTTTGTGGCACTGGGACCGAGCTGGCCCGGACGAGGGGTGG 180
 DB 836 GGCATATCTTCCCTACTTTGTGGCACTGGGACCGAGCTGGCCCGGACGAGGGGTGG 895
 OY 181 CCAGCAGGCGCATGTCACCTGCTGTAGAGTCACTGCTGCTGCTGCTGCTGCTGCT 240
 DB 896 CCAGCAGGCGCATGTCACCTGCTGTAGAGTCACTGCTGCTGCTGCTGCTGCTGCT 955
 OY 241 CTTCAAGCTGTCCCGGCACTCAAGAGGCGCTGCAAAATCTTGGGCGAGAGCTTGGGCGC 300
 DB 956 CTTCAAGCTGTCCCGGCACTCAAGAGGCGCTGCAAAATCTTGGGCGAGAGCTTGGGCGC 1015
 OY 301 CATGCGTGAGCTGGGCGCTCTCATCTTTCCTTTCATGCTGCTGCTGCTGCTGCTGCT 360
 DB 1016 CATGCGTGAGCTGGGCGCTCTCATCTTTCCTTTCATGCTGCTGCTGCTGCTGCTGCT 1075
 OY 361 CGCCGCTACTTGTGCGGAAGTTGACCGGGTGCATCCCTTCTACTAGATCCCTGAGTC 420
 DB 1076 CGCCGCTACTTGTGCGGAAGTTGACCGGGTGCATCCCTTCTACTAGATCCCTGAGTC 1135
 OY 421 CTTTGTGTGGGCGTAGTACCATGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 DB 1136 CTTTGTGTGGGCGTAGTACCATGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1195
 OY 481 TGTGGGTGGCAGATAGTGGGCTCTGTGTGTCATTTGGGCGTGTGCTGCTGCTGCTGCT 540
 DB 1196 TGTGGGTGGCAGATAGTGGGCTCTGTGTGTCATTTGGGCGTGTGCTGCTGCTGCTGCT 1255
 OY 541 GCCAGTGGCGCTGCTAT 556
 DB 1256 GCCAGTGGCGCTGCTAT 1271

RESULT 5
 AAD28734
 ID AAD28734 standard; DNA: 691 BP.
 AC AAD28734;
 DT 07-MAY-2002 (first entry)
 XX

Human ion channel gene, ion-166.
 Human: ion channel; neurological disorder; psychiatric disorder;
 schizophrenia; attention deficit hyperactivity disorder; depression;
 proliferation disease; migraine; ischemia; neurodegenerative disease;
 macular degeneration; Alzheimer's disease; congestive heart failure;
 glaucoma; Parkinson's disease; cardiovascular disease; arrhythmia;
 high blood pressure; restenosis; metabolic disease; neuroprotective;
 obesity; hormonal disorder; polycystic ovarian syndrome; gene therapy;
 alopecia; anxiety; stroke; neuroleptic; nootropic; cancer; diabetes; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 566..658
 FT /tag= a
 FT /product= "Human ion channel ion-166"
 FT /note= "CDS does not include start and stop codon"
 FT /partial

WO200192303-A2.
 PD 06-DEC-2001.
 PF 25-MAY-2001; 2001WO-US16967.
 PR 26-MAY-2000; 2000US-207119P.
 PR 26-MAY-2000; 2000US-207152P.
 PR 26-MAY-2000; 2000US-207257P.
 PA (PHAA) PHARMACIA & UPJOHN CO.

PI Benjamin CW, Roberts SL, Karnovsky AM, Ruble CL, Goto LF;
 DR WPI: 2002-147617/19.
 DR P-PSDB: AAE18034.
 XX
 PT New human ion channel polypeptides and nucleic acids, useful for
 PT treating or diagnosing neurological, psychiatric or neurodegenerative
 PT diseases, e.g. depression, anxiety, stroke, ischemia, or Alzheimer's or
 PT Parkinson's disease
 XX
 PS Claim 1: Page 76; 126pp; English.
 XX
 CC The invention relates to ion channel polypeptides designated as ion-x
 CC (where x is 157-175) and their corresponding nucleic acids. The ion-x
 CC sequences and their modulators are useful for the treatment of human
 CC diseases and conditions such as neurological or psychiatric disorders.
 CC These compounds are useful for treating schizophrenia, attention deficit
 CC hyperactivity disorder, depression, anxiety, stroke, migraine, ischemia
 CC or neurodegenerative disease (e.g. macular degeneration, Alzheimer's
 CC disease, glaucoma, or Parkinson's disease). The compounds that modulate
 CC ion channels can be used for treating cardiovascular diseases (e.g.
 CC congestive heart failure, arrhythmia, high blood pressure or restenosis),
 CC metabolic diseases and disorders (e.g. diabetes or obesity), hormonal
 CC disorders (e.g. polycystic ovarian syndrome or alopecia) and
 CC proliferation diseases and cancers. The ion channels are also useful as
 CC targets for discovering ligands or drugs to treat many diverse disorders
 CC and defects. The ion-x sequences and their modulators may also be used
 CC in diagnostic assays for such diseases or conditions. Ion-x nucleic
 CC acids are used in gene therapy. The present sequence is a DNA encoding
 CC human ion channel designated as ion-166.
 SQ Sequence 691 BP; 113 A; 207 C; 185 G; 186 T; 0 other;

Query Match 95.7%; Score 532; DB 24; Length 691;
 Best Local Similarity 100.0%; Pred. No. 2e-139;
 Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTTGTGGTGGAGAGCGTGTATTTGTTGCTTCTCTTGGAGCTGCTGACGCT 60
 DB 160 GTTCTTGTGGTGGAGAGCGTGTATTTGTTGCTTCTCTTGGAGCTGCTGACGCT 219
 OY 61 CCTGTCTGTCCCAAGCAGGCTATCTTCAAGAAGTGATGAACTCATGATTTTGT 120
 DB 220 CCTGTCTGTCCCAAGCAGGCTATCTTCAAGAAGTGATGAACTCATGATTTTGT 279
 OY 121 GGCATATCTTCCCTACTTTGTGGCACTGGGACCGAGCTGGCCCGGACGAGGGGTGG 180
 DB 280 GGCATATCTTCCCTACTTTGTGGCACTGGGACCGAGCTGGCCCGGACGAGGGGTGG 339
 OY 181 CCAGCAGGCGCATGTCACCTGCTGTAGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 340 CCAGCAGGCGCATGTCACCTGCTGTAGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCT 399
 OY 241 CTTCAAGCTGTCCCGGCACTCAAGAGGCGCTGCAAAATCTTGGGCGAGAGCTTGGGCGC 300
 DB 400 CTTCAAGCTGTCCCGGCACTCAAGAGGCGCTGCAAAATCTTGGGCGAGAGCTTGGGCGC 459
 OY 301 CATGCGTGAGCTGGGCGCTCTCATCTTTCCTTTCATGCTGCTGCTGCTGCTGCTGCT 360
 DB 460 CATGCGTGAGCTGGGCGCTCTCATCTTTCCTTTCATGCTGCTGCTGCTGCTGCTGCT 519
 OY 361 CGCCGCTACTTGTGCGGAAGTTGACCGGGTGCATCCCTTCTACTAGATCCCTGAGTC 420
 DB 520 CGCCGCTACTTGTGCGGAAGTTGACCGGGTGCATCCCTTCTACTAGATCCCTGAGTC 579
 OY 421 CTTTGTGTGGGCGTAGTACCATGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 DB 580 CTTTGTGTGGGCGTAGTACCATGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
 OY 481 TGTGGGTGGCAGATAGTGGGCTCTGTGTGTCATTTGGGCGTGTGCTGCTGCTGCTGCT 532
 DB 640 TGTGGGTGGCAGATAGTGGGCTCTGTGTGTCATTTGGGCGTGTGCTGCTGCTGCTGCT 691

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RESULT 6
AA04953
ID AA04953 standard; cDNA; 1598 BP.
XX
AC AA04953;
XX
DT 11-APR-1996 (first entry)
XX
DE Mouse Kv1.7 voltage-gated potassium channel coding sequence.
XX
KW Mouse Kv1.7 voltage-gated potassium channel;
KW Insulin antagonist drug screening; insulin agonist drug screening;
KW non-insulin-dependent diabetes mellitus; ds.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1..1598
FT /tag=a
FT /note="specification states sequence is 1599.
FT Incomplete stop codon given"
XX
PN MO9523858-A1.
XX
PD 08-SEP-1995.
XX
PF 23-FEB-1995; 95WO-US02221.
XX
PR 10-AUG-1994; 94US-0288405.
PR 04-MAR-1994; 94US-0207401.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Chandry G, Chandry KG, Gutman GA, Kalman K;
XX
DR WPI; 1995-320573/41.
DR P-PSDB; AAR82937.
XX
PT New voltage-gated potassium channel gene - used to identify
PT material(s) which can increase insulin release e.g. for treating
PT non-insulin dependent diabetes mellitus.
XX
PS Claim 1; Page 22-23; 38pp; English.
XX
CC The DNA encodes a mouse Kv1.7, which is a Shaker-related voltage-
CC gated potassium channel. It may be used in drug screening for
CC identification of therapeutics which modulate the channel and,
CC therefore, modulate insulin secretion. Selective antagonists
CC increase insulin release and thereby reduce hyperglycaemia
CC associated with non-insulin-dependent diabetes mellitus.
XX
SQ Sequence 1598 BP; 232 A; 521 C; 502 G; 343 T; 0 other;
Query Match 78.5%; Score 436.6; DB 16; Length 1598;
Best Local Similarity 86.7%; Pred. No. 1.7e-112;
Matches 481; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
OY 2 TTCTGTGGTGGAGAGCGGTATTTGTGTGTCCTTGAGCTGCGTAGCGCTC 61
DB 853 TTCTTTGTGTGGAGAGCCCTGTATCTGCTGCTTCCCTTAGCGTGTGCATCTG 912
OY 62 CTGGCTGTCCAGCAAGAGCTATCTTCAAGACGTGATGAACCTCATGATTTTGTG 121
DB 913 GTGGCGCTGCCCTAGCAAGGTGTCTTCAAGATGTATGAACTAATTTGACTTCGTG 972
OY 122 GCTATCCTTCCCTACTTTTGTGACATGGGACCGAGCTGGCCCGGAGCGAGGGGTGGC 191
DB 973 GGCATCTGCTCTACTTCTGCGGCGCTGGGACGAGTTACCCGCGAGCGGGGTGGGC 1032
OY 182 CAGCAGGCCATCTCATCTGGCATCCGAGAGTATCCGATGGTGGCTGCTTCCGATC 241
DB 1033 CAGCGGGTATGTCCCTGGCATCCGAAGGTCATCCGATTTGGTGTGCTTCCGATC 1092

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OY 242 TTCAGCTGTCCCGGCACTTCAAGGCGCTGCAGAAATCTTGGGGCCAGACGCTTGGGGCTCC 301
DB 1093 TTCAGCTGTCCAGGCAATTCGAAAGGGGTCTACAGATCTTGGGGTCAGACACTGGGGCTCC 1152
OY 302 ATGCGTGAGCTGGGCGCTCTCATCTTTTCTTTCATCGGTGTGGTCTTTTCCAGC 361
DB 1153 ATCGTGAGCTAGCTCTCCCATCTCTCTTCTTCATTTGGCGGTGGCTCTTTTCCAGC 1212
OY 362 GCGGTCTACTTTCGCGAAGTTGACCGGGGTGGAGTCCCATTTCACTAGCATCCCTGAGTCC 421
DB 1213 GCAGTCTACTTCTCTGAGTGACCGGGGTGGAGACCATTTTCACGACATCCCGGAGTCC 1272
OY 422 TTCTGTGGGCGGTAGTCAACCATGACTACAGTTGGCTATGAGACATGGCACCCGTCAC 481
DB 1273 TTTTGTGGGCGAGTGTGACCATGACACAGCGTTGGCTATGGGACATGGACCCGTCAC 1332
OY 482 GTGGGTGGCAAGATAGTGGGCTCTGTGTGCCATTTGGCGGCGCTGTACTATTTCCCTG 541
DB 1333 GTGGGTGGCAAGATCGTGGGCTCTGTGTGCCATTTGGCAGGTGTGTCACCATCTCTG 1392
OY 542 CCAGTGGCGGTCATT 556
DB 1393 CTTGTGCTGTCAATT 1407

RESULT 7
AAH21452
ID AAH21452 standard; DNA; 1836 BP.
XX
AC AAH21452;
XX
DT 18-SEP-2001 (first entry)
XX
DE Human Kv1.5 DNA.
XX
KW Inhibitor; eukaryotic; potassium channel; TRK1; TRK2; TOK1;
KW activator; ds.
XX
OS Homo sapiens.
XX
PN WO200151519-A2.
XX
PD 19-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-EP00055.
XX
PR 11-JAN-2000; 2000DE-1000651.
XX
PA (AVENTIS PHARMA DEUT GMBH.
XX
PI Leberer E, Leeuw T, Ritscher A;
XX
DR WPI; 2001-442137/47.
XX
PT Identifying inhibitors and activators of eukaryotic potassium channels,
PT for use as pharmaceuticals, comprises using yeast cells that express
PT heterologous, but no endogenous, potassium channels -
XX
PS Disclosure: Page 45-46; 78pp; German.
XX
CC This sequence represents a novel method for identifying inhibitors or
CC activators (A) of a eukaryotic potassium channel (KC) by applying a test
CC compound to a mutant Saccharomyces cerevisiae cell in which: (1) the
CC three endogenous KC (TRK1, TRK2 and TOK1) are not expressed; but (11) a
CC eukaryotic KC is expressed heterologously, where the effect of the
CC compound on the eukaryotic KC is then determined. The method is used to
CC identify inhibitors or activators (A) of a eukaryotic potassium channel.
CC (A) are potentially useful as pharmaceuticals. The method is easily
CC automated for parallel processing of many samples, using either different
CC concentrations of test compounds and/or different levels of heterologous
CC gene expression. It allows identification of compounds that inhibit human
CC KC selectively. This sequence represents the human Kv1.5 encoding DNA

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CC described in the method of the invention.

Sequence 1836 BP; 323 A; 614 C; 580 G; 319 T; 0 other;

Query Match 60.1%; Score 334.2; DB 22; Length 1836;
Best Local Similarity 75.8%; Pred. No. 1e-83;

Matches 436; Conservative 0; Mismatches 118; Indels 21; Gaps 1;

```
OY 2 TTCTTCGTGGAGAGCGTGTGATTTTGTGTTCTCTCTCTGAGTGGCGTACCCCTC 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 964 TTCTTCATGTGGAGACACGTCGTGATGTTGATTCACCTTCGAGCTGCGCTTC 1023
OY 62 CTGTCTGTCCAGCAAGGCTATCTTCTTCAAGAACGTATGAACTCATCATTTGTG 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1024 TTGCGCTGGCCAGCAAGGAGGTTCTCCGGAAACATCATGACATCATGTTGGTG 1083
OY 122 GGTATCTTCCCTACTTTTGTGACAGCGACCGACCTGGCCGACGAGGAGGCGG 181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1084 GCCATCTTCCCTACTTCAACCTCGGGACCGAAGTGGCAGAGCAGCAGGAGGCG 1143
OY 182 -----CAGCAGGCGATGTCACCTGCGCATCTCCGTGAGATCATCCGA 220
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1144 GGAGGAGCGCGCCAGAAATGGGAGGCGCATGTCCTGGCCATCTCCGAGTCATCCG 1203
OY 221 TTGTCGCTGTCTTCCGATCTTCAAGCTGTCCCGGACACTCAAAAGGCGCTGCAATCTTG 280
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1204 CTGGTCGGGGTGTCCGACATCTTCAAGCTCTCCGGCACTCCAAAGGCGCTGCAATCTTG 1263
OY 281 GGCAGAGCGCTTGGCGCTTCATGCGTGAAGCTGGCGCTCTCATCTTTTCTCTTCATC 340
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1264 GGCAGAGCGCTTGGCGCTTCATGCGTGAAGCTGGCGCTCTCATCTTTTCTCTTCATC 1323
OY 341 GGTGTGTCCTCTTTTCCAGCGCGCTTACTTTCGGAAGTTGACCGGGTGGACCTCCAT 400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1324 GGGGTATCTCTTCTTCCAGTGGCGCTTACTTTCGCAAGGCTGACCAACGAGGAACCTTC 1383
OY 401 TTCACTAGCATCCCTAGTCTTCTGTGTTGGGCGGTAGTACCATGATGATGTTGCTAT 460
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1384 TTCTTCATGATCCCTTCCAGCGCTTCTGTGGGCGGTGTCACCATGACCATGTTGGGCTAC 1443
OY 461 GGAGACATGGACCGCTCACTGTGGGTGGCAGAGATAGTGGGCTCTGTGTGCTATGCG 520
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1444 GGGGACATGAGGCGCATCTGTTGGGGCAGAGATGCTGGGCTGTGTGCTATGCGC 1503
OY 521 GGGGTGCTGACTATTTTCCCTGCGCAAGTGGCGGCTAT 555
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1504 GGGGTCTTCACCATTTGCCCTGCTGTGCCGCTCAT 1538
```

RESULT 8

ABN95856

ID ABN95856 standard; DNA; 2867 BP.

XX ABN95856;

DT 13-AUG-2002 (first entry)

DE Gene #2354 used to diagnose Liver cancer.

XX Gene: liver cancer; ds; hepatocellular carcinoma; hepatotropic;
XX metastatic liver tumour; cytostatic; expression profile; disease state;
XX disease progression; drug toxicity; drug efficacy; drug metabolism.

OS Homo sapiens.

PN WO200229103-A2.

PD 11-APR-2002.

PF 02-OCT-2001; 2001WO-US30589.

PR 02-OCT-2000; 2000US-237054P.

XX

PA (GENE-) GENE LOGIC INC.

PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

DR WPI; 2002-426119/45.

PT Diagnosing and detecting the progression of liver cancer,

PT hepatocellular carcinoma or metastatic liver tumor in a patient,

PT involves detecting the level of expression of two or more genes in a

PT liver tissue sample

PS Claim 1; SEQ ID NO 2354; 298bp; English.

XX The invention relates to a novel method for diagnosing and detecting the

XX progression of liver cancer, hepatocellular carcinoma or metastatic liver

XX tumor in a patient, and differentiating metastatic liver cancer from

XX hepatocellular carcinoma in a patient, involving detecting the level of

XX expression of two or more genes represented in ABN93503-ABN97455 in a

XX tissue sample. The method of the invention has hepatotropic, and

XX cytostatic activity. The method is useful for diagnosing and detecting

XX the progression of liver cancer, hepatocellular carcinoma and metastatic

XX liver carcinoma in a patient. The method is useful for identifying

XX expression profiles which serve as useful diagnostic markers as well as

XX markers that can be used to monitor disease states, disease progression,

XX drug toxicity, drug efficacy and drug metabolism.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2867 BP; 565 A; 839 C; 845 G; 618 T; 0 other;

XX

Query Match 60.1%; Score 334.2; DB 24; Length 2867;

Best Local Similarity 75.8%; Pred. No. 1.2e-83;

Matches 436; Conservative 0; Mismatches 118; Indels 21; Gaps 1;

```
OY 2 TTCTTCGTGGAGAGCGTGTGATTTTGTGTTCTCTCTCTGAGTGGCGTACCCCTC 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1198 TTCTTCATGTGGAGACACGTCGTGATGTTGATTCACCTTCGAGCTGCTGCGCTTC 1257
OY 62 CTGTCTGTCCAGCAAGGCTATCTTCTTCAAGACGTGATGAACTCATCATTTTGTG 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1258 TTGCGCTGGCCAGCAAGGAGGTTCTCCGGAAATCATGAACTCATCATGATGTTGGTG 1317
OY 122 GGTATCTTCCCTACTTTTGGGACATGGGCGACGAGTGGACCGGAGCAGGAGGTTGGG 181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1318 GCCATCTTCCCTACTTTCATCACCTGCGGACCGAACTGGCAGAGCAGCAGGAGGCG 1377
OY 182 -----CAGCAGGCGCATGTCACCTGCGCATCTCCGTGAGATCATCCGA 220
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1378 GGAGGAGCGCGCCAGAAATGGGAGGCGCATGTCCTGGCCATCTCCGAGTCATCCGC 1437
OY 221 TTGTCGCTGTCTTCCGATCTTCAAGCTGTCCCGGACACTCAAAAGGCGCTGCAATCTTG 280
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1438 CTGGTCGGGGTGTCCGACATCTTCAAGCTCTCCCGCACATCCAAAGGCGCTGCAATCTTG 1497
OY 281 GGCAGAGCGCTTGGGCGCTCATGCGGAGCTGGGCGCTCTCATCTTTTCTCTTCATC 340
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1498 GGCAGAGCGCTTGGGCGCTCATGCGGAGCTGGGCGCTCTCATCTTTTCTCTTCATC 1557
OY 341 GGTGTGTCCTCTTTTCCAGCGCGCTTACTTTCGGAAGTTGACCGGGTGGACTCCCAT 400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1558 GGGGTATCTCTTTCACAGTGGCGCTTACTTTCGAGAGGCTGACCAACCGGAGAACCAT 1617
OY 401 TTCACTAGCATCCCTAGTCTTCTGTGGGCGGTAGTACCATGATGATGATGTTGCTAT 460
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1618 TTCTTCAGCATTCCTGACGCGCTTCTGTGGGCGGTGATGACCATGATGATGTTGCTAT 1677
OY 461 GGAGACATGGACCGCATCTGTGGGCGCAAGATAGTGGGCTCTGTGTGCTATGCG 520
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1678 GGGGACATGAGGCGCATCTGTGGGCGCAAGATGCTGGGCTGTGTGTGCTATGCGC 1737
OY 521 GGGGTGCTGACTATTTTCCCTGCGCAAGTGGCGGCTAT 555
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db 1738 GGGCTCTCACACATGCGCTGCTGCGCCGTCA 1772

RESULT 9
ABL65917
ID ABL65917 standard; DNA: 2867 BP.
XX
AC ABL65917;
XX
DT 15-MAY-2002 (first entry)
XX
DE Lung cancer related gene sequence SEQ ID NO:4254.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW Stomach; lung; prostate; pancreas; carcinoma; antitumour; carcinosus;
KW Cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN W0200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001MO-US10838.
XX
XX 05-JUN-2000; 2000US-209473P.
XX 05-JUN-2000; 2000US-209531P.
XX 18-SEP-2000; 2000US-23133P.
XX 18-SEP-2000; 2000US-231617P.
XX 20-SEP-2000; 2000US-234009P.
XX 20-SEP-2000; 2000US-234034P.
XX 20-SEP-2000; 2000US-234052P.
XX 22-SEP-2000; 2000US-234509P.
XX 22-SEP-2000; 2000US-234567P.
XX 25-SEP-2000; 2000US-234923P.
XX 25-SEP-2000; 2000US-234934P.
XX 25-SEP-2000; 2000US-235077P.
XX 25-SEP-2000; 2000US-235082P.
XX 25-SEP-2000; 2000US-235134P.
XX 25-SEP-2000; 2000US-235280P.
XX 26-SEP-2000; 2000US-235637P.
XX 26-SEP-2000; 2000US-235638P.
XX 27-SEP-2000; 2000US-235711P.
XX 27-SEP-2000; 2000US-235720P.
XX 27-SEP-2000; 2000US-235840P.
XX 27-SEP-2000; 2000US-235863P.
XX 28-SEP-2000; 2000US-236028P.
XX 28-SEP-2000; 2000US-236032P.
XX 28-SEP-2000; 2000US-236033P.
XX 28-SEP-2000; 2000US-236034P.
XX 28-SEP-2000; 2000US-236109P.
XX 28-SEP-2000; 2000US-236111P.
XX 29-SEP-2000; 2000US-236842P.
XX 29-SEP-2000; 2000US-236891P.
XX 02-OCT-2000; 2000US-237172P.
XX 02-OCT-2000; 2000US-237173P.
XX 02-OCT-2000; 2000US-237278P.
XX 02-OCT-2000; 2000US-237294P.
XX 02-OCT-2000; 2000US-237295P.
XX 02-OCT-2000; 2000US-237316P.
XX 03-OCT-2000; 2000US-237425P.
XX 03-OCT-2000; 2000US-237598P.
XX 03-OCT-2000; 2000US-237604P.
XX 03-OCT-2000; 2000US-237606P.
XX 03-OCT-2000; 2000US-237608P.
XX 01-NOV-2000; 2000US-244867P.
XX 01-NOV-2000; 2000US-245084P.
XX
XX (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;

XX
XX WPI: 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a
XX chemical agent to be tested for anti-neoplastic activity, and
XX determining a change in expression of a gene of a signature gene set -
XX
XX Claim 1; SEQ ID 4254; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an
XX anti-neoplastic agent. The method involves exposing cells to a chemical
XX agent to be tested for anti-neoplastic activity, determining a change in
XX expression of at least one gene (I) of a signature gene set, where (I)
XX comprises a sequence (S) selected from 8447 sequences (given in ABL61664
XX to ABL70110), or is at least 95% identical to (S), where a change in
XX expression is indicative of anti-neoplastic activity. (I) has cytostatic
XX activity and can be used in gene therapy. M1 can be used for screening
XX an anti-neoplastic agent, and can be used for producing a product which
XX is the data collected with respect to the anti-neoplastic agent as a
XX result of M1, and the data is sufficient to convey the chemical
XX structure and/or properties of the agent. M1 can be used in the
XX treatment of cancer such as colon, breast, stomach, lung, thyroid,
XX oesophageal, ovarian, kidney, prostate or pancreatic cancer,
XX adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
XX infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
XX carcinoma, papillary carcinoma and Wilm's tumour.
XX
XX Sequence 2867 BP; 565 A; 839 C; 845 G; 618 T; 0 other;
XX
XX
XX Query Match 60.1%; Score 334.2; DB 24; Length 2867;
XX Best Local Similarity 75.88; Pred. No. 1.2e-83;
XX Matches 436; Conservative 0; Mismatches 118; Indels 21; Gaps 1;
XX
XX
XX 2 TTCTGCTGGGAGACGCTGTGATTTGTTGCTCTTGTAGCTGTGACGCTC 61
XX 1198 TTCTTCATCGTGGAGACAGACAGTGGCTATCTGTACCTTCAGCTGCTGCGCTTC 1257
XX
XX 62 CTGCTGTGTCACAGAGCTATCTTCAAGACGTATGAACCTCATGATTTGTG 121
XX 1258 TTGCTGCTGCCACAGACAGAGAGGTCTCCGGAACATCATGATGATGTGTG 1317
XX
XX 122 GCTATCCTTCCCTACTTTTGTGCACTGGGACAGGAGTGGCCGGGAGGAGGTGGG 181
XX 1318 GCCATTTCCCTTCACTTATCCTTGACCGAATCGACAGACAGGAGGAGGAGG 1377
XX
XX 182 -----CAGCAGGACATGTCAGTGGCCATCGAGAGTATCGA 220
XX 1378 GGAGAGGCGCGCCAGATGGGACAGGACGATGCTGGCCATCTCCGAGTATCGCG 1437
XX
XX 221 TTGCTGCTGTCTTCCGATCTTCAAGCTGTCCGCGACATCAAGGCGTGAATCTTG 280
XX 1438 CTGCTCCGGGTGTTCCGATCTTCAAGCTGTCCGCGACATCAAGGCGTGAATCTTG 1497
XX
XX 281 GGCAGAGCGCTGGGCGCTCATGCGGATGCGGCGCTCCGATCTTTCCTTCATC 340
XX 1498 GGCAGAGCTTGGACGCGCTCATGAGGAGTGGGCTGCTCATCTTCTTCATC 1557
XX
XX 341 GGTGTGCTCTTCTTTCAGAGCGCTCACTTGTGCGAATGTCAGCGGTGACCTCCAT 400
XX 1558 GGGGTATCTCTTCTTCAAGTGGCGTCTACTGTGCAAGGCTGACACAGGAGGAGCCAT 1617
XX
XX 401 TTCACTAGCATCCCTGAGTCTGTGTGGGCGGTACTACACATGACTACATTTGGCTAT 460
XX 1618 TTCTCTAGCATCCCTGAGGCTTCTGTGGGAGTGTGACATGACACTGTGGGCTAC 1677
XX
XX 461 GGAGACATGGACCGGCTCATGTGGGAGGAGTATGAGTGGCTGTGTCGATGGC 520
XX 1678 GGGGACATGAGGCGCATCTGTGGGAGGAGTGTGGGCTGTGCTGTGGGCTGCC 1737
XX
XX 521 GGGCTGCTGACTATTTCTGCTGCGAGTGGCCGCTAT 555
XX 1738 GGGCTCTCACACATGCGCTGCTGCGCCGTCA 1772

RESULT 10
AB199654
ID AB199654 standard; cDNA; 3147 BP.
XX
AC AB199654;
XX
DT 07-MAR-2002 (first entry)
XX
DE Mouse ischemic condition related cDNA sequence SEQ ID NO:683.
XX
KW Mouse; ischemia; compressive ischemia; occlusive ischemia;
KM vasospastic ischemia; ischemic condition; ischemic disease; ss.
XX
OS Mus musculus.
XX
PN W020018188-A2.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-JP04192.
XX
PR 18-MAY-2000; 2000JP-0145977.
XX
PI (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
DR WPI: 2002-034733/04.
XX
P-PSDB: ABB57250.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
PT genes -
XX
PS Claim 2; Page 1705-1709; 2690pp; English.
XX
CC The present invention describes a method for examining ischemic
CC conditions, comprising measuring the expression levels of particular
CC genes (1) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (1). The method
CC is useful for examining the ischemic condition (e.g. compressive
CC ischemia, occlusive ischemia or vasospastic ischemia) by measuring
CC expression levels of particular genes (AB199654 to AB199912, encoding
CC the protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The
CC expression levels or expression profiles produced by these genes are
CC used as an indicator when screening for ischemic condition-improving
CC drugs or therapeutics for ischemic diseases. AB199913 and AB199914
CC represent PCR primers for a mouse ischemic condition related sequence,
CC which are used in the exemplification of the present invention.
XX
SQ Sequence 3147 BP; 704 A; 859 C; 887 G; 697 T; 0 other;
XX
Query Match 56.1%; Score 311.8; DB 24; Length 3147;
Best Local Similarity 73.6%; Pred. No. 2.4e-77;
Matches 413; Conservative 0; Mismatches 142; Indels 6; Gaps 1;
QY 2 TTCTTCGTGGAGACGCTGTATTTGTTGCTTCTTGAAGCTGTGATGCGCTC 61
DB 2117 TTCTTCATTTGTGAACCTTGTATCATCTGTTCTTTTGAGCTGTGCGCTC 2176
QY 62 CTGCTCTGTCAAGCAAGGCTATCTTTCAAGACGTATGAACCTCATGATTTGTG 121
DB 2177 TTGGCTGCTCCAGACAGACGACTTCTTAAGACATCATGAACCTCATGACATTTG 2236
QY 122 GCATCTCTGCTACTTGTGGACGTGGGACGAGCTGGCGCGGACGAGG-----G 175
DB 2237 GGCATCATCCCTTATTTTCATTACCTGTGGACGAGATAGCTGACGAGGGAATCAG 2296
QY 176 GTGGGCGACGAGGCGCATGCTGCGCATCTGAGAGTCAATCCGATTGCTGCTCTTC 235
||||| ||||||| || ||||||| || ||||||| ||||| || || ||

DB 2297 AAGGGCGAGCGACCACTTCCCTGGCCATCCCTCAGGGTCATCCGCTGTGAAGGCTTC 2356
QY 236 CGCATCTTCAAGCTGTCGCCGACACTCAAGGCGCTGCAATCTTGGGCGAGCGCTCGG 295
DB 2357 AGAATCTTCAAACTCTCCGCGACCTCCAGAGGCGCTTAGATCTCCGGCCAGACCTTAAA 2416
QY 296 GCGTCATGCGGTGAGCTGGGCGCTCCATCTCTTTCATCGGCTGGTCCCTTT 355
DB 2417 GCTAGTATGAGGAGGATGAGGCGCTCTCATCTTTTCCCTTCATTTGGGGCATATCTGTT 2476
QY 356 TCACGCGCGCTTACTTTGCCGAAGTTGACCGGCTGACATCCATTCATCATCATCTCCT 415
DB 2477 TCTAGCCGACATGTACTTTGGGAGCGGCAAGAGCTGATGCGACTTCTCCAGATATCCC 2536
QY 416 GAGTCCTTCTGCGGGGAGTACATCATCATCTGCTGCTTGGAGCATGAGCACC 475
DB 2537 GATGCTTCTGCGGGGAGGCTGCTCATGACCTGCGATGCGTGGATGCGTATACCT 2556
QY 476 GTCACGTGGGTGGCAAGATAGTGGCTCTCTGTGTCATGCGGCGCTGCTGACTTAT 535
DB 2597 GTGACATTTGGAGGCAAGATCGTGGCTCTGTGTGCCATCGCTGGTGTGTCACAT 2656
QY 536 TCCCTGCCAGTCCCGTCAT 556
DB 2657 GCCCTGCCCGACCTGTCAAT 2677
||||| || || |||||
RESULT 11
AAS29512
ID AAS29512 standard; cDNA; 2157 BP.
XX
AC AAS29512;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human endocrine polypeptide encoding cDNA SEQ ID NO 12.
XX
KW Endocrine protein; human; mouse; rabbit; goat; horse; food additive;
KW celt; dog; chicken; sheep; immunosuppressive; antirheumatic; vasotropic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective;
KW cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
KW ophthalmologic; vulnary; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ss;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; endocrine disorder;
KW gastrointestinal disorder; renal disorder; respiratory disorder;
KW wound healing; skin aging; organ transplantation; food preservative;
KW tissue regeneration; anti-fertility.
XX
OS Homo sapiens.
XX
PN W0200155364-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01308.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216860.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000: 2000US-0220963.
 PR 26-JUL-2000: 2000US-0220964.
 PR 14-AUG-2000: 2000US-0224518.
 PR 14-AUG-2000: 2000US-0224519.
 PR 14-AUG-2000: 2000US-0225213.
 PR 14-AUG-2000: 2000US-0225214.
 PR 14-AUG-2000: 2000US-0225266.
 PR 14-AUG-2000: 2000US-0225267.
 PR 14-AUG-2000: 2000US-0225268.
 PR 14-AUG-2000: 2000US-0225270.
 PR 14-AUG-2000: 2000US-0225447.
 PR 14-AUG-2000: 2000US-0225757.
 PR 14-AUG-2000: 2000US-0225758.
 PR 14-AUG-2000: 2000US-0225759.
 PR 18-AUG-2000: 2000US-0226279.
 PR 22-AUG-2000: 2000US-0226681.
 PR 22-AUG-2000: 2000US-0226686.
 PR 22-AUG-2000: 2000US-0227182.
 PR 23-AUG-2000: 2000US-0227009.
 PR 30-AUG-2000: 2000US-0228924.
 PR 01-SEP-2000: 2000US-0229287.
 PR 01-SEP-2000: 2000US-0229343.
 PR 01-SEP-2000: 2000US-0229344.
 PR 01-SEP-2000: 2000US-0229345.
 PR 05-SEP-2000: 2000US-0229509.
 PR 05-SEP-2000: 2000US-0229513.
 PR 06-SEP-2000: 2000US-0230437.
 PR 06-SEP-2000: 2000US-0230438.
 PR 08-SEP-2000: 2000US-0231242.
 PR 08-SEP-2000: 2000US-0231243.
 PR 08-SEP-2000: 2000US-0231244.
 PR 08-SEP-2000: 2000US-0231413.
 PR 08-SEP-2000: 2000US-0231414.
 PR 08-SEP-2000: 2000US-0232080.
 PR 08-SEP-2000: 2000US-0232081.
 PR 12-SEP-2000: 2000US-0231968.
 PR 14-SEP-2000: 2000US-0232397.
 PR 14-SEP-2000: 2000US-0232398.
 PR 14-SEP-2000: 2000US-0232399.
 PR 14-SEP-2000: 2000US-0232400.
 PR 14-SEP-2000: 2000US-0232401.
 PR 14-SEP-2000: 2000US-0233063.
 PR 14-SEP-2000: 2000US-0233064.
 PR 14-SEP-2000: 2000US-0233065.
 PR 21-SEP-2000: 2000US-0234223.
 PR 21-SEP-2000: 2000US-0234274.
 PR 25-SEP-2000: 2000US-0234997.
 PR 25-SEP-2000: 2000US-0234998.
 PR 26-SEP-2000: 2000US-0235484.
 PR 27-SEP-2000: 2000US-0235834.
 PR 27-SEP-2000: 2000US-0235836.
 PR 29-SEP-2000: 2000US-0236327.
 PR 29-SEP-2000: 2000US-0236367.
 PR 29-SEP-2000: 2000US-0236368.
 PR 29-SEP-2000: 2000US-0236369.
 PR 29-SEP-2000: 2000US-0236370.
 PR 02-OCT-2000: 2000US-0236802.
 PR 02-OCT-2000: 2000US-0237037.
 PR 02-OCT-2000: 2000US-0237038.
 PR 02-OCT-2000: 2000US-0237039.
 PR 02-OCT-2000: 2000US-0237040.
 PR 13-OCT-2000: 2000US-0239935.
 PR 13-OCT-2000: 2000US-0239937.
 PR 20-OCT-2000: 2000US-0240960.
 PR 20-OCT-2000: 2000US-0241221.
 PR 20-OCT-2000: 2000US-0241785.
 PR 20-OCT-2000: 2000US-0241786.
 PR 20-OCT-2000: 2000US-0241787.
 PR 20-OCT-2000: 2000US-0241808.
 PR 20-OCT-2000: 2000US-0241809.
 PR 20-OCT-2000: 2000US-0241826.
 PR 01-NOV-2000: 2000US-0244617.
 PR 08-NOV-2000: 2000US-0246474.

PR 08-NOV-2000: 2000US-0246475.
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 PR 11-DEC-2000: 2000US-0254097.
 PR 05-JAN-2001: 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI: 2001-451936/48.
 P-PSDB; AAU18283.
 Isolated polypeptide for treating, preventing and/or prognosing disorders of the endocrine system such as reproductive disorders, endocrine cancers and also for testing and detection e.g. diagnosis -
 Claim 1; SEQ ID No 12; 604pp; English.
 Sequences AAS29511-AAS29736 represent cDNA molecules, which encode the endocrine polypeptides of the invention. Endocrine polypeptides and their associated polynucleotides of the invention are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by determining the presence or absence of a mutation in an endocrine polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral ischemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi.

CC ocular disorders such as corneal infection, endocrine disorders such as
CC premature labour and infertility, gastrointestinal disorders such as
CC Crohn's disease, renal disorders such as glomerulonephritis and
CC respiratory disorders such as asthma. The polypeptides can also be used
CC to aid wound healing, to prevent skin aging due to sunburn, to maintain
CC organs before transplantation, to regenerate tissues and in chemotaxis.
CC The polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO

Query Match 49.2%; Score 273.4; DB 22; Length 2157;
Best Local Similarity 75.4%; Pred. No. 1.2e-66;

Matches 340; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

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RESULT 12

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ID ABK43428 standard; cDNA; 2159 BP.

XX ABK43428;

DT 05-JUN-2002 (first entry)

DE DNA encoding novel central nervous system protein #8.

XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy; gene; ss.

OS Homo sapiens.

XX WO200155318-A2.

XX

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XX 17-JAN-2001; 2001WO-US01332.
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 PR 05-JAN-2001: 2001US-0259678.
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 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-581633/65.

DR P-PSDB; AA087098.
 XX
 PT New isolated nucleic acid encoding a protein for diagnosing,
 PT preventing, treating or ameliorating medical conditions and used as
 PT food additives or preservatives -
 XX
 PS Claim 1; SEQ ID No 18; 837pp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule (I) encoding a
 CC novel central nervous system protein. (I) and polypeptides (II) encoded
 CC by (I), are used to treat a medical conditions and in diagnosis of a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. Rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
 CC adenocarcinomas and irritable bowel syndrome, reproductive system
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 CC leukemia, disorders involving neovascularisation e.g. malignancies,
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 CC acute kidney failure and blood related disorders e.g. myocardial
 CC infarction. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC
 Query Match 49.2%; Score 273.4; DB 23; Length 2159;
 Best Local Similarity 75.4%; Pred. No. 1.2e-66;
 Matches 340; Conservative 0; Mismatches 111; Indels 0; Gaps 0;
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 ID ABA06356 standard; cDNA; 492 BP.
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DT 10-JAN-2002 (first entry)
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DE Human cDNA SEQ ID NO: 22.
XX
KW Human; gene therapy; neural disorder; immune system disorder;
muscular disorder; reproductive disorder; gastrointestinal disorder;
pulmonary disorder; cardiovascular disorder; renal disorder;
proliferative disorder; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200154474-A2.
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PD 02-AUG-2001.
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AAS29636
ID AAS29636 standard; cDNA; 492 BP.
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AC AAS29636;
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DT 21-NOV-2001 (first entry)
XX
DE Human endocrine polypeptide encoding cDNA SEQ ID No 136.
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KW Endocrine protein; human; mouse; rabbit; goat; horse; food additive;
KW cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotrophic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective;
KW cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
KW ophtalmological; vulnerary; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ss;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; endocrine disorder;
KW gastrointestinal disorder; renal disorder; respiratory disorder;
KW wound healing; skin aging; organ transplantation; food preservative;
KW tissue regeneration; anti-infertility.
XX
OS Homo sapiens.
PN W0200155364-A2.
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PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225265.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226581.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
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PR 05-SEP-2000; 2000US-0229509.
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PR 06-SEP-2000; 2000US-0230437.
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PR 08-SEP-2000; 2000US-0231242.
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PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
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PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
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PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235836.
PR 27-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
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PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
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PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241785.
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PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
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PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.

PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-02559678.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM.
 DR WPI; 2001-451936/48.
 DR P-PSDB; AAU18407.
 XX
 PT Isolated polypeptide for treating, preventing and/or prognosing
 PT disorders of the endocrine system such as reproductive disorders,
 PT endocrine cancers and also for testing and detection e.g. diagnosis -
 XX
 PS Claim 1; SEQ ID NO 136; 604pp; English.
 XX

Sequences AAS29511-AAS29736 represent cDNA molecules, which encode the
 endocrine polypeptides of the invention. Endocrine polypeptides and their
 associated polynucleotides of the invention are useful in the diagnosis,
 treatment and prevention of various types of disorders in e.g. humans,
 mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A
 pathological condition can be determined by determining the presence or
 absence of a mutation in an endocrine polynucleotide. The treatable
 disorders include autoimmune diseases such as rheumatoid arthritis,
 hyperproliferative disorders such as neoplasms of the breast or liver,
 cardiovascular disorders such as cardiac arrest, cerebrovascular
 disorders such as cerebral ischemia, nervous system disorders such as
 Alzheimer's disease, infections caused by bacteria, viruses and fungi,
 ocular disorders such as corneal infection, endocrine disorders such as
 premature labour and infertility, gastrointestinal disorders such as
 Crohn's disease, renal disorders such as glomerulonephritis and
 respiratory disorders such as asthma. The polypeptides can also be used
 to aid wound healing, to prevent skin aging due to sunburn, to maintain
 organs before transplantation, to regenerate tissues and in chemotaxis.
 The polypeptides can also be used as a food additive or preservative to
 increase or decrease storage capabilities.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC

Query Match 42.1%; Score 233.8; DB 22; Length 492;

Best Local Similarity 75.7%; Pred. No. 9.2e-56; Mismatches 103; Indels 5; Gaps 4;

QY 106 CCTCATGATTTTGTGGTATCTCTTCCCTACTTGTGGCACTGGGACCGAGTGGCCG 165
 DB 14 CCGGATCGACATGTGGCCATCTTATTATCATCTGTGGTACGAGCTGGCCGA 73
 QY 166 GCAGCGAGGGGTGGCCAGGCGCATGTCACTGGCCATCTAGAGTCAATCCGATTGT 225
 DB 74 ACACAGGCGCATGACAGGCGCATGTCTGGCCATCTGAGGCTCATCCGCTGT 133
 QY 226 GCGTGTCTCCGATCTTCAAGCTGTCCGCGCACTCAAGGCGCTCAATCTTGGGCCA 285
 DB 134 AAG-GTCTTCCGATCTTCAAGCTGTGCGCCACTCCAAAGGCGCTCAGATCTCGGCA 192
 QY 286 GACGCTTGGGCTCCATGCTGAGCTGGGCTCTCATCTTTCTCTTCATCGGT 345

DB 193 AACRCAGAGCATTCATGCGGAGTGGGTTGCTCATCTTCTTCATGTGAGT 252
 QY 346 GGTCTCTTTCCAGGCGGTCTACTTTGCCGAGTGAACGGGTGAGTCCCATTTAC 405
 DB 253 CATCTCTTCTCCAGTGCATCTTACTTGTGAGTGAAGCCAGAGTCCCATTTCTC 312
 QY 406 TACATCCCTGAGTCTTCTGTGGCGGTAGTACCATGACTTACAGTT-GGCTATGAG 464
 DB 313 TAGCATCTCGATGAGTCTTGTGGGCGAGTGTACCATGACATGTTAGGCTATGGGG 372
 QY 465 ACATGCGACC--CGTCACTGTGGTGGCAAGATAGTGGGCTCTGTGTCCATT-GCGG 521
 DB 373 ACATGTGCCCGACACCCAGGGGGGTAAAGATTGTGGGCACTGTGTCCATTGGCAG 432
 QY 522 GCGTGTGATTTTCCCTGCCAGTCCC 550
 DB 433 GGGTCTCACCATTTGCCCTTGTGGCC 461

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2003, 02:24:22 ; Search time 22.8547 Seconds
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Searched: 441362 seqs, 153338381 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	436.6	78.5	1599	1	US-08-288-405A-9
2	326.2	58.7	1994	1	US-08-527-152-1
3	179.4	32.3	696	1	US-07-955-916-5
4	168.2	30.3	1805	1	US-07-955-916-6
5	159	28.6	2064	4	US-09-178-109-3
6	159	28.6	2072	4	US-09-142-791A-3
7	159	28.6	2104	4	US-09-142-791A-1
8	157.8	28.4	3424	4	US-09-336-643A-9
9	157.8	28.3	2104	4	US-09-142-791A-5
10	145	26.1	2483	1	US-08-464-340A-3
11	145	26.1	2483	5	PCT-US94-08449A-3
12	137.2	24.7	2127	5	PCT-US94-08449A-1
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14	130.8	23.5	196	1	US-08-288-405A-18
15	130.8	23.5	2293	4	US-09-336-643A-5
16	124.2	22.3	1927	4	US-09-336-643A-3
17	122.2	22.0	3102	4	US-09-336-643A-17
18	115	20.7	3080	4	US-09-336-643A-7
19	106.4	19.1	139	1	US-07-961-268-3
20	97.4	17.5	139	1	US-07-961-268-4
21	97.4	17.5	896	4	US-09-105-058C-1
22	77	13.8	2028	4	US-09-634-920-1
23	57.6	10.4	2734	3	US-09-135-021-79
24	57.6	10.4	2821	4	US-09-135-010A-115
25	57.6	10.4	2821	4	US-09-597-735-115
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36	55	9.9	930	4	US-09-105-058C-17	Sequence 17, Appli
37	55	9.9	2565	4	US-09-105-058C-26	Sequence 26, Appli
38	55	9.9	2914	4	US-09-177-650-6	Sequence 6, Appli
39	53.8	9.7	93	1	US-08-288-405A-16	Sequence 16, Appli
40	53	9.5	702	4	US-08-843-417-3	Sequence 3, Appli
41	53	9.5	2573	4	US-08-669-656A-3	Sequence 3, Appli
42	53	9.5	6344	4	US-08-843-417-1	Sequence 1, Appli
43	53	9.5	6524	4	US-08-669-656A-1	Sequence 1, Appli
44	53	9.5	6527	4	US-08-669-656A-7	Sequence 7, Appli
45	53	9.5	7052	4	US-08-669-656A-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-288-405A-9
; Sequence 9, Application US/08288405A
; Patent No. 5559009
; GENERAL INFORMATION:
; APPLICANT: Chandy, Kantanthara G.
; APPLICANT: Kalman, Katilin
; APPLICANT: Chandy, Grischa
; APPLICANT: Gutman, George A.
; TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
; ADDRESSEE: Attn: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,405A
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,431
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-59844-1/MHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELETYPE: 910 277299
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1599
; US-08-288-405A-9

Query Match 78.5%; Score 436.6; DB 1; Length 1599;
Best Local Similarity 86.7%; Pred. No. 2.8e-109;
Matches 481; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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DB 913 GTGGCCCTGAGCAAGCGGTGTGTTTCAAGATGTGATGAACCTATTTGATTTG 972
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QY 182 CAGAGGCGCATGTACAGCGGCATCTTCAAGATCATCCGATTTGGCTGTCTTCGAGTC 241
DB 1033 CAGCGGCTATGTCTGCGGCATCTTCAAGGATCATCCGATTTGGCTGTCTTCGAGTC 1092
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DB 1153 ATGCGTGAGCTGGGCGCTCTCATCTTTTCTCTTCATTCGCTGTGCTTTTTCAGC 1212
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QY 422 TTCTGTGTGGGCGGTAGTACCATGATGATGATTTGGCTATGAGACATGGGCGCTGAT 481
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DB 1333 GTGGGTGGCAAGATGATGGGCTCTGTGTGTCATTTGGGCGGCTGCTGACTATTTCCCTG 1392
QY 542 CCAAGTGGCGCTCAT 556
DB 1393 CCAAGTGGCGCTCAT 1407

RESULT 2
US-08-527-152-1
Sequence 1, Application US/08527152
Patent No. 5827655
GENERAL INFORMATION:
APPLICANT: Chandu, Kanianthara G.
APPLICANT: Cahalan, Michael D.
APPLICANT: Grissmer, Stephan
APPLICANT: Goldin, Alan L.
APPLICANT: Dehiefs, Brent A.
APPLICANT: Gutman, George A.
TITLE OF INVENTION: Assay, Methods and Products Based On n
TITLE OF INVENTION: K+ Channel Expression
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobach, Test, Albritton & Herbert,
ADDRESSEE: Attn: W.H. Dregler
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/527,152
FILING DATE: UNKNOWN
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/170,418
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/558,568
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dregler, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-54444-2/MHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1994 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 150..1736
US-08-527-152-1

Query Match 58.7%; Score 326.2; DB 1; Length 1994;
Best Local Similarity 74.2%; Pred. No. 2.6e-79;
Matches 412; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

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QY 62 CTGCTGTGTCCAGCAAGCGGTATCTTTCAAGAACGTGAACATCATGATTTGTG 121
DB 951 TTCTGTGTGGGCGGTAGTACCATGATGATTTGGCTATGAGACATGGGCGCTGAT 1010
QY 122 GCTATCTTCTCTTCTTGTGGCACTGGGACCGAGCTGGCCCGGACGAGGGGTGG 181
DB 1011 GCGATCTTCTCTTCTTGTGGCACTGGGACCGAGCTGGGCGGCTGAGCGCATTAAGGG 1070
QY 182 CAGAGGCGCATGTACAGCGGCATCTTCAAGATCATCCGATTTGGCTGTCTTCGAGTC 241
DB 1071 CAGAGGCGCATGTACAGCGGCATCTTCAAGATCATCCGATTTGGCTGTCTTCGAGTC 1130
QY 242 TTCAAGCTGTCCGCACTCAAAAGGCGCTCAAAATCTTGGGCGAGCGCTTCGCGCTCC 301
DB 1131 TTCAAGCTGTCCGCACTCAAAAGGCGCTCAAAATCTTGGGCGAGCGCTTCGCGCTCC 1190
QY 302 ATGCGTGAGCTGGGCGCTCTCATCTTTTCTCTTCATTCGCTGTGCTTTTTCAGC 361
DB 1191 ATGCGTGAGCTGGGCGCTCTCATCTTTTCTCTTCATTCGCTGTGCTTTTTCAGC 1250
QY 362 GCGCTCTACTTTGCGCAAGTTGAACGGGCTGGGAGCTCCCATTTCACTACATTCCTGAGTC 421
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QY 422 TTCTGTGTGGGCGGTAGTACCATGATGATGATTTGGCTATGAGACATGGGCGCTGAT 481
DB 1311 TTCTGTGTGGGCGGTAGTACCATGATGATGATTTGGCTATGAGACATGGGCGCTGAT 1370
QY 482 GTGGGTGGCAAGATGATGGGCTCTGTGTGTCATTTGGGCGGCTGCTGACTATTTCCCTG 541
DB 1371 GTGGGTGGCAAGATGATGGGCTCTGTGTGTCATTTGGGCGGCTGCTGACTATTTCCCTG 1430
QY 542 CCAAGTGGCGCTCAT 556
DB 1431 CCAAGTGGCGCTCAT 1445

RESULT 3

US-07-955-916-5

Sequence 5, Application US/07955916

Patent No. 5397702

GENERAL INFORMATION:

APPLICANT: CAHALAN, Michael D.

APPLICANT: CHANDY, Kanianthara G.

APPLICANT: GRISMER, Stephen

APPLICANT: GHANSHANI, Sanjiv

APPLICANT: GUTMAN, George A.

APPLICANT: DETHELEFS, Brent A.

TITLE OF INVENTION: ASSAY FOR AND TREATMENT OF AUTOIMMUNE

DISEASES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Walter H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/955,916

FILING DATE: 19921002

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-54474-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 696 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-07-955-916-5

Query Match 32.3%; Score 179.4; DB 1; Length 696;

Best Local Similarity 62.0%; Pred. No. 1,1e-39;

Matches 354; Conservative 0; Mismatches 181; Indels 36; Gaps 3;

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14 TCGAGGGCGTGTGTTGCTGCTGATTCCTTCATGCTGATGCTGATCTTCTGCG 73
72 CAAGAGGCTATCTTCTTCAGAGAGTATGACTCATTCATTTTGGCGTATCTCT 131
74 CCAACAGGTATAGATTCAAGAACTCGCTCAACATCATTTGTTGGCCATCTCT 133
132 CCTACTTTGGCAGTGGGACCGAGCTGCGCGGAGGAGGAGGAGGAGGAGGAGGCA 191
134 CCTTCACTGAGAGTGGG-----GCTAGAGGCGCTGTCTCCCAAGGAGGAGGAGG 187
192 TGTCACTGGCCATCTGAGAGTCAATCGATGTTGGTGTCTTCCGATCTTCAAGCTGT 251
188 TG---CTGGGCTTCGCGCGTGTGCTGCTGCGCATCTTGGCAGCTTAAAGCTGA 244
252 CCGGAGCTCAAGAGGCGCTGCAATCTTGGGCGAGAGCGTGGGCGCTTCATGCGTGA 311
245 CCGGAGCTTGTGGCGTGGGCGTCTGGGCGACAGCGTCCGAGGAGGAGGAGGAG 304
312 TGGGCGCTCTCATCTTTTCTCTTCATGAGTGTGTCTCTTTTTCAGAGGCGCTGAG 371

RESULT 4

US-07-955-916-6

Sequence 6, Application US/07955916

Patent No. 5397702

GENERAL INFORMATION:

APPLICANT: CAHALAN, Michael D.

APPLICANT: CHANDY, Kanianthara G.

APPLICANT: GRISMER, Stephen

APPLICANT: GHANSHANI, Sanjiv

APPLICANT: GUTMAN, George A.

APPLICANT: DETHELEFS, Brent A.

TITLE OF INVENTION: ASSAY FOR AND TREATMENT OF AUTOIMMUNE

DISEASES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Walter H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/955,916

FILING DATE: 19921002

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-54474-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 1805 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-07-955-916-6

Query Match 30.3%; Score 168.2; DB 1; Length 1805;

Best Local Similarity 60.8%; Pred. No. 1.7e-36;

Matches 347; Conservative 0; Mismatches 188; Indels 36; Gaps 3;

12 TGGAGAGCGTGTATTTGTTGCTTCCTTTGAGCTGCTGAGCCCTCGTGGTGTGAC 71
879 TCGAGGGCGTGTGTTGCTGCTGATTCCTTCATGAGTGTGTCTCTTTTTCAGAGG 938

OY	72	C A A C G A G G G A T C T T C C T T A A A A G C G T A G A A C C T A T C A T T T T T T T G G C A T C T T C	131
Db	939	C C A A C A A G G T G G A A T T A T C A T A M A M A C T C C C T C A T A T C A T T T A C T T T T G G G C A T T T C C	998
OY	132	C T T A C T T T G T G G C A C T G G G C A C C G A G C T G C C C G G C A G C G A G G G T G G G G C A G C A G G C C A	191
Db	999	C C T T C T A C C G T G A G G T G G G -- C C T A A G C G G C T G T C T C T A A A A G C C G C C A M A G A C G T T --	1054
OY	192	T G T C A T G G G C A T C C G A G A G T A T C C G A T T G G T G G T C T T C C G A C A T C T T C A A G C T G T	251
Db	1055	-- C T G G G C T T C T B C G G G T G T C C G T T G T G G G C A T C C T G G C A T T T T C A A G C T G A	11039
OY	252	C C G G C A C T A A A G G G C C T G C A A A T C T T G G G C A G C G T T G G G G C T T C A T G C G T G A G C	311
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OY	312	T G G G C C G C A C A C T C T T T T C C T C T C A T G G G T G G T G C T C T T T T T G C A G C G C C T A C T	371
Db	1170	T C T G C T G C T T A T C A T C T T C T T C T G G C C C T G G A T G C T C A T C T T T G C A C A C T A G A T C T A C T	12239
OY	372	T T G C C G A ----- A G T T A G C C G G G T G A C T C C C A T T T T C A	404
Db	1230	A C G C C G A G A G A T A G G G G C A C A C C C A A T A G A C C C A G C C C A C G A M A C A C A C A C T T T A	1289
OY	405	C T A C A C T C C T G A G T C C T T T G T T G G G C G G T A G T A C A C A T A C T A G A G T T G G C T A T G A G	464
Db	1290	A A A A C A T C C C A A T O G G T C T T G T G T G G G C T G T G T C A C A T A G A C A G A C A C T G G G C T A T A G A G	1349
OY	465	A C A T G G C A C C C G C A C T G T G G G T G G C A A G A T A G T A G G G C T C T T G A T G G C A C T T G C G G C G	524
Db	1350	A C A T G A T C C C A C A G A C G T G T G T G A A T G C T G T G G A G C C T T G T G T G C T G C T G G G	1409
OY	525	T G T G A C T A T T T C C C T T C C A G T C C C C C T A C T	555
Db	1410	T G C T G A C C A T T T G C C A T G C G G T C C C T G A C T A C T	1440

RESULT 5
 US-09-178-109-3
 : Sequence 3, Application US/09178109
 : Patent No. 6395477
 : GENERAL INFORMATION:
 : APPLICANT: Cockett, Mark I.
 : APPLICANT: Dilks, Daniel W.
 : APPLICANT: Chang Ling, Hual-Ping
 : APPLICANT: Sokol, Patricia T.
 : TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
 : FILE REFERENCE: ahp-98089
 : CURRENT APPLICATION NUMBER: US/09/178,109
 : CURRENT FILING DATE: 1998-10-23
 : NUMBER OF SEQ ID NOS: 4
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 3
 : LENGTH: 2064
 : TYPE: DNA
 : ORGANISM: human
 US-09-178-109-3

Query Match	28.6%	Score 159;	DB 4;	Length 2064;
Best Local Similarity	58.7%	Pred. No. 5.6e-34;		
Matches 326;	Conservative	0;	Mismatches 205;	Indels 24;
				Gaps 2

QY	2	TTTCTTGAGGAGAGACGCTGTGATATTTGTTGGTTCCTTTGAGCTGCGTACGCGCTC	61
	748	TTTCTTCTGCTGGACAGCGGCTGGGTATGATCTTCAACCGTGGAGTACTCTCTGGCGCTC	807
Db			
QY	62	CTGGCTGTGTCCAAACGACATCTTCTTCAAGACGTGATGAACCTCATGATTTTGTG	121
Db	808	TTTCGGGCTCTCCAGCGCTACTCCGCTTCACTCCGCAACGCTCATGACATATGAGAGCTGTG	867
QY	122	GCTATCTTCCCTACTTTGTGGACACTGGGACCCGACGCTGGCGCCCGGACAGAGGGGTGGGC	181

Db	868	GCATCATGGCCACTACTACATCGGTGTGGTCAT-----GACCAAC	906
QY	182	CACGAGCCCATGTCTACTGGCCATCTGAGAGTCATCCGATTGGTGGCTGTCTTCCGCATC	241
Db	907	AACGAGGACCTGTCCGGCGGCTTCGTCA--GCGTCCGGGTCTTCCGGCTTCCAGGATC	963
QY	242	TTTCAAGGTGTCCGGGCATCTCAAGGGGCGTCGAATTTGGGGCAGCGGCTTGGGCGCTC	301
Db	964	TTTCAAGTTTTTCCGGCCACTCCAGGGCGTCGGGATCTTGGGTACACATCGAAGAGCTGT	1023
QY	302	ATGGGTAGCTGGGGCCCTCATCTTTTTCCTTCATGTGGTGGTCTCTTTTCCAGC	361
Db	1024	GCTTCCGAAGCTGGGCTTTCTTCTTCTTCCCTCACCATGGCCATCATATCTTTGCCACT	1083
QY	362	GCCCTCACTTTGGCCGAAGTTGAACGGGGAGACTCCCATTTTCATGACATCCGTGAGTCC	421
Db	1084	GTGATGTTTATGGCGAAGAGGGCTCTGTGGCCAGCAATTCACAAGATCCCTGCTCG	1143
QY	422	TTTGTGTGGGGCGGTATGCACCATGACTACAGTTGGCTATGGAAGACATGGACCCCTCACT	481
Db	1144	TTTTGTATACCATTTGTTCACCATGACCACTGGGTTACGGAGACATGGTGGCTTAAGAG	1203
QY	482	GTGGGTGGCAAGATAGTGGGCTCTGTGTGGCATTTGGCGGGGTGCTGACTATTTTCCGTG	541
Db	1204	ATTTCAGAGGAGAGATCTTGGCTCATCTGTGCTTGAATGGGGGCTGTGCTATTTGCCCTG	1263
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Db	1264	CCAGTCCCTGTGATT	1278

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RESULT 6
US-09-142-791A-3
: Sequence 3, Application US/09142791A
: Patent No. 6368623
: GENERAL INFORMATION:
: APPLICANT: Antoine Michel Alain Brill
: APPLICANT: Thierry Paul Gerard Calmels
: APPLICANT: Jean-Francois Simon Pierre Falvire
: APPLICANT: Jean-Luc Javre
: APPLICANT: Sabine Rouanet
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GH-30012
: CURRENT APPLICATION NUMBER: US/09/142, 791A
: CURRENT FILING DATE: 1999-02-02
: PRIOR APPLICATION NUMBER: PCT/EP98/01901
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: UK 9706377.0
: PRIOR FILING DATE: 1997-03-27
: PRIOR APPLICATION NUMBER: EP 97402971.2
: PRIOR FILING DATE: 1997-12-09
: PRIOR APPLICATION NUMBER: EP 97403007.4
: PRIOR FILING DATE: 1997-12-11
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 2072
: TYPE: DNA
: ORGANISM: HOMO SAPIENS
US-09-142-791A-3

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Query Match	28.6%	Score 159;	DB 4;	Length 2072;
Best Local Similarity	58.7%;	Pred. No. 5.7e-34;		
Matches 326;	Conservative	0;	Mismatches 205;	Indels 24;
				Gaps 2

Oy	2	TTTTCTGCGGAGAGCGCTGTATTGTTGGCTTCCTTTGAGCTGGATACGCTC	61
Db	676	TTCTTCTCCCTCGACACGGCGCTGGCTCATATCTTCAACGGTGGAGTACCTCTGGCGCTC	735
Oy	62	CTGCTCTCTCCACGACAGGCTATCTTCTCAAGAACGTCGATGAACCTCATCATTTTGTG	121
Db	736	TTTCGGGCTCCACGCGCTACCGCTTATCCGACGGCTCATGACATCATGACGTGTG	795

APPLICATION NUMBER: PCT/US94/08449A
 FILING DATE: SUBMITTED HERewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: FERRARO, GREGORY D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-105
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2483 BASE PAIRS
 TYPE: NUCLEIC ACID
 STRANDEDNESS: SINGLE
 TOPOLOGY: LINEAR
 MOLECULE TYPE: CDNA
 PCT-US94-08449A-3

Query Match 26.1%; Score 145; DB 5; Length 2483;
 Best Local Similarity 55.4%; Pred. No. 3,8e-30;

Matches 302; Conservative 0; Mismatches 240; Indels 3; Gaps 1;

QY 11 GTGAGACGCTGTATTTGTTGTTCTCCTTGGAGCTGCTGAGCGCTCTGCTGT 70
 DB 1357 GTGAGACGCGCTGTATTTGTTGTTCTCCTTGGAGCTGCTGAGCGCTCTGCTGT 1416
 QY 71 CCAGAGAGGCTATCTTCTTCAAGAACGTATACCTCATCTTTTGCTATCTT 130
 DB 1417 CCCAAGAGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1476
 QY 131 CCCTACTTGTGACATGCGACCGAGCTGCGCCGAGCGAGGGGGGCGACAGGCC 190
 DB 1477 CCCTTACTGAGCTGACGCTGACGCTGACGCTGCTGCTGCTGCTGCTGCTGCTG 1536
 QY 191 ATGTCACTGCGCATCTGAGAGTCAATCCGATGCTGCTGCTGCTGCTGCTGCTGCTG 250
 DB 1537 GTGACACAGGCGCTGAGAG--GCGCTGCGGATGATGCGGATGCGGCGCATCTCAAGCTG 1593
 QY 251 TCCGCGCATCAAGAGGCGCTGCAATCTTGGGCGACAGCTTGGGCGCTCATGCTGAG 310
 DB 1594 GCGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1653
 QY 311 CTGCGGCTCTCATCTTTTCTCTCTCATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 370
 DB 1654 CTGCGGCTCTCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1713
 QY 371 TTTGCCGAAGTTGACCGGGTGAAGCTCCATTTCAGTACGATCCCTGAGTCTTCTGCTG 430
 DB 1714 ACCATGAGCAGAGACCATCCAGAGACCTGTTAAGAACATCCCGAGTCTTCTGCTG 1773
 QY 431 GCGGTATGACCATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 490
 DB 1774 GCGGTATGATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1833
 QY 491 AAGATAGTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 550
 DB 1834 AAGCTCAAGCGGCGCATGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1893
 QY 551 GTTCAT 555
 DB 1894 CCCAT 1898

RESULT 13
 US-08-464-340A-1
 ; Sequence 1, Application US/08464340A
 ; Patent No. 5710019
 ; GENERAL INFORMATION:
 ; APPLICANT: LT, ET AL.

TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ADDRESS: CECCHI, STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464, 340A
 FILING DATE: June 5, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/08449
 FILING DATE: 28 JUL 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: FERRARO, GREGORY D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-415
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2127 BASE PAIRS
 TYPE: NUCLEIC ACID
 STRANDEDNESS: SINGLE
 TOPOLOGY: LINEAR
 MOLECULE TYPE: CDNA
 US-08-464-340A-1

Query Match 24.7%; Score 137.2; DB 1; Length 2127;
 Best Local Similarity 56.6%; Pred. No. 4.6e-28;

Matches 325; Conservative 0; Mismatches 228; Indels 21; Gaps 3;

QY 3 TCTTGTGTGAGAGCGTGTATTTGTTGTTCTTCTTGTGAGTGTGCTGCTGCTGCTG 62
 DB 1084 TCTTGTGTGAGAGCGTGTATTTGTTGTTCTTCTTGTGAGTGTGCTGCTGCTGCTGCTG 1143
 QY 63 TGTGTGTCAAGCAGGCTATCTTCTCAAGACGATGATGACATGATGATGATGATGATG 122
 DB 1144 TGTGTGTCAAGCAGGCTATCTTCTCAAGACGATGATGACATGATGATGATGATGATG 1203
 QY 123 CTATCTTCT 170
 DB 1204 CTATCTTCT 1263
 QY 171 GAGGGGTGGGCGAG-----CAGCCATGTCTACTGACCATCTGAGATGATGATGATG 224
 DB 1264 CCGGCGCGGCGCAACAGCTACTGCAAGAGTGGGCTGTGCTGCTGCTGCTGCTGCTGCTG 1323
 QY 225 TGGGTGTCTTCCGATCTTCAAGCTGTCCGCGACATCAAGAGGCGCTGCAAAATCTTGGGCG 284
 DB 1324 TGGGTGTCTTCCGATCTTCAAGCTGTCCGCGACATCAAGAGGCGCTGCAAAATCTTGGGCG 1383
 QY 285 AGACGCTTGGGCGCTCATGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 344
 DB 1384 TACGCGCGCGCGCGCTGACCGCGGAGATTTGGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1443
 QY 345 TGGTCTCTTTTTCAGCGCGCTCTACTTTCGGAAGTTACCGGGTGAAGCTCC---ATT 401
 DB 1444 TGGCGCTTCTTTCAGCGCGCTCTACTTTCGGAAGTTACCGGGTGAAGCTCC---ATT 1503
 QY 402 TCACATGACATCCCTGAGTCTTCTGCTGCGGTATGACATGATGATGATGATGATGATG 461
 DB 1504 TCACATGACATCCCTGAGTCTTCTGCTGCGGTATGACATGATGATGATGATGATGATG 1563

FEATURES	source
Plate: 0070	row: M column: 07
Seq primer:	CACACAGGAAACACCTATGACC
Class:	plasmid ends
High quality sequence stop:	636.
Location/Qualifiers	
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0070M07"
/clone_id="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F+"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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BASE COUNT	181 a	163 c	161 g	131 t
ORIGIN				
Query Match		54.2%	Score 301.2;	DB 17; Length 636;
Best Local Similarity		72.9%;	Pred. No. 3.4e-68;	
Matches 401; Conservative		0;	Mismatches 148;	Indels 1; Gaps 1;

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Db	636	GTGGTGGAGACCTTGTGCATCATCTGGTTCTCTTTGAGCTCTTGCTGGCTATTTCCT	577
Qy	68	TGTCCACGCAAGGCTATCTTTTCAAGACGTATGAACCTCATGATTTTGTGGCTATC	127
Db	576	TGCCCACTAAAGCACCTTCTCAGAAATCATGAACCTGATAGATATGTGGCAATC	517
Qy	128	CTTCCCTACTTTGTGGCACTGGGACCGAGCTGGGCGGCGAGCGGGGTGGGCGAG	187
Db	516	ATTCTCTATTTTATTCACCTCTGGCAGCTAGCTGGCTGAACGACAAAGTAAATGGCAGCAG	457
Qy	188	GCCATGTACTTGGCCATCTGAGATCATCCGATTTGTGCTGTCTTCCGACTTTCAG	247
Db	456	GCCATGTGCTGGCCATCTGAGATCATCCGCTAGTAAAGGTTTCCGACTTTCAG	397
Qy	248	CTGATCCGGGACCTAAAGGGCTGCAAACTTTGGGCGCAGAGCTTGGGGCTCATAGGT	307
Db	396	CTTCTCCGCCATTTCTAAAGGCTCAGATCTTAAAGACGACGCTGAAGGCTTCCATGGG	337
Qy	308	GAGCTGGGCTCTCATCTTTTCTCTCTCTCTCTGAGTGTGCTCTCTTCCAGCGCGCTC	367
Db	336	GAGCTGGGCTGTTCATTTCTCTTATTCATTAATGGGGCTATCTTTCTCAGTGAATC	277
Qy	368	TACTTTGCCGAAGTTGACCGGGTGAGCTCCCATTTCTACATAGATCTCCCTTCTGG	427
Db	276	TACTTTGCTGAGGAGCAGCCCTCTTCTGGGGTTTTTAAACATATCCGGAGTGCCTTGG	217
Qy	428	TGGCGGTAGTACCATGACTACAGTTGGCTATGAGACATGAGCCGCTACTGTGGCT	487
Db	216	TGGCGAGTAGTAAACCATTTACAACCTGTGGTTATGTGTATAGCACCCAGTACCATAGA	157
Qy	488	GGCAGATAGTGGGCTCTCTGTGTGCATTTGCGGGCGTGC-TGACATATTTTCCCTGCAGT	546

Db	156	GGCAGAGTTTGTGGGCTCTTTTGTGCATCCGAGSTGTCTTGTGACATTTCATTACCAAT	97
QY	547	GCCCGTCATT	556
Db	96	TCTGTGATT	87

RESULT 2					
CNS02RD3/C					
LOCUS		900 bp	DNA	linear	GSS 14-MAY-2000
DEFINITION	CNS02RD3				
	Tetraodon nigroviridis genome survey sequence T7 end of clone				
	159H12 of library G from Tetraodon nigroviridis, genomic survey				

ACCESSION	sequence.
VERSION	AL210432.1
KEYWORDS	GI:7869251
SOURCE	GSS: genome survey sequence.
ORGANISM	Tetradodon nigroviridis.
	Tetradodon nigroviridis

REFERENCE
Roest-Crolius, H., Jallón, O., Dasilva, C., Bouneau, L., Fisher, C.,
1 (bases 1 to 900)

TITLE	JOURNAL	REFERENCE
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence	Unpublished	2 (bases 1 to 900)

AUTHORS	TITLE	JOURNAL	DATE	DOI
Roest-Crotilius, H., Jallion, O., Dasilva, C., Fitzames, C., Fisher, C., Bonneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissbach, J.	Characterization and repeat analysis of the compact genome of the freshwater pufferfish <i>Tetraodon nigroviridis</i>	Unpublished	2003	10.1002/1469-7580(200304)1469:7580::AID-HEM2003040101

REFERENCE	3 (bases 1 to 900)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000)
COMMENT	This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetradon nigroviridis genome. For more information please take a look at

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SOURCE
1. 900
location/Qualifiers
/organism="Tetradodon nigroviridis"
/db_xref="taxon:99883"
/codon="15qnt2"

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Query Match	53.8%	Score 299.2	DB 17	Length 900
BASE COUNT	206 a	242 c	283 g	166 t
ORIGIN	/clone_11b="c" /note="Genoscope sequence ID : C0AG159DD06Lp1-end : T7" 3 others			

[illegible][illegible][illegible]

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11465 row: n column: 23
High quality sequence stop: 772.

FEATURES	Location/Qualifiers
source	1. .772

BASE COUNT	150 a	240 c	236 g	146 t
ORIGIN				

Query Match	50.2%;	Score 279.2;	DB 13;	Length 772;
Best Local Similarity	76.7%;	Pred. No. 2.1e-62;		
Matches 376;	Conservative	0;	Mismatches 93;	Indels 21;
				Gaps 2

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Db	19	TTCTCCGGGAACATCATGAAACATCATGATGTGGTGGGATCTTCCCTCATTCATACC	78
QY	146	CTGGGGACCCGAGCTGGCCCGGACGAGGGGTG- -----GGCCAGC	185
Db	79	CTGGGGACCCGAACTGGGACGAGACAGCCACAGGGCGCGAGAGCGGCCCAAAATGGGACG	138
QY	186	AGGCGATGTCATCTGGCCATCCCTGAGTATCATCCGATGGTGGCGGCTTCGGATCTTCA	245
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QY	246	AGCTGTCCCGGCACTCAAAAGGGCCTGCAAAATCTTGGGCGAGAGCTTCGGGGCTCCATGC	305
Db	199	AGCTGTCCCGGCACATCCAAAGGGGCTGCAGATCCGGGCAAGACCTTGCAAGCCCTCATGA	258
QY	306	GTGAGCTGGGGCTCTCATCTCTTTTCCCTTCAATCGGTGGTGCCTTTTTCACAGGGCCG	365
Db	259	GGGAGCTGGGGCTCTCATCTCTTTTCCCTTCAATCGGGTCACTCTTCTTCCAGTGGCG	318
QY	366	TCCTACTTTGCCAAGTTGACCGGGGTGAGCTCCCAATTTCACTAGCATCCCTGAGTCTCTT	425
Db	319	TCCTACTTCCGAGAGGCTGACACCAACAGGA - ACCCATTTCTTACATATCCCTGAGGCTCTT	377
QY	426	GGTGGGGGTGTACCATCATCTTACATTTGGGTATGAGACATGAGGACCCGCTCACTGTG	485
Db	378	GGTGGGAGTGTACCATCATGACACTGTGGCTACAGGGGACATGAGGCCCATCATCTGTG	437
QY	486	GTGGCAAGATAGTGGGCTCTCTGTGTCCATGTGGGGCTGCTGACTATTTTCCCTGGCAG	545
Db	438	GGGGCAAGATAGTGGGCTCGGCTGTGTGCCATMGCCGGGGTCTCAGACATTGGCCCTGGCTG	497
QY	546	TGCCCCGTAT 555	
Db	498	TGCCCGTCAT 507	

DEFINITION
daif3e03.y1 NICHD XGC Brn1 Xenopus laevis cDNA clone IMAGE:4740197
5' similar to TR:070259 070259 VOLTAGE-GATED POTASSIUM CHANNEL
KV1.7, mRNA sequence.
BC812963
BC812963.1 GI:14183943
EST.
African clawed frog.
SOURCE

FEATURES

Location/Qualifiers

BASE COUNT	135 a	120 c	133 g	171 t
ORIGIN				

Query Match	48.9%;	Score 271.8;	DB 12;	Length 559;
Best Local Similarity	72.1%;	Pred. No. 1.6e-60;		
Matches 354;	Conservative 0;	Mismatches 137;	Indels 0;	Gaps 0;

[illegible]

Db 368 ATGAGGAAATGGGGCTGTGATATTTTCCTTTTCATTTGGGGTATACCTTCTCCAGC 427

QY 362 GCGGTACTTGGCCAGTACCGCGGAGCTCCCATTTACATGATCCCTGAGTCC 421

Db 428 TTAGTCTACTTGGCTGCTGATCATGCGGATACAAAGTTTACAGTATCCCTGAGCA 487

QY 422 TTCTGTGGCGGCTAGTACCATGACTACAGTGTGCTATGAGACATGACCCCTGACT 481

Db 488 TTTTGTGGGCTGTGCTGACATGACATGACAGTATGCTGATGTGCTACTGAAACA 547

QY 482 GTGGGTGCCAA 492

Db 548 GTAGGGGGA 558

RESULT 6

LOCUS BM128683 575 bp mRNA linear EST 12-MAR-2002

DEFINITION 1f14f08.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens

CDNA clone IMAGE:5676446 5' similar to SW:CIK3_HUMAN P22001

VOLTAJE-GATED POTASSIUM CHANNEL PROTEIN KVL3 ; mRNA sequence.

ACCESSION BM128683.1 GI:17123227

VERSION EST.

KEYWORDS human.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 575)

AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistein,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvilli,R., Williams,T., Jackson,Y. and Bowers,Y.

TITLE Endocrine Pancreas Consortium

JOURNAL Unpublished (2000)

COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center for information on obtaining a clone please contact: Juliana Brown (brownjefas.harvard.edu) This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov

High quality sequence stop: 429.

FEATURES

source

Location/Qualifiers

1..575

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5676446"

/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"

/sex="Both"

/tissue_type="Islets of Langerhans"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Organ: Pancreas; Vector: pSPORT1; Site:1: Not 1; Site:2: Sal 1; Starting library constructed using Superscript Plasmid Library Kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaudo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an EcoT of 20. Single-stranded (unhybridized) plasmids were isolated

BASE COUNT 118 a 164 c 156 g 137 t

ORIGIN

Query Match 48.2%; Score 267.8; DB 13; Length 575;

Best Local Similarity 75.6%; Pred. No. 1.8e-59;

Matches 332; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 118 TGTGGTATCTTCCCTACTTTGTGGCAGCGGACCGACCGCCCGAGGAGGAG 177

Db 1 TGTGGCATCATCTTCTATTATTAACCTGTGGGTACGAGCTGGCAAGACAGGCA 60

QY 178 GGGCCAGCAGGCGCATGTGACGCAATCCGAGATCATCGATGTGGTGGTCCG 237

Db 61 TGCACAGCAGGCGCATGTGACGCAATCCGAGATCATCGGCTGTAGGGCTTTCCG 120

QY 238 CATCTTCAAGCTGTCCCGGACATCAAGGCGCTGCAAACTTGGCGCAGCCTTGGGC 297

Db 121 CATCTTCAAGCTGTCCCGGACATCAAGGCGCTGCAAACTTGGCGCAGCCTTGGGC 180

QY 298 CTCATGCGGAGCTGGGCGCTCCCATCTTTCTCTTCATGCGGTGGTCTCTTTC 357

Db 181 GTCCATGCGGAGCTGGGCGCTCCCATCTTTCTCTTCATGCGGTGGTCTCTTTC 240

QY 358 CACGCGCGTCTACTTTGGCCGAAGTTGACCGGGTGAAGTCCCATTTTCACTAGCATCCCTGA 417

Db 241 CACGCGCGTCTACTTTGGCCGAAGTTGACCGGGTGAAGTCCCATTTTCACTAGCATCCCTGA 300

QY 418 GTCTTCTGTGTGGCGGTAGTACCATGACTACAGTTGGCTATGAGACATGGCACCCGT 477

Db 301 TGCTTCTGTGTGGCGGTAGTACCATGACTACAGTTGGCTATGAGACATGGCACCCGT 360

QY 478 CACTGTGGTGGCAAGATAGTGGGCTCTGTGTCATGCGGCGCTGCTGACTATTTC 537

Db 361 GACCATGCGGGGCGCAAGATAGTGGGCTCTGTGTCATGCGGCGCTGCTGACTATTTC 420

QY 538 CTGCGCGTCCCGCTATT 556

Db 421 ATTGCCAGTCCCGTATT 439

RESULT 7

LOCUS BM128211 593 bp mRNA linear EST 12-MAR-2002

DEFINITION 1f10f09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens

CDNA clone IMAGE:5676160 5' similar to SW:CIK3_HUMAN P22001

VOLTAJE-GATED POTASSIUM CHANNEL PROTEIN KVL3 ; mRNA sequence.

ACCESSION BM128211 GI:17122763

VERSION EST.

KEYWORDS human.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 593)

AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistein,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvilli,R., Williams,T., Jackson,Y. and Bowers,Y.

TITLE Endocrine Pancreas Consortium

JOURNAL Unpublished (2000)

COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:

Db 401 ACTGCTACTTACTTCCGAGTCGACGACCAACAGCAGCTTTGTTAGCATPACCAGT 460
OY 419 TCCCTTGTGGTGGCGGTAGTACCATGACTTGGCTATGACATGACACCGCCGTC 478
|||||
Db 461 GGCTTCTGTGGCGCGGTGTTACATGACTGCGTTATGGGACATGTGTCCATC 520
OY 479 ACTGTGGTGGCAGATAGTGGGCTCTGTGTGTCCTATGCGGGGCTGCTGACTATTTCC 538
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Db 521 ACCTTGGAGGCAAAATGATGGGACAGCTGTGCGCATCGTGAGAGTCTAACCATGTCT 580
OY 539 CTGGCAGTCCCGCTCATT 556
|||||
Db 581 CTGCTGTCCCGTCATT 598
RESULT 9
CNS035KP/c 1085 bp DNA linear GSS 15-MAY-2000
LOCUS Tetradon nigroviridis genome survey sequence PUC-Or1 end of clone
DEFINITION 214101 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION AL228850
VERSION AL228850.1 GI:7887843
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigroviridis.
ORGANISM Tetradon nigroviridis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetradon.
REFERENCE 1 (bases 1 to 1085)
Roest-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F.,
Saurin,W. and Weissbach,J.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence
Unpublished
TITLE 2 (bases 1 to 1085)
Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
Unpublished
JOURNAL 3 (bases 1 to 1085)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (12-APR-2000)
JOURNAL This sequence is a single read and was generated as part of a large
COMMENT scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.
FEATURES
source
1. 1085
/organism="Tetradon nigroviridis"
/db_xref="taxon:99883"
/clone="214101"
/clone_lib="G"
/note="Genoscope sequence ID : C0AG214AE01SP1-end ;
PUC-Or1"
BASE COUNT 201 a 308 c 372 g 198 t 6 others
ORIGIN
Query Match 46.1%; Score 256.4; DB 17; Length 1085;
Best Local Similarity 75.0%; Pred. No. 2.3e-56;
Matches 342; Conservative 0; Mismatches 96; Indels 18; Gaps 1;
OY 2 TTCTTCGTGGTGGAGAGCTGTGTTGTTGTTCTCTTGGAGCTGTGGAGCCCTC 61
|||||
Db 457 TTCTTCATGTCGAGAGCGTTCATCATCTGTTCTCTTGGAGCTCATCGTGGCTTC 398
OY 62 CTGGTCTGTCAAGAGGCTATCTTCTTCAAGAACGTGATGACCTCATGATTTTGTG 121
|||||

Db 397 TTGGCCTGCCAGCAGAGGCGCCTTCTTCAGAACATGATGACATCGATCGTG 338
OY 122 GCTATCTCTCCCTACTTGTGACACTGGGACACGAGCTGGC----- 163
|||||
Db 337 GCCATCATCTCCCTACTTCAATCAAGCTGGGAGAGAGCTGGCCGACGAGGCAACAAGAG 278
OY 164 CGGACGCGAGGGGATGGGCCAGAGGCGATGCTACTGGCCATCTGAGACTATCCGATTG 223
|||||
Db 277 GGCAGAGGGGCGGCTGGGCGAGAGGCGACCTGCTGGCCATCTGAGGTATCCGCCCTG 218
OY 224 GTGCGTGTCTCCGATCTTCAAGCTGTCCCGGCACTCAAAAGGCGCTGCAATCTTGGGC 283
|||||
Db 217 GTCCGCGTCTCCGATCTTCAAGCTGTCCCGGCACTCAAAAGGCGCTGCAATCTTGGGC 158
OY 284 CAGACGCTCGGGGCGCTCCATGCGTGGAGCTGGGCGCTCCATCTTCTTCCATCGGT 343
|||||
Db 157 CAGACCTTAAGGCGCAGCATGCGCGAGCTGGGCTGCTATCTTCTTCCATCGGG 98
OY 344 GTGTCCTCTTTTCCAGCGCGCTTACTTTGGCGAAGTTGACCGGGTGGACTCCCATTTTC 403
|||||
Db 97 GTCATCTCTTCTCCAGCGCTGTCTACTTTCGCGAGGCGGAGACAGACATCTTACTTC 38
OY 404 ACTGATCTCCCTGAGTCTTCTGTGGGCGGTAGTC 439
Db 37 ACCAGATCCCGCAGCGCTTGTGGGCGGCTTTC 2
RESULT 10
AG163977 629 bp DNA linear GSS 09-JAN-2002
LOCUS Pan troglodytes DNA, clone: RP43-031A01.T7, genomic survey
DEFINITION sequence.
ACCESSION AG163977
VERSION AG163977.1 GI:16693655
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphocytes DNA, clone_lib:RP43-43 Chimpanzee
Male BAC Library clone:RP43-031A01.T7.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
REFERENCE 1
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoh,K.Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of library RP43-43
Unpublished
JOURNAL 2 (bases 1 to 629)
REFERENCE Direct Submission
AUTHORS Tokohi,Y., Watanabe,H. and Sakaki,Y.
TITLE Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical
JOURNAL and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
COMMENT 1-7-22 Sushiro-Chou, Tsunumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbese@sc.riken.go.jp, URL:http://hgp.9sc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RP43-43 This BAC
end was generated during the Red process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. 629
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-031A01.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP43-43 Chimpanzee Male BAC Library"
BASE COUNT 144 a 168 c 153 g 164 t
ORIGIN

Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Db 350 TCTGTCTGTCTCAAGCAGCTATCTTCTTGAAGACGTATGAACCTCATCATGATTTTGT 409

QY 121 GGCATCTCTTCCCTACTTTTGTGGCAGTGCGCA-CCGAGCTGGCCCGCAGCAGGAGTGG 179

Db 410 GGCATCTCTTCCCTACTTTTGTGGCAGTGCGCA-CCGAGCTGGCCCGCAGCAGGAGTGG 469

QY 180 GCCAGCAGCCATGCTACT--GGCCATCTGAGAGTATCCGATTTGGTGGCTGCTTCC- 236

Db 470 GCCANCAAGCCATGCTACTTGGCCATCTTGAAGATCCGATTTGGTGGCTGCTTCCG 529

QY 237 GCATCTCAAGCTGGCCCGCAGCTCAAGG 267

Db 530 GATCTTCAAGCTGTCCCGACTMAAANG 560

RESULT 14
BE654741 434 bp mRNA linear EST 06-SEP-2000
LOCUS
DEFINITION UT-M-BG1-ah-e-11-0-UT.r1 NIH_BMAP_MSC_N Mus musculus cDNA clone
ACCESSION BE654741
VERSION BE654741
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 434)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL MEDLINE
COMMENT 97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mstremail.nih.gov
cDNA library preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
Seq primer: M13 Reverse
FEATURES
Location/Qualifiers
1. 434
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UT-M-BG1-ah-e-11-0-UT"
/clone_1lb="NIH_BMAP_MSC_N"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pTZ19-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The NIH_BMAP_MSC_N library is a normalized library constructed from mouse spinal cord. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806 1996. Tissue provided by Ms. Annie Novakovich, Zivic-Miller Laboratories."

BASE COUNT 86 a 117 c 111 g 120 t

ORIGIN

Query Match 36.2%; Score 201.4; DB 10; Length 434;
Best Local Similarity 74.6%; Pred. No. 3,8e-42;
Matches 253; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 218 CGATTGTGGCTGTCTTCCGATCTTCAAGCTGTCCGGCAGCTCAAGGGCCTCAATC 277

Db 1 CGCCTAGTAAGGGTTTTCGCCATCTTCAAGCTTCCGCCATTTCAAGGGCTCAGATC 60

QY 278 TTGGGCCACGCTTGGGACCTCCATGCGTGGAGTGGGACCTCCATCTTTTCTCTTC 337

Db 61 CTAGACAGACGCTGAAAGGCTTCCATGCGGAGCTGGGGCTGCTCATATTTCTCTTC 120

QY 338 ATCGGTGTGCTCTTTTCCAGGCGCGTCTACTTTGCCGAATTTGACCGGGTGGACTCC 397

Db 121 ATTGGGCTATCTTTTCTTCCAGTGCATCTTGTGTGAGGACAGACCTTCTTCG 180

QY 398 CATTTACTACATCCCTGAGTCTTGTGGTGGCGGAGTACACCATGACTAGTGGC 457

Db 181 GGTTTTACAGTATCCGGAATCCCTTGTGGGACAGTAAACCATGACACAGTGTGT 240

QY 458 TATGAGACATGGACCCGCTCATGTGGTGAGATAGAGGCTCTGTGTCATC 517

Db 241 TATGCTATATGACACCCAGTACCATAGAGGCAAGATTTGGGCTCTTTTGTGCATC 300

QY 518 GCGGGCGTGTGACTATTTCCCTGCCAGTGGCCGCTATT 556

Db 301 GCAGGTGCTTGTACCATTTGATTCGACGTTCCGCTGTGATT 339

RESULT 15
CNS04EVP 990 bp DNA linear GSS 21-MAY-2000
LOCUS
DEFINITION Tetradon nigroviridis genome survey sequence T7 end of clone
105118 of library G from Tetradon nigroviridis, genomic survey sequence.
ACCESSION AL287566.1 GI:8026065
VERSION AL287566.1
KEYWORDS GSS: genome survey sequence.
SOURCE Tetradon nigroviridis.
ORGANISM Tetradon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
1 (bases 1 to 990)
Roest-Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using Tetradon nigroviridis DNA sequence
Unpublished
JOURNAL REFERENCE
AUTHORS 2 (bases 1 to 990)
Roest-Crolius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis
Unpublished
JOURNAL REFERENCE
AUTHORS 3 (bases 1 to 990)
Genoscope.
TITLE Direct Submission
COMMENT Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.
FEATURES
Location/Qualifiers
1. 990
/organism="Tetradon nigroviridis"
/db_xref="taxon:99883"
/clone="105118"
/clone_1lb="G"
/note="Genoscope sequence ID : COBG105BE09LP1-end : T7"

BASE COUNT 209 a 295 c 280 g 169 t 37 others

ORIGIN

Query Match 36.0%; Score 200.4; DB 17; Length 990;
Best Local Similarity 69.4%; Pred. No. 9,9e-42;

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2003, 06:36:10 ; Search time 326 seconds

(without alignments)
3861.555 Million cell updates/sec

Title: US-09-804-014A-8

Perfect score: 2918

Sequence: 1 MERRRGSRRQKDEKGDPG.....VPELPPIWAPREHLVTEV 559

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n model -DEV=ylh
-Q=/cgn2.1/USPTO/spool/US09804014/runatc.10022003_161447_27185/app_query.fasta_1.711
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFTX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -FPANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09804014.ecgn1.1.1.0 -tnamec.10022003_161447_27185 -NCP=6 -ICP=3
-NO_XLPXY -NO_MMAP -LARGEOUTER -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMECUT=120
-WARN_TIMECUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_101002: *
1: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT: *
2: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT: *
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5: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT: *
6: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT: *
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8: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT: *
9: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT: *
10: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT: *
11: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT: *
12: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT: *
13: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT: *
14: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT: *
15: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT: *
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17: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT: *
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23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT: *
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2918	100.0	1747	22	AA513338	Human cDNA encoding
2	2418	82.9	1792	24	AAD37899	Human ion channel
3	2373	81.3	1686	23	AA578540	DNA encoding novel
4	2288.5	78.4	1341	24	ABE57038	Human potassium ch
5	2203	75.5	1598	16	AA704953	Mouse Kv1.7 Voltag
6	1495.5	51.3	3147	24	AB199654	Mouse ischaemic co
7	1447.5	49.6	2867	24	AB958566	Gene #2354 used to
8	1447.5	48.8	2867	24	AB165917	Lung cancer relate
9	1425	48.8	2867	22	AAH21452	Human Kv1.5 DNA.
10	1365.5	46.8	2237	23	AB113285	Drosophila melanog
11	1089.5	37.3	7642	24	AB133117	Human immune syste
12	1028	35.2	7642	24	AB133116	Human immune syste
13	1021.5	35.0	7488	24	AB133113	Human immune syste
14	1016.5	34.8	8758	24	AB133119	Human immune syste
15	1014	34.7	691	24	AAD28734	Human ion channel
16	1000.5	34.3	7488	24	AB133112	Human immune syste
17	950.5	32.6	7500	24	AB133114	Human immune syste
18	937	32.1	994	24	AB019702	Oligonucleotide fo
19	937	32.1	994	24	AB019703	Oligonucleotide fo
20	925	31.7	8758	24	AB133118	Human immune syste
21	911.5	31.2	994	24	AB019704	Oligonucleotide fo
22	911.5	31.2	994	24	AB019705	Oligonucleotide fo
23	901.5	30.9	7500	24	AB133115	Human immune syste
24	756.5	25.9	3424	20	AA211901	Human potassium ch
25	746.5	25.6	2157	22	AA529512	Human endocrine po
26	746.5	25.6	2159	23	ABK43428	DNA encoding novel
27	746.5	25.6	2711	22	AAH21246	Human Kv4.1 cDNA.
28	746	25.6	2578	22	AAH99538	Human protein enco
29	745	25.5	2578	23	AAH99538	
30	739.5	25.3	2578	23	AAH99538	
31	734.5	25.2	2578	24	AAH99538	
32	733	25.1	2578	23	AAH99538	
33	732.5	25.1	1927	20	AA211898	Human potassium ch
34	730	25.0	1927	24	AA211898	
35	728	24.9	2064	24	ABN84401	Human Kv4.3 potass
36	728	24.9	2121	24	ABN84400	Human Kv4.3 potass
37	725	24.8	2121	21		
38	722.5	24.8	2351	22	AAH21247	Human Kv4.2 cDNA.
39	721	24.7	2072	19	AAV61572	Human Kv potassium
40	721	24.7	2104	19	AAV61571	Human Kv potassium
41	718.5	24.6	1716	23	ABV29811	Drosophila melanog
42	709	24.3	2104	19	AAV61573	Human Kv potassium
43	696	23.9	3102	20	AA211905	Human potassium ch
44	669	22.9	3102	23	AA211905	
45	651.5	22.3	3102	24	AA211905	

ALIGNMENTS

RESULT 1
ID AA513338 standard; cDNA: 1747 BP.

AC AA513338;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA encoding NOV4 protein.

XX Human: NOV4; ss; cytosolic; nontropic; neuroprotective; vulnary;
KW cerebroprotective; antiparkinsonian; hypotensive; antistimatic;
KW antidiabetic; antipsoriatic; antiinflammatory; immunosuppressive;
KW antitherosclerotic; dermatological; cancer; neurological disorder;
KW Parkinson's disease; diabetes mellitus; asthma; enamel defect;
KW immune disorder; autoimmune disease; respiratory disorder;
KW bone disorder; musculoskeletal disorders; leukaemia; lymphoma;
KW cell growth regulation disorder; lesional psoriatic skin;

KW	atherosclerosis; abdominal aortic aneurysm.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	5'UTR	1..37
FT		/*tag= a
FT	CDS	38..1717
FT		/*tag= b
FT		/product= "NOV4"
FT	3'UTR	1718..1747
FT		/*tag= c
XX		
PN	WO200168851-A2.	
XX		
PD	20-SEP-2001.	
XX		
XX		
PF	12-MAR-2001; 2001WO-US07735.	
XX		
PR	10-MAR-2000; 2000US-0188277.	
PR	10-MAR-2000; 2000US-0188316.	
PR	14-MAR-2000; 2000US-0189139.	
PR	14-MAR-2000; 2000US-0189140.	
PR	17-MAR-2000; 2000US-0190231.	
XX	17-MAR-2000; 2000US-0190401.	
XX		
PA	(CURA-) CURAGEN CORP.	
PI	Padigaru M, Vernet CM, Fernandes E, Shimkets RA, Spaderna SK;	
PI	Majumder K, Li L;	
XX		
DR	WPI: 2001-570869/64.	
DR	P-PSDB: AAU08660.	
XX		
PT	Novel polypeptides and nucleic acids homologous to members of collagen,	
PT	potassium channel, tuffelin family of proteins for diagnosing, treating	
PT	cancer, atherosclerosis, neurological, skin and enamel defect disorders	
PT	-	
XX		
XX	Claim 9; Page 15-16; 128pp: English.	
PS		
XX		
CC	The invention relates to isolated NOVX (NOVX1-11) polypeptides and	
CC	the polynucleotides that encode them. NOVX polypeptides, polynucleotides	
CC	and anti-NOVX antibodies are useful for treating or preventing a	
CC	pathology associated with NOVX polypeptide in humans and for treating a	
CC	syndrome associated with human disease e.g. disorders characterised by	
CC	altered cell motility, proliferation and migration e.g. cancer,	
CC	angiogenesis and wound healing (NOVX-3), neurological disorders, e.g.	
CC	episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's	
CC	disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,	
CC	asthma, hypertension and seizure (NOV4), enamel defects, such as	
CC	amelogenesis imperfecta and disorders involving enamel defects,	
CC	including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic	
CC	neurological disorders, e.g. paraneoplastic limbic of brain-stem	
CC	encephalitis occurring during testicular cancer, diabetes, reproductive	
CC	health, metabolic and endocrine disorders, gastrointestinal disorders,	
CC	immune disorders and autoimmune diseases, respiratory disorders, bone	
CC	disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell	
CC	growth regulation disorders (NOV8), leisional psoriatic skin (NOV9-10) an	
CC	atherosclerosis, abdominal aortic aneurysm and neurological disorders	
CC	(NOV11). NOVX polypeptide is also useful for identifying an agent that	
CC	binds to it and a cell expressing NOVX polypeptide is useful for	
CC	identifying a therapeutic agent for use in treatment of a NOVX related	
CC	pathology. The antibodies and a polypeptide having 95% sequence identity	
CC	to NOVX polypeptide are useful for treating a pathological state in a	
CC	mammal. The present sequence encodes NOV4, a possible voltage gated	
CC	potassium channel.	
XX		
SO	Sequence 1747 BP; 255 A; 582 C; 575 G; 335 T; 0 other;	

Alignment Scores:

Pred. NO.:

Score:

6,93e-148

2918.00

Length: 1747

Matches: 559

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-804-014A-8 (1-559) x AAS1338 (1-1747)

QY	1	MetGlnAArgArgArgThGlySerArgArgGlnLysAspGlyGlyLysGlyVAspProGly	20
DB	38	ATGGAGAGACGGAGGACAGATATCCGGCGGCGAGAAGCGAGAAAGAGGACCCCGG	97
QY	21	ThrGlyLysAlaGlnSerArgArgGlyLArgArgArgArgGlyArgAlaGlyArgAla	40
DB	98	ACGGGAAGAGCCACAGCAGGCGCGGGCGCGCGCGGGGAGGAGGCGGGCGG	157
QY	41	SerArgGlnArgAlaArgGlyLArgProValAlaLeuArgProAlaGlyValThlValPro	60
DB	158	TCCCGGCAAGGGCGCGGGGTCCCTCCCTCCCGCCCGCGGGGGTACAGTCC	217
QY	61	ProProSerArgProSerArgProAlaGlyLeuPheThyTAlaArgThProAspThGly	80
DB	218	CCTCCCTCCCGCCCTACGCCCCCTCCCGGGCATTTTACGGCGCGACACCGGACCGGA	277
QY	81	HisArgAlaGlyAlaAlaValGlyValThrArgArgPheAlaGlyArgGlyCysAla	100
DB	278	CACCGGGGTGGGGCGCGGTGGGGCCACAGCTGGTTCGGGGTCCGGCGCTGGCGG	337
QY	101	ArgHisGlyAlaAlaValProAlaAlaProCysGlyCysGlyValArgLeuValLeuAsn	120
DB	338	CGCCATGGAGCGCGGGTCCCGCGCCCGCGGGGTCTCTCGAGCGGTGTCTCAAC	397
QY	121	ValAlaGlyLeuArgPheGlnLThrArgAlaArgThrLeuGlyArgPheProAspThrLeu	140
DB	398	GTGGCGGGCTCGCTTCGAGACGGCGGCGGACAGCTGGGCGCTTCCGACACTCG	457
QY	141	LeuGlyAspProAlaArgArgGlyLArgPheThyTAspAspAlaArgArgGlyLThyPhePhe	160
DB	458	CTAAGGGGACCCACGGCGCGCGCGCTTTCACGACGACGGCGCCCGGATATTTCTTC	517
QY	161	AspArgHisArgProSerPheAspAlaValLeuThyTThyTArgInsGlyGlyArgLeu	180
DB	518	GACGGGCAACGGCCAGCTTCGACGCCGTGCTACACTACAGTCCGGTGGGGCGGTG	577
QY	181	ArgArgProAlaHisValProLeuAspValPheLeuGlnGluValAlaPheThyGlyLeu	200
DB	578	CGGCGCGCGGCGACAGTCCCTCGACCTTCTTCGGGAAGGTGGCGCTTCACGGGCTG	637
QY	201	GlyAlaAlaAlaLeuAlaArgLeuArgLysAspGlnGlyCysProValProProGlnArg	220
DB	638	GGCGGGGGGCGCTTGGCACGCTTGGCGGACGAGACAGGGCTCCGGTCCCGCGACGC	697
QY	221	ProLeuProArgArgAlaPheAlaArgGlnLeuThyPheLeuPheGlnPheProGlnSer	240
DB	698	CCCCGCCCGCGCGCTTCGCGCGGACAGCTGTGGGTCTTTCGAGTTTCCGAAAGC	757
QY	241	SerGlnAlaAlaArgValLeuAlaValValSerValLeuValIleLeuValSerIleVal	260
DB	758	TCTCAGCGCGCGGTCTCGCGTACTTCCTCGTGGTCATCCGTCCTCATCGTC	817
QY	261	ValPheCysLeuGlnThrLeuProAspPheArgAspAspArgAspGlyThrGlyLeuAla	280
DB	818	GCTCTCTCGCTCGAGAGCTGCTGACTTCGGGACGACGCGGACGGGCGGCTTGCT	877
QY	281	AlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGlySerSerGlnMetPro	300
DB	878	GCTGACGCGGACGCGCGCGGTGTTCCTCCCGCTCGGATGAGCTCCAGCAATATCTT	937
QY	301	GlyAsnProProArgLeuProPheAsnAspProPhePheValGlnThrLeuCysIle	320
DB	938	GGAATTCACACCCGCTCTCCCTTCAATGACCCGTTCTTCGTGGTGGAGACGCTGTGATT	997
QY	321	CysTrpPheSerPheGlnLeuLeuValArgLeuLeuValCysProSerLysAlaIlePhe	340

Db 998 TGTGGTCTCTCTTGAGCTGCTGAGCCCTTCGTCCTGTCACGACGACGCTATCTTC 1057
 QY 341 PhelysAsnValMetAsnLeuIleAspPheValAlaIleLeuProTyrPheValAlaLeu 360
 Db 1058 TTCACAAAGCTGATGACCTCATCTGATTTTGCGCTATCTCTCTCTCTCTCTCTCTCT 1117
 QY 361 GLTyrGluLeuAlaArgGlnArgGlyValGlyGlnGlnAlaMetSerLeuAlaIleLeu 380
 Db 1118 GGCACCGACCTGGCCCGGACGAGGAGGTGGCCGACAGGCCATGTCACCTGGCCATCTTC 1177
 QY 381 ArgValIleArgLeuValArgValPheArgIlePheLeuSerArgHisSerGly 400
 Db 1178 AAGTGTATCCGATTTGGTGGTGTCTTCCTCCATCTTCACAGCTGTCCCGACACTCAAGGGG 1237
 QY 401 LeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgGluLeuGlyLeuIlePhe 420
 Db 1238 CTCGCAATCTTGGCCGACGCTTCGCGCTTCATCTGAGCTGGGCTCTCTCATCTCTT 1297
 QY 421 PheLeuPheIleGlyValValLeuPheSerSerAlaValTyrPheAlaGluValAspArg 440
 Db 1298 TTCCTCTCATCGGTGTGGTCTCTCTTTCACGCGCGCTCTACTTTCGCAAGTTGACCG 1357
 QY 441 ValAspSerHisPheThrSerIleProGluSerPheTyrTrpAlaValAlaThrMetThr 460
 Db 1358 GTGGACTCCCATTTTCACTGACATCCCTGAGTCTTGTGGCGGTGAGTCAACCATGACT 1417
 QY 461 ThrValGlyTyrGlyAspMetAlaProValThrValGlyGlyIleValGlySerLeu 480
 Db 1418 ACAGTTGGCTATGAGACATGGCACCCGTCACCTGTGGTGGCAAGATAGGGGCTCTCTG 1477
 QY 481 CysAlaIleAlaGlyValLeuThrIleSerIleProValProValIleValSerAsn 500
 Db 1478 TCGGCATTCGCGGGCTGTGACTATTTCCCTGCGAGTCCGCTCATTTGCTCCAAATTTC 1537
 QY 501 SerTyrPheTyrHisArgGluThrGlyGlyGluAlaGlyMetCysHisValAsp 520
 Db 1538 ACCTACTTTTATCACCGGAGACAGAGGCGGAAAGAGCTGTGGATGTTTCAAGCCATGTGAC 1597
 QY 521 MetGlnProCysGlyProLeuGluGlyLysAlaAsnGlyIleValAspGlyGlyVal 540
 Db 1598 ATGCACCTCTTGCCCACTGGAGGCAAGGCCAATGGGGGGCTGTGGAGGGGAGGTA 1657
 QY 541 ProGluLeuProProLeuTyrAlaProProArgGluHisLeuValThrGluVal 559
 Db 1658 CCTGAGCTACCACTCCACTGCTGGGACACCCCGAGGGAACACTGTGTCACGAGAAG 1714
 RESULT 2
 AAD37899 standard; cDNA; 1792 BP.
 ID AAD37899
 AC AAD37899;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human ion channel protein encoding cDNA.
 XX
 KW Human; novel human protein; NHP; ion channel protein; forensic biology;
 KW Pharmacogenomic; drug screening; mental disorder; biological disorder;
 KW symptomatic manifestation; phenotypic manifestation; medical disorder;
 KW gene; ss.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 93..1463
 FT /*tag= a
 FT /product= "Human ion channel protein"
 FT /note= "This region is specifically claimed as
 FT SEQ ID NO: 1 in claim 1 of the specification"
 XX
 PN WO200231150-A2.
 XX
 PD 18-APR-2002.

XX
 PF 10-OCT-2001; 2001WO-US31900.
 XX
 PR 10-OCT-2000; 2000US-239623P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Fiddle CJ, Hilbun E, Gerhardt B, Turner CA;
 DR WPI: 2002-452348/48.
 DR P-PSDB; AAE23655.
 PT Novel human ion channel polynucleotide encoding protein sharing
 PT structural similarity with mammalian ion channel proteins, e.g.
 PT potassium channels useful in therapeutic, diagnostic and
 PT pharmacogenomic applications -
 XX
 PS Disclosure; Page 36; 36pp; English.
 CC
 CC The present invention relates to novel human proteins (NHPs), human ion
 CC channel proteins and polynucleotides encoding such proteins. Sequences of
 CC the invention are useful in therapeutic, diagnostic and pharmacogenomic
 CC applications. They are useful for the identification of protein coding
 CC sequences, for mapping a unique gene to a particular chromosome, as
 CC additional DNA markers for restriction fragment length polymorphism
 CC (RFLP) analysis and in forensic biology, for screening libraries,
 CC isolating clones, preparing templates for cloning and sequencing, as
 CC hybridization probes, in microarrays or other assay formats, to screen
 CC collections of genetic material from patients who have a particular
 CC medical condition, to identify mutations associated with a particular
 CC disease and also as a diagnostic or prognostic assay. NHPs are useful
 CC for the detection of mutant human proteins or inappropriately expressed
 CC proteins for the diagnosis of disease, for the generation of antibodies,
 CC for screening for drugs effective in the treatment of symptomatic or
 CC phenotypic manifestations of perturbing the normal function of the
 CC protein in the body, for identification of other cellular gene products
 CC related to the protein and as reagents in assays for screening for
 CC compounds that can be used as pharmaceutical agents in the therapeutic
 CC treatment of mental, biological or medical disorders and diseases. The
 CC present sequence is a cDNA encoding human ion channel protein.
 XX
 SQ Sequence 1792 BP; 265 A; 534 C; 592 G; 399 T; 2 other:
 Alignment Scores:
 Pred. No.: 4 26e-121 Length: 1792
 Score: 2418.00 Matches: 473
 Percent Similarity: 97.938 Conservative: 1
 Best Local Similarity: 97.734 Mismatches: 5
 Query Match: 82.864 Indels: 6
 DB: 24 Gaps: 2
 US-09-804-014a-8 (1-559) x AAD37899 (1-1792)
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 Db 14 GCGGCGCGAGGCGGGCGCGGACCGGGGCGGGGCTGGGGGCCACAGTGGTGGGGG 73
 QY 96 ARGArgGlyCysAlaArgHisGlyAlaAlaValProAlaAlaProCysGlyCysGlu 115
 Db 74 CGCGGGGGCGCGCGCGCATGGAGCGCGGTCGCCCGCG--CCGTCGCGCTCTCCGAG 131
 QY 116 ARGLeuValIleuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGlyArg 135
 Db 132 CGGCTGTGCTCAACGTGGCGCGGGGCTGCGCTTGAACACGGGCGCGACGCTGGCCCG 191
 QY 136 PheProAspThrLeuLeuGlyAspProAlaArgArgGlyArgPheTyrAspAspAlaArg 155
 Db 192 TTCGCGAGACCTGTCTAGGGGACCCAGCGCGCGCGCTTTCACGACGACGGCGG 251
 QY 156 ARGGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyrGln 175
 Db 252 CGGAGTATTCTTCGACCGGACCGCGCCAGCTTGAGCGCGCTGCTACTACTACGAG 311

Best Local Similarity: 89.80% Mismatches: 18
 Query Match: 81.32% Indels: 39
 DB: 23 Gaps: 5
 US-09-804-014a-8 (1-559) x AAS78540 (1-1686)

19 ProglyThrGlyLysAlaGlnSerArgGlyArgArgArgArgGlyAlaGly 38
 132 CCGGGAGCTGGG-----GCTGGAGATGCCCTT 158
 39 ArgAlaSerArgGlnArgAlaArgGlyArgProValAlaLeuArgProAlaGlyAlaThr 58
 159 GGAGCTCGGACGATAGCA-----GAGAGAGCTGGGCTGTGA 197
 59 ValPro---ProProSerArgProSerArgProAlaGlyLeu-PheTyrAlaArgThr 77
 138 GGGCTCTTCATGAAGCTTGGTACGCCCTCGCGGCTATTTTACGCGGACACC 257
 77 GAsPThrGlyHisArgAlaGlyAlaA----- 86
 258 GGACACCGGACACCGGGCTGGGGCGGCG- GCGGCGGCGGCGGACGCGCGGCGGCGGCG 316
 87 -----ValGlyAlaThrArgArgPheAlaGlyArgGlyCysAlaAr 101
 317 CGCACCGGGCGGCGGCTGGGGCCACACGTGCGGGTCCGCGGGCTGCGCGCGG 376
 101 gHisGlyAlaAlaValProAlaAlaProCysGlyCysGlyAlaArgLeuValLeuAsnVa 121
 377-CCATGGAGCGCGGCTGCCGCG-CCGTGGCGCTGCTCGAGCGGCTGCTCAACGT 434
 121 lAlaGlyLeuArgPheGlnThrArgAlaArgThrLeuGlyArgPheProAspThrLeuLe 141
 435 GCGCGGGCTGGCTTCGACACCGGGCGGCGACGCTGGGCCCTTCCCGACACTGTGCT 494
 141 uGlyAspProAlaArgArgGlyArgPheTyrAspAspAlaArgArgGlyTyrPhePheAs 161
 495 AGGGAGCCAGCGCGCGCGCTTACACGACGCGCGCGGCTATTTCTTCCA 554
 161 pArgHisArgProSerPheAspAlaValLeuTyrTyrGlnInsGlyArgLeuArg 181
 555 CGGGACCGGCCAGCTTGACGCGCTGCTACTACTACAGTCCGGTGGGGGCTGGCG 614
 181 gArgProAlaHisValProLeuAspValPheLeuGlnGlyValAlaPheTyrGlyLeuG 201
 615 GCGGCGGCGGCGACGTGCCCTCGACGTCTTCTCGAAGAGTGGCCTTACGGGCTGGG 674
 201 yAlaAlaAlaLeuAlaArgLeuArgGlnAspGlnGlyCysProValProProGlnArgPr 221
 675 CCGGCGGCGCTGGACGCTCGCGAGGAGGAGGCGCTCCGCGTGCCTCCGACGCGCC 734
 221 oLeuProArgArgAlaPheAlaArgGlnLeuTyrLeuLeuPheGlnPheProGlnSerSe 241
 735 CCTGGCCCGCGCGCTTGCCCGGACGTGGCTGCTTTTCGAGTTTCCGAGAGCTC 794
 241 rGlnAlaAlaArgValLeuAlaValAlaValSerValLeuValIleLeuValSerIleValVa 261
 795 TCAGGCGGCGGCGCTGCTCGCGTACTCTCGTGTGTCATCTCTGCTCCATCTGCTGCT 854
 261 lPheCysLeuGlnTyrThrLeuProAspPheArgAspAspArgAspGlyTyrGlyLeuAla 281
 855 CTTCCTGCTCGAGAGCTCTGACTTCGCGACGACGCGGACGCGGAGGCGGCTTCTGCT 914
 281 aAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGlySerSerGlnMetProG 301
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 301 yAsnProProArgLeuProPheAsnAspProPhePheValAlaGlnThrLeuCysIleCy 321
 972 AATTCACCGCGCGCTTCAATGACCGCTTCTCGTGGTGGAGACCGCTGTGATTTTG 1031
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 1032 TTGGTTCTCTTGAAGCTGTGTGAGCTCTGCTGCTGCCAAGCAAGGCTATCTTCTT 1091

341 eLysAsnValMetAsnLeuIleAspPheValAlaIleLeuProTyrPheValAlaLeuG 361
 1092 CAAGAACGTGATGACCTCATGATTTTGCTGCTATCTCCCTACTGTTGTGGCACTGGG 1151
 361 yThrGlnLeuAlaArgGlnArgGlyValGlyGlnGlnAlaMetSerLeuAlaIleLeuAr 381
 1152 CACCGAGTGGCGCGGACGACGAGGGGTGGCGCAGCGGCATATGTCACGGCATCTCGAG 1211
 381 gValIleArgLeuValArgValPheArgIlePheIleuSerLeuSerIleSerIleGlyLe 401
 1212 AGTCATCCGATGTGGCTGCTCTTCGCACTTTCACGCTGTCCCGCAAGGCGCT 1271
 401 uGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgIleuLeuGlyLeuIlePhePh 421
 1272 GCAATCTTGGCGGACAGCCTTCGGGCTTCATGCTGAGCTGGGCTCTCATCTTTT 1331
 421 eLeuPheIleGlyValAlaLeuPheSerSerAlaValTyrPheAlaGlnValAspArgVa 441
 1332 CCTCTCATCGGTGTGCTCTTTTCCAGCGCGCTCACTTGGCGAGTTGACCGGGT 1391
 441 lAspSerHisPheThrSerIleProGlnSerPheTyrTrpAlaValAlaIleThrThr 461
 1392 GGACTCCCATTCATCAGCATCCCTGAGTCTTGTGCTGGCGGTGATCACCATGACTAC 1451
 461 rValGlyTyrGlyAspMetAlaProValAlaThrValGlyGlyLysIleValGlySerLeu 481
 1452 AGTTGGCTATGGAGCATGGACCCCTCACTGTGGGTGGCAAGATGTGGCTCTGTG 1511
 481 sAlaIleAlaGlyValLeuThrIleSerLeuProValIleValSerAsnPheSe 501
 1512 TGGCATTTGGGGGTGCTGACTATTTCCGTGGCAGGCGCCGTCATGTTCCCAATTGAG 1571
 501 rTyrPheTyrHisArgGlnThrGlnGlyGlnGlnAlaGlyMetPheSerHisValAspMe 521
 1572 CTACTTTTATCACCGGAGACAGAGGCGAGAGGCTGGAGATTTCAGCATGTGGACAT 1631
 521 tGlnProCysGlyProLeuGlnGlyLysAlaAsnGlyGlyLeuValAspGlyGlu 539
 1632 GCAGCTTGTGGCCCTGAGGAGGCAAGGCCAATGGGGGCTGTGTGACGGGGAG 1686

RESULT 4
 ABL57038
 ID ABL57038 standard; cDNA; 1341 BP.
 AC ABL57038;
 DT 22-JUL-2002 (first entry)
 DE Human potassium channel 12189 partial cDNA.
 XX Potassium channel, ion transport; 12189; noctropic; anticonvulsant;
 KW neuroprotective; antiparkinsonian; hypotensive; neuroleptic;
 KW antidepressant; antianemic; tranquillizer; anorectic; antimigraine;
 KW antiarteriosclerotic; vasotropic; vulnerability; antiarrhythmic;
 KW cardiant; antiinflammatory; cytoskeletal; osteopathic; hepatotropic;
 KW antidiabetic; immunosuppressive; antiarthritis; antirheumatic;
 KW antipsoriatic; antilyroid; antiulcer; dermatological; antiandemic;
 KW antistimetic; antiallergic; ophthalmological; immunomodulator;
 KW analgesic; virucide; human; gene therapy; gene; ss.
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT 1..1341
 FT CDS /tag= a
 FT /product= "12189"
 FT /partial
 FT /note= "The CDS does not include a start codon"
 PN WO200194390-A2.
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 PD 13-DEC-2001.


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QY 453 TTTPTGAlaValValThrmethrThrValGlyTyrGlyAspMetAlaProValThrVal 472
Db 1018 TGGTGGCGGTGATGCACATGACTACAGTTGGTATGAGACATGGCACCCCGTCACTGTG 1077
QY 473 GLYGLYLeuValGlySerLeuGlySerAlaIleAlaGlyValLeuThrIleSerLeuPro 492
Db 1078 GGTGGCAAAATAGTGGCTCTCTGTGTGCAATTTGGCGGTGCTGACTATTTCCGTGCCA 1137
QY 493 ValProValIleValSerAsnPheserTyrPheTyrHisArgGluThrGluGluGlu 512
Db 1138 GTGCCCGTCATGTCTCCCAATTTCCAGCTATTATACACCGGGAGACAGAGGCGCAAGAG 1197
QY 513 AlaGlyMetPheSerHisValAspMetGlnProCysGlyProLeuGluGlyValAsn 532
Db 1198 GCTGGATGTTGACCATGTGACATGACACCTTGTGGCCACTGGAGGCAAGGCCAAT 1257
QY 533 GlyGlyLeuValAspGlyLeuValProGluLeuProProLeuThrProAlaProProArg 552
Db 1258 GGGGGCTGTGGACGGGAGGAGTACTGAGCTACCACTCCACTGTGGCACCACCCCAAGG 1317
QY 553 GluHisLeuValThrGluVal 559
Db 1318 AACACCTGTGTACCGAAGTG 1338

RESULT 5
AAT04953
ID AAT04953 standard; cDNA; 1598 BP.
XX
AC AAT04953;
XX
DT 11-APR-1996 (first entry)
XX
DE Mouse Kv1.7 voltage-gated potassium channel coding sequence.
XX
KW Mouse Kv1.7 voltage-gated potassium channel;
KW Insulin antagonist drug screening; insulin agonist drug screening;
KW non-insulin-dependent diabetes mellitus; ds.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1..1598
FT /tag=a
FT /note="specification states sequence is 1599.
FT Incomplete stop codon given"
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PN W09523658-A1.
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PD 08-SEP-1995.
XX
PF 23-FEB-1995; 95WO-US02221.
XX
PR 10-AUG-1994; 94US-0288405.
PR 04-MAR-1994; 94US-0207401.
XX
PA (REGC ) UNIV CALIFORNIA.
PI
XX Chandy G, Chandy KG, Gutman CA, Kaiman K;
XX
DR WPI: 1995-320573/41.
DR P-PSDB: AAR82937.
XX
PT New voltage-gated potassium channel gene - used to identify
PT material(s) which can increase insulin release e.g. for treating
PT non-insulin dependent diabetes mellitus.
XX
PS Claim 1: Page 22-23; 38pp; English.
XX
CC The DNA encodes a mouse Kv1.7, which is a Shaker-related voltage-
CC gated potassium channel. It may be used in drug screening for

```

CC identification of therapeutics which modulate the channel and,
 CC therefore, modulate insulin secretion. Selective antagonists
 CC increase insulin release and thereby reduce hyperglycemia
 CC associated with non-insulin-dependent diabetes mellitus.

XX Sequence 1598 BP; 232 A; 521 C; 502 G; 343 T; 0 other;

Alignment Scores:

Pred. No.:	124e-109	Length:	1598
Score:	2203.00	Matches:	452
Percent Similarity:	84.93%	Conservative:	10
Best Local Similarity:	83.09%	Mismatches:	61
Query Match:	75.50%	Indels:	22
DB:	16	Gaps:	8

US-09-804-014a-8 (1-559) x AAT04953 (1-1598)

```

QY 22 GLYLeuAlaGlnSerArgArgArgArgArgGlyArgAlaGlyArgAlaSer 41
Db 11 GGGAAAGCTCAAGAGATCCACGGAAAGCGCGGTGGCAGTGTTCACAGGTGGAA 70
QY 42 ArgGlnArgAlaArgGlyArgProValAlaLeuArgProAlaGlyValThrValProPro 61
Db 71 CGCGACAGGCGC-----CCCTTAGC-CCGCGGGGGTAAACCCGCCCTT 114
QY 62 ProSerArgProSerArgProAlaGlyLeuPheTyrAla-----Arg 75
Db 115 CCCCCGCCCCGTGGCCG-----ACTTTCATGCTATTTTTCACCGCCGACACCGG 165
QY 76 ThrProAspThrGlyHisArgAlaGlyAlaValAlaGlyValThrArgArgPheAlaGly 95
Db 166 ACACCCGACGTGGGT-----GGCTGGGGGTGGGGGCCACAGCTCCGTTACACGGT 216
QY 96 ArgArgGlyCysAlaArgHisGlyAlaValAlaProAlaAlaProCysGlyCysGlu 115
Db 217 CGCCCGGCGTGTGCGGCCATGAGACACAGTCCGCCGCC-----CTGCGCTCTCGAG 273
QY 116 ArgLeuValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGlyArg 135
Db 274 CGGCTGTGCTCAACGTGGCGGGGTGGCTTGCGAGACCGCGCGACAGCTCGGCGC 333
QY 136 PheProAspThrLeuLeuGlyAspProAlaArgArgGlyArgPheTyrAspAspAlaArg 155
Db 334 TTCGGGACACGCTGCGGGGGGACCCGCGTGGCGGACCGCCTTCAACGAGCGGGCGC 393
QY 156 ArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyrGln 175
Db 394 GCGGAGATTTCTTCCACACGACCGGCCAGCTTGATCGGTGCTCTACTACACAG 453
QY 176 SerGlyGlyArgLeuArgArgProAlaHisValProLeuAspValPheLeuGluGluVal 195
Db 454 TCGGGCGCGGCTGAGACGCGCGCACGTCCTCCATCTTCCGTGGAGAGGTG 513
QY 196 AlaPheTyrGlyLeuGlyAlaAlaAlaLeuAlaArgLeuArgGluAspGluGlyCysPro 215
Db 514 TCTTTCACGGCGTGGGG---CGGCGGCTGGCGGCTGGGAGAGACGAGGCTCGCGC 570
QY 216 ValProProGluArgProLeuProAlaArgAlaPheAlaArgGluLeuThrLeuPhe 235
Db 571 GTC---GCCGAGCGCGCGTGGCC---CCGCCCTTGGCGGCTGAGCTGTGGCTCTTC 624
QY 236 GluPheProGluSerSerGlnAlaAlaArgValLeuAlaValAlaSerValLeuValIle 255
Db 625 GAATTCCTGAGAGCTGCGAGGCTGGCGGCTGCTGCGCTGCTCCGACTGTCATC 664
QY 256 LeuValSerIleValValPheCysLeuGluThrLeuProAspPheArgAspAspArgAsp 275
Db 685 CTGCTCCCATGCTGTGCTTTTGCCTCGAGACACTGCAACACTTCCGCGACGACCGGAT 744
QY 276 GlyThrGlyLeuAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGly 295
Db 745 GACCCGGGCGTCCGCGCGGAGCGGCTGACTACGCTCTGCTCGCTCGGCTCAATGCG 804

```


Query Match: 49.61% Indels: 107
 DB: 24 Gaps: 20
 US-09-804-014a-8 (1-559) x ABN95856 (1-2867)

QY 2 GUAARGARGARGHGLYSERARG-----ARGGLNLYSASPGLGLYLUGLY 17
 DB 34 GAGAGGCGAGAGGAGCGAGCGCTTGTACCTCAGGCGCAAGCGAGGAGCGCCGC 93
 QY 18 ASP-----PROGLYTHRGILYSLAGLN-----SER 26
 DB 94 CAGCAACCCAGCTCTCCACAGAGGCGCGCGAGCTGGAGCGGAGCGCTGACGCC 153
 QY 27 ARGARGLYARGARGARGARGGLYARGALAGLYARG---ALASERARGLNARGALA 45
 DB 154 AGGCGCGCGGAGCGCTGAGAGGCGCGCGAGCGGCTGGGCGGCGACATGCC 213
 QY 46 -----ARGGLYARGPROVALALALEUARGPROALA-GLYVALTHRYVALPROPTOPR 62
 DB 214 CTGTGCTCCGCGCGCATGAGAGATCGCTGTGCTGCGTGGAGAACGGCGGTGATGACC 273
 QY 62 OSER-----ARGPROSERARGPROLAGLYLEUPHETHRYALARGTHPROAS 78
 DB 274 GTCAGAGAGAGCGCATGAGCGCGCGCGCTGCGCGCACAGCGGAGAGAGCTCCAG 333
 QY 78 PTHRGILNLSARGALAGLYALALA-----GLYALATH 90
 DB 334 TGTCCCGCGAGCGGTGCTCAGCATGAGCGCCCAAGAGCGCGCGCCAAAGGCGCGCGC 393
 QY 90 RARGARGPHEALAGLYARGARGLYCYS----- 99
 DB 394 GCGCAGAGAGACGGGAGCTGGGAGTGGCCCTTGGCTCGCGTCCGCGACCCGGAGTG 453
 QY 100 -----AL 100
 DB 454 CGGCGCTTGGCTCCGCTGCCAGAGAGAGCTGCCAGCGCGCTCGAGCGCGCGCTCCGAGAGC 513
 QY 100 AARGHISGLYALALAVALPROALA-----AL 109
 DB 514 GAGGAGAGAAAGAGCGATCCCGCGCTGGGACGCGTGGAGAGCACAGGCTTGGGACGGCG 573
 QY 109 APROCGGLYCYSGSLARGLEUVALLEUASNVALALAGLYLEUARGPHEGLUPTHAR 129
 DB 574 TCCCTGGC---ACCAC-CAGGCGGTCCACATCATCTCGCGCTTGGAGAGCA 629
 QY 129 GALAARGTHRGLEUARGPHEPROASPTHRGLEUGLYASPROALAARGARGLYAR 149
 DB 630 GCTGGGACACCGAGCGCAGTCCCAACACATCTCTGGGAGACCCCGCAAGCGCTGCC 689
 QY 149 GPHETYRASPAPALARGARGGLUTYRPHEPHEASPARGHISARGPROSERPHEASPA 169
 DB 690 GTACTGTGACCCCTGAGGAAGAGTACTTCTTGACCGCAACCGCGCGCTCGACGG 749
 QY 169 AVALLEUARGTHRYTRGINSERGLYARGLEUARGARGPROALAHISVALPROLEUAS 189
 DB 750 TATCTCTACTACTACACGAGTCCGGGCGCGCTGGAGGCGCGTCAACGCTTCCCTGGA 809
 QY 189 PVALPHELEUGLUGLVALALAPHETYRGLYLEUGLYALALALALEUALAARGLEUAR 209
 DB 810 CGGTTCGGGAGAGAGTACGCTTCTACACGCTGGGAGAGCGACCATGAGCGCTTCGG 869
 QY 209 GGLUASPGLUGLYCYSPROVALPROPROGLUARGPROLEUPROARGARGALAEALAR 229
 DB 870 CGAGGATGAGGCGTTCATTAAGAGAGAGAGAGAGCCCTGCTCGCAACGAGTTCACGG 929
 QY 229 GGLNLEUTRPLEUENHEGLUPHEPROGLUSERSERGLNLAALALARGVALLEUALA 249
 DB 930 CCAGGTTGGCTTATCTTCAGATATCGGAGAGCTTGGCGCGCGGCGCATCGCAT 989
 QY 249 VALSERVALLEUVALLEUVALSERILEVALVALPHECYSLEUGLUTHRLEUPROAS 269
 DB 990 CGTCTCGGCTTGTGTTATCTCTCATCTCATCATCCTTCTGCTTGGAGAGACCTGCTGA 1049

QY 269 PHEARGASPAPARGASPLGTYHTRGLYLEUALALALALALALAGLYPROVALPH 289
 DB 1050 GTTCAGGATGAGAGCGTGCCTCCGCAACCTCCGCGCGCCAGCAGCGCTCCCGCG-- 1107
 QY 289 EPROALAPRO---LEUASNGLYSERGLNME-----PROGLYASINPRO----- 303
 DB 1108 -CCGCGCGCTGGGCGCACGAGCGCGGCGTATGCGCCCGCGCTTGGCGCTTACGTTGCC 1166
 QY 304 -PROARGLEUPRO-----PHEASNASPPROPHAPHEVALVALGLUTHRLEUCYSILECY 321
 DB 1167 ACCGCTCTGCGCGAGACCGCTGCGCGACCCCTTTATCTGTGAGACACAGTGGCTCAT 1226
 QY 321 STRPHEASERPHGLULEUENVALARGLEUENVALCYSPROSERLYSALALIEPHEPH 341
 DB 1227 CTGTTCACCTTCAGAGCTGCTGCGCTTCTTCCGCTGCGCGCGCAAGGACAGGTTCTC 1286
 QY 341 ELYSASNVALMEKASNLEUENLEASPPHEVALALALIELEUPROTHRYPHEVALALAEUG 361
 DB 1287 CCGGACATCATGACATCATCATGATGATGATGATGATGATGATGATGATGATGATGATG 1346
 QY 361 YTHRGILULEUALARGSLNARG-----GLYVALGLYGLNLA 374
 DB 1347 CACCGAATGCGAG 1406
 QY 374 AMETSERLEUALALIELEUARGVALLEARGLEUVALARGVALPHEARGILIEPHELYS 394
 DB 1407 CATGTCCCTGCGCATCTCCGAGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1466
 QY 394 USERARGHISERLYSGLYLEUGLILIEUGLILIEUGLILIEUGLILIEUGLILIEUGLIL 414
 DB 1467 CTCCCGCACCTCCAGAGGCGTGCAGATCTGGGAGAAACCTTCAGGCTTCATGAGGAGA 1526
 QY 414 ULEUGLYLEUENLEUPHEPHELEUPHELEUGLYVALLEUENLEUPHEPHEPHEVALA 434
 DB 1527 GCTGGGCTGCTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1586
 QY 434 RPHEALAGLYVALASPARVALASPSERHISPHETHSERILEPROGLUSERPHETPTR 454
 DB 1587 CTTCGAGAGGCTGACCAACAGAGGAGCAATTTCTTACAGATCCCTGACCGCTTCTGCTG 1646
 QY 454 PALAVALVALPHEMETHRYTHRYVALGLYTRGLYASMETALAPROVALTHRYVALGLY 474
 DB 1647 GCGAGTGTACCATGACCTGTGGCTACGGGAGCATGAGGCGCATCATCTGTGGGG 1706
 QY 474 YLYSILIEVALISERLEUCYSALALALAGLYVALLEUENLEUENLEUENLEUENLEUEN 494
 DB 1707 CANAGATGTGGCGCTGT 1766
 QY 494 OVALILIEVALISERASPHESERTYRPHETRYHISARGLUTHRGILYGLUGLUALAG 514
 DB 1767 CGTCATGCTGTCCAACTTCACTTCTTACACCGGGAACGAGATCAGAGAGCGCGGC 1826
 QY 514 YMETPHESETHIS-----VALASPMELINPROCYGLY-----PR 526
 DB 1827 AGTCTTTAAG 1885
 QY 526 OLEUGLILYLYSALAASNGLYLEUVAL-----ASPLGLYUVA 540
 DB 1886 AGCGAAG 1945
 QY 540 LPROGLULEUPROPROLEUTRIPALAPROPTOARGGLU 553
 DB 1946 CAGACAGTGCCTGAGAGGG---CAGCTGCGCCCTAGAGAA 1982

RESULT 8
 ABL65917
 ID ABL65917 standard; DNA: 2867 BP.
 XX ABL65917;
 AC ABL65917;
 XX 15-MAY-2002 (first entry)
 DE Lung cancer related gene sequence SEQ ID NO:4254.

XX	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW	gene; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200194629-A2.
PD	13-DEC-2001.
XX	
PF	30-MAY-2001; 2001WO-US10838.
XX	
PR	05-JUN-2000; 2000US-209473P.
PR	05-JUN-2000; 2000US-209531P.
PR	18-SEP-2000; 2000US-233133P.
PR	18-SEP-2000; 2000US-233617P.
PR	20-SEP-2000; 2000US-234009P.
PR	20-SEP-2000; 2000US-234034P.
PR	20-SEP-2000; 2000US-234052P.
PR	22-SEP-2000; 2000US-234509P.
PR	22-SEP-2000; 2000US-234567P.
PR	25-SEP-2000; 2000US-234923P.
PR	25-SEP-2000; 2000US-234924P.
PR	25-SEP-2000; 2000US-235077P.
PR	25-SEP-2000; 2000US-235082P.
PR	25-SEP-2000; 2000US-235134P.
PR	25-SEP-2000; 2000US-235280P.
PR	26-SEP-2000; 2000US-235637P.
PR	26-SEP-2000; 2000US-235638P.
PR	27-SEP-2000; 2000US-235711P.
PR	27-SEP-2000; 2000US-235720P.
PR	27-SEP-2000; 2000US-235840P.
PR	27-SEP-2000; 2000US-235863P.
PR	28-SEP-2000; 2000US-236028P.
PR	28-SEP-2000; 2000US-236032P.
PR	28-SEP-2000; 2000US-236033P.
PR	28-SEP-2000; 2000US-236034P.
PR	28-SEP-2000; 2000US-236109P.
PR	28-SEP-2000; 2000US-236111P.
PR	29-SEP-2000; 2000US-236842P.
PR	29-SEP-2000; 2000US-236891P.
PR	02-OCT-2000; 2000US-237172P.
PR	02-OCT-2000; 2000US-237173P.
PR	02-OCT-2000; 2000US-237278P.
PR	02-OCT-2000; 2000US-237294P.
PR	02-OCT-2000; 2000US-237295P.
PR	02-OCT-2000; 2000US-237316P.
PR	03-OCT-2000; 2000US-237425P.
PR	03-OCT-2000; 2000US-237598P.
PR	03-OCT-2000; 2000US-237604P.
PR	03-OCT-2000; 2000US-237606P.
PR	03-OCT-2000; 2000US-237608P.
PR	01-NOV-2000; 2000US-244867P.
PR	01-NOV-2000; 2000US-245084P.
XX	
PA	(AVAL-) AVALON PHARM.
XX	
PI	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI	Soppet DR, Weaver Z;
XX	
DR	WPI; 2002-188264/24.
XX	
PT	Screening for anti-neoplastic agent involves exposing cells to a
XX	chemical agent to be tested for anti-neoplastic activity, and
XX	determining a change in expression of a gene of a signature gene set
PS	Claim 1; SEQ ID 4254; 44pp; English.
XX	
CC	The present invention describes a method (M1) for screening for an
CC	anti-neoplastic agent. The method involves exposing cells to a chemical
CC	agent to be tested for anti-neoplastic activity, determining a change in

expression of at least one gene (1) of a signature gene set, where (1) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (1) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, CC adenocarcinoma, ovarian, kidney, prostate or pancreatic cancer, CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour.

xx

Sequence 2867 BP; 565 A; 839 C; 845 G; 618 T; 0 other:

50

Alignment Scores:

Pred. NO.:	6,38e-69	Length:	2867
Score:	1447.50	Matches:	338
Percent Similarity:	61.31%	Conservative:	63
Best Local Similarity:	51.68%	Mismatches:	148
Query Match:	49.61%	Indels:	107
DB:	24	Gaps:	20

US-09-804-014A-8 (1-559) x ABL65917 (1-2867)

```
0Y      2  GUAArgArGrArGrThrArgGlySerArg-----ArgGlnLysAspGlyLysGly 17
          |||||:::||||| ||| ||| ||| ||| |||:::
Db      34  GAGAGGCGAGAGAGGAGGCGAGCGCTTTGTAGCGTCAGGCGCCAGGAGGAGTGCGGCG 93

0Y      18  Asp-----ProGlyThrGlyLysAlaGln-----Ser 26
          ||| ||| ||| |||:::
Db      94  CAGACACCCCGACGCTCCCGCAGAGAGGCGCGCGAGCGTGGAGCGAGCGCTGACGCC 153

0Y      27  ArgArgGlyArgArgArgArgArgArgGlyArgGlyArg--AlaSerArgGlnArgAla 45
          ||||| ||| ||| ||||| ||| ||| ||| ||| |||
Db      154  AGCGCGCGCGGAGCGAGCGTAGTAGGGGGCGGGGAGCGGTGACGTGGGGCGAGCATGCC 213

0Y      46  -----ArgGlyArgProValAlaLeuAluArgProAla-glyValThlValProProPr 62
          ||| ||| ||| ||||| ||| ||| ||||| |||
Db      214  CTCTGCTCCCGCGGCATGAGATCGCGCTGTCGTCCTGAGAACGGCGGTCCATGTACC 273

0Y      62  oSer-----ArgProSerArGrProAlaGlyLeuPheTyAlaArgThProAs 78
          |||| ||||| |||::: |||
Db      274  GTCACAGAGAGCGCATGACGCGCCCGGCGAGCGTGGCCAGGCCACAGGGGAGAGCTCCAG 333

0Y      78  rThGlnHisArgAlaGlyAlaAlaAlaAla-----GlyAlaTh 90
          ||| ||| ||| |||::: ||| ||| ||| |||
Db      334  TGTCGCCCGAGAGCGGTGGGCTCAGACGATGGGGCCCAAGAGACCGGGCGCAAGGGCGCGG 393

0Y      90  rArgArgPheAlaGlyArgArgGlyLys-----99
          ||||| ||| ||| |||
Db      394  GCGCAGAGAGACGCGGACCTGGGAGATGCGGCCCTTGCTCCGCTGCGAGCCGAGAGTG 453

0Y      100 -----Al 100
          ||| ||| ||| |||
Db      454  CGGCGCTTGCGCTCGCTGCCAGAGAGAGCTGCCAGCGGCTCGAGCGCGGCTCCGAGAGAC 513

0Y      100  aArgHisGlyAlaAlaValProAla-----Al 109
          ||| ||||| ||| ||| |||
Db      514  GAGAGAGGAGAGAGCGATGCCCGGCTGGGCGAGCGTGAGAGACCAAGGCTGTGGCGACGGG 573

0Y      109  aProCysGlyLysCysGlyArgLeuValLeuAsnValAlaGlyLeuArgPheGlyThrArg 129
          ||||| ::::|::: ||| ||| ||| ||| ||| |||
Db      574  TCCCTCT---ACGAC-CAGCGCGCTCCACATCAACATCTCCGCGCTCTTGGAGACGCA 629

0Y      129  gAlaArgThrLeuGlyArgPheProAspThrLeuLeuGlnGlyAspProAlaArgArgGlyArg 149
          ||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      630  GCTGGGACCCAGGCGGACGATTTCCCAACACACTCTCTGGGGGAGCCCGGCCAAGCGCTGCC 689

0Y      149  gPheArgAspAspAlaArgArgGlyArgPhePheAspArgHisArgProSerPheAspAl 169
          ::::|::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 690 GTACTTGACCCCTGAGAGACGACTTCTTGACCCGACCCGCGGCTTCAGCG 749
 Qy 169 aValLeuTyrTyrGlnSerGlyGlyArgLeuArgProAlaHisValProLeuAs 189
 Db 750 TATCCTTACTACTACACCGCGGCGCGCTCGGAGCGCGCTCAACGCTCCCTGGA 809
 Qy 189 pValPheLeuGlnGluValAlaPheTyrGlyLeuGlyAlaAlaLeuAlaLeuAla 209
 Db 810 CGTCTTCGCGACGACGATACGCTTCTACACAGCTGGGGAGAGCCATGTAGAGCCCTTCGG 869
 Qy 209 gGluAspGluGlyCysProValProProGluArgProLeuProArgArgAlaPheAlaAr 229
 Db 870 CGAGAGATGAGGGCTTCACTTAAGAAGAGAGAACCCCTGCTCCGCAACGATTCAGCG 929
 Qy 229 gGlnLeuTyrLeuLeuPheGlnPheProGluSerSerGlnAlaAlaAlaArgValLeuAla 249
 Db 930 CAAGCTGTGGCTTATCTTCGATATCCGAGAGCTGTGGGCGCGGCGGCGCATCGCAT 989
 Qy 249 lValSerValLeuValAlaLeuValSerTlleValAlaPheCysLeuGlnLutThrLeuProAs 269
 Db 990 CGTCTCGCTGTGTATCTCATCTCATCTCATCTGCTGCTTGGAGAGACCTGCTGTA 1049
 Qy 269 pPheArgAspArgAspArgpGlyTyrGlyLeuAlaAlaAlaAlaAlaGlyProValLph 289
 Db 1050 GTTCAGGAGATGAACTGAGCTGCTCCGCCACCTCCGCGCGCCACCAAGCCTCCCGCG 1107
 Qy 289 eProAlaPro---LeuAsnGlySerSerGlnMet-----ProGlyAsnPro----- 303
 Db 1108 -CCGCGCCCTGGGGCCAAAGCGAGCGGGGTCATGCGCCCGCTCTGCGCTACAGTGGCG 1166
 Qy 304 -ProAlaGLeuPro-----PheAsnAspProPhePheValAlaGluThrLeuGlyIleCy 321
 Db 1167 ACCGCTCTCCCAAGACCCCTGGCGGACCCCTTCTCATCTGTCGAGACCACTGCTCGCAT 1226
 Qy 321 sTyrPheSerPheGlnLeuLeuValArgLeuLeuValAlaCysProSerGlyAlaIlePhePh 341
 Db 1227 CTGTTACCTCTGAGCTGCTCGTGGCTTCTTGCGCTGCCCAAGAGGAGGGTCTTC 1286
 Qy 341 eLysAsnValMetAsnLeuLeuAspPheValAlaIleLeuProTyrPheValAlaLeuG 361
 Db 1287 CCGGAAACATCATGAACTCATGATGATGATGATGATGATGATGATGATGATGATGATG 1346
 Qy 361 yThrGlnLeuAlaArgGlnArg-----GlyValGlyGlnGlnAla 374
 Db 1347 CACCGAACTGCGAGACAGACGAGGCGCGAGAGCGCGCAGATGAGGCGAGCGAGCG 1406
 Qy 374 aMetSerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgLlePheLysle 394
 Db 1407 CATGTCCCTGGCCATCTCCGAGTCATCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1466
 Qy 394 uSerArgHisSerLysGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgL 414
 Db 1467 CTCGCGGCACTCCAAAGGGGTGCGAGATCCGAGGCAACACTTGGAGCGCTCCATGAGGA 1526
 Qy 414 uLeuGlyLeuLeuIlePhePheLeuPheIleGlyValValLeuPheSerSerAlaValTyr 434
 Db 1527 GCTGGGGCTCTCATCTTCTCTTCTCATCGGGGTCATCTCTTCTCCAGTGGCGCTCA 1586
 Qy 434 rPheAlaGlnValAspArgValAspSerHisPheThrSerTlleProGluSerPheTyr 454
 Db 1587 CTTCGCGAGAGCTGACCAACGAGGAACTTCTTAGACATCCCTGAGCCCTTGTGCTG 1646
 Qy 454 pAlaValAlaThrMetThrThrValGlyTyrGlyAspMetAlaProValThrValGlyG 474
 Db 1647 GGCAGATGATACCATGACACTGTGGGCTACGGGAGCATAGGCCATCTGTGGGGG 1706
 Qy 474 yLysIleValGlySerLeuGlySerLeuAlaIleAlaGlyValLeuThrTlleSerLeuProValPr 494
 Db 1707 CAAGATCGTGGCTCGCTGTGTCATCGCGGGGTCTCACAATGTCCTGCTGCTGCGC 1766
 Qy 494 oValIleValSerAsnPheSerTyrPheTyrHisArgGluThrGlnGluGluAlaG 514
 Db 1767 CGTCATCGTCTCCAACTTCAACTTCTTACACCGGGAACGATATCAGAGAGCGCGCG 1826

Qy 514 yMeLpHeSerHis-----ValAspMeLglnProCysGly-----Pr 526
 Db 1827 AGTCTTAAGAAAGACAGGAGGACTCATGAGCCAGAG--GCCGGGGCTGTGACAGAGACTCC 1885
 Qy 526 oLeuGlnGlyLysAlaAsnGlyLeuVal-----AspGlyGluVal 540
 Db 1886 AGCGAAGGTCTAGCGAGGAGGAGGATCTTCTGCAAGCTGGGGGAGCCCTGGAGAAATG 1945
 Qy 540 lProGluLeuProProProLeuTyrPalProProArgGlu 553
 Db 1946 CAGACAGTGCCTCGAGAGG---CAGCTGCCCTCAGAGAA 1982
 RESULT 9
 AAH21452
 ID AAH21452 standard; DNA; 1836 BP.
 AC AAH21452:
 XX 18-SEP-2001 (first entry)
 DT Human Kv1.5 DNA.
 DE
 XX Inhibitor: eukaryotic; potassium channel; TRK1; TRK2; TOK1;
 KW activator: ds.
 XX Homo sapiens.
 OS WO200151519-AZ.
 PN 19-JUL-2001.
 PD 05-JAN-2001; 2001MO-EP00055.
 PF 11-JAN-2000; 2000DE-1000651.
 PR (AVET) AVENTIS PHARMA DEUT GMBH.
 PA Leberer E, Leeuw T, Ritscher A;
 PI WPI; 2001-442137/47.
 DR
 XX Identifying inhibitors and activators of eukaryotic potassium channels,
 PT for use as pharmaceuticals, comprises using yeast cells that express
 PT heterologous, but no endogenous, potassium channels
 PS Disclosure; Page 45-46; 78pp; German.
 XX This sequence represents a novel method for identifying inhibitors or
 CC activators (A) of a eukaryotic potassium channel (KC) by applying a test
 CC compound to a mutant *Saccharomyces cerevisiae* cell in which: (i) the
 CC three endogenous KC (TRK1, TRK2 and TOK1) are not expressed; but (ii) a
 CC eukaryotic KC is expressed heterologously, where the effect of the
 CC compound on the eukaryotic KC is then determined. The method is used to
 CC identify inhibitors or activators (A) of a eukaryotic potassium channel.
 CC (A) are potentially useful as pharmaceuticals. The method is easily
 CC automated for parallel processing of many samples, using either different
 CC concentrations of test compounds and/or different levels of heterologous
 CC gene expression. It allows identification of compounds that inhibit human
 CC KC selectively. This sequence represents the human Kv1.5 encoding DNA
 CC described in the method of the invention.
 XX
 SQ Sequence 1836 BP; 323 A; 614 C; 580 G; 319 T; 0 other;
 Alignment Scores:
 Pred. No.: 6, 61e-68 Length: 1836
 Score: 1425.00 Matches: 333
 Percent Similarity: 64.81% Conservative: 60
 Best Local Similarity: 54.65% Mismatches: 146
 Query Match: 48, 83% Indels: 65
 DB: 22 Gaps: 15
 US-09-804-014A-8 (1-559) x AAH21452 (1-1836)

DB 1680 TACGGAACCTAACCGAAGCAAAACAATAACAAACCATATCTTAACCATCTTAA 1621
QY 381 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 401
DB 1620 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1561
QY 401 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 421
DB 1560 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1501
QY 421 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 441
DB 1500 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1441
QY 441 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 461
DB 1440 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1381
QY 461 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
DB 1380 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1321
QY 481 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 501
DB 1320 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1261
QY 501 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 519
DB 1260 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1206
RESULT 12
ABL33116
ID ABL33116 standard; DNA: 7642 BP.
XX ABL33116;
AC ABL33116;
XX 26-MAR-2002 (first entry)
DT Human immune system associated gene SEQ ID NO: 1089.
XX Human immune system associated gene SEQ ID NO: 1089.
DE Human immune system associated gene SEQ ID NO: 1089.
XX Human immune system associated gene SEQ ID NO: 1089.
KW Human: immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antiasthmatic; cytosine methylation; antiasthmatic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antineoplastic; antineoplastic; antidiabetic; antipsoriatic;
KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX Homo sapiens.
OS Homo sapiens.
PN WO200200928-A2.
XX WO200200928-A2.
PD 03-JAN-2002.
XX 03-JAN-2002.
PE 02-JUL-2001; 2001WO-EP07537.
XX 02-JUL-2001; 2001WO-EP07537.
PR 30-JUN-2000; 2000DE-1032529.
XX 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX 01-SEP-2000; 2000DE-1043826.
PA (EPIC-) EPIGENOMICS AG.
XX (EPIC-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX Olek A, Piepenbrock C, Berlin K;
DR WPI; 2002-130909/17.
XX WPI; 2002-130909/17.
PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
XX cytosine methylation -
XX cytosine methylation -
PS Claim 1; SEQ ID NO 1089; 32pp + Sequence Listing; German.
XX Claim 1; SEQ ID NO 1089; 32pp + Sequence Listing; German.

CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 7642 BP; 2050 A; 279 C; 1786 G; 3527 T; 0 other;
Alignment Scores:
Pred. No.: 4,89e-46 Length: 7642
Score: 1028.00 Matches: 236
Percent Similarity: 54.35 Conservative: 50
Best Local Similarity: 45.47 Mismatches: 158
Query Match: 35.23 Indels: 99
DB: 24 Gaps: 10
US-09-804-014A-8 (1-559) x ABL33116 (1-7642)
QY 7 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 22
DB 4856 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4915
QY 22 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 22
DB 4916 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4975
QY 23 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 28
DB 4976 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5035
QY 29 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 48
DB 5036 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5074
QY 49 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 68
DB 5075 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5101
QY 69 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 88
DB 5102 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5125
QY 89 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 101
DB 5126 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5185
QY 101 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 116
DB 5186 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5245
QY 116 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 136
DB 5246 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5305
QY 136 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 156
DB 5306 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5365
QY 156 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 176
DB 5366 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5425
QY 176 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 196
DB 5426 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5485
QY 196 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 216
DB 5486 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5545


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      TTTCAAAATACCCGAAATCCGAAACCGCCAAATCATCGCCATCTCTCGCTATATATC 1961
Db 2020 TTTCAAAATACCCGAAATCCGAAACCGCCAAATCATCGCCATCTCTCGCTATATATC
QY 255 LLeuValSerLLeuAlaValPheCysLeuLLeuThrLeuProAspPheArgAspArg 274
      :::::::::::::: :::: :::::::::::::: ::::
Db 1960 ATCTCATCTCATCTCATCTATTTTACCTAAAAAGCTCCCCGAACTAAAAAATACAAA 1901
QY 275 AspGlyThrGlyLeuAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsn 294
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Db 1900 AACTTCACGAAAC-----ACGCTCACCGCAGCTGACCAACACACGATCATC 1856
QY 295 GlySerSerGlnMetProGlyAsnProProArgLeuProPheAsnAspProPheVal 314
      :::: ::::
Db 1855 TACAAATTCACAAATC-----TTACAAACACCCCTTCTCTCATC 1820
QY 315 ValGluThrLeuGlyCysIleCysTrpPheSerPheGluLeuValArgLeuValCys 334
      :::: ::::
Db 1819 CTAAAAACGCTATATATCATCTATTTCTCTCGAAGCTAAATATACGCTTCTGCGCTAC 1760
QY 335 ProSerLysAlaIlePhePheLysAsnValMetAsnLeuIleAspPheValAlaIleLeu 354
      :::: ::::
Db 1759 CCCAAACAAACGAACTCTCTCAAAAAACATCATAAACCTCAAAACATATATACCATCAT 1700
QY 355 ProGlyPheValAlaLeuGlyThrGluLeuAlaArgGlnArg-----GlyValGlyGln 372
      :::: ::::
Db 1699 CCTTATTTTCATCAGCGTAAACACCGAAATATCTAAACAAAAAACCACAAAAACGCA 1640
QY 373 GlnAlaMetSerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIlePhe 392
      :::: ::::
Db 1639 CAACCAACCTCCCTACCATCTCAATCAATATCCGCTTAATATAATTTTAAATCTTTC 1580
QY 393 LysLeuSerArgHisSerLysGlyLeuGlnIleLeuGlyIleThrLeuArgAlaSerMet 412
      :::: ::::
Db 1579 AATCTCTCCCGCCACTCTCAAAACCTCAAAATCTTAAACCAACCCCAAAACATTAATA 1520
QY 413 ArgGluLeuGlyLeuLeuIlePhePheLeuPheIleGlyValValLeuPheSerSerAla 432
      :::: ::::
Db 1519 AAAAAACATAAAGTACTCATCTTTTCTCTTCATCAAGAAATCATCTATTTTCTTAATACA 1460
QY 433 ValTrpPheAlaGluValAlaPargValAspSerHisPheThrSerIleProGluSerPhe 452
      :::: ::::
Db 1459 ATATACCTTTACCGAAGAAATAAATAAATGCGACTTCTCCATATATCCCGATACTTTC 1400
QY 453 TrpTrpAlaValValThrMetThrThrValGlyTrpGlyAspMetAlaProValThrVal 472
      :::: ::::
Db 1399 TAATAAAGCATTAATATCATATACCATATTAATAATACGTAATACCTCATTAACAAT 1340
QY 473 GlyGlyLysIleValGlySerLeuGlyAlaIleAlaGlyValIleThrIleSerLeuPro 492
      :::: ::::
Db 1339 AAAAAACAAATCGTAATCTCTTATATACCTTCCTTAATATATACCAATTAATACCTACCC 1280
QY 493 ValProValIleValSerAsnPheSerTrpPheTrpHisArgGluThrGluGlyGluGlu 512
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Db 1279 GTACTCTATCATATATCAATTTCACTATTTTACACCAAGCAAAACATAAATAAAAAAAA 1220
QY 513 AlaGlyMetPheSerHisValAsp 520
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RESULT 14
ID ABL33119 standard; DNA; 8758 BP.
XX
XX ABL33119;
XX
XX 26-MAR-2002 (first entry)
XX

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DE Human immune system associated gene SEQ ID NO: 1092.
XX
XX Human; immune system disease; cytosine methylation; antiasthmatic;
KW antierleucosclerotic; antinaemic; cytosine; neotropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antirheumatic; antidiabetic; antipsoriatic;
KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
KW antineoplastic; cancer; eye disease; Alzheimer's disease; AIDS; epilepsy;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
XX Homo sapiens.
XX
XX W0200200928-A2.
XX
XX 03-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP07537.
XX
XX 30-JUN-2000; 2000DE-1032529.
XX
XX 01-SEP-2000; 2000DE-1043826.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI: 2002-130909/17.
XX
XX Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation.
XX
XX Claim 1; SEQ ID NO 1092; 32pp + Sequence Listing; German.
XX
XX CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
XX SQ Sequence 8758 BP; 2209 A; 217 C; 2178 G; 4154 T; 0 other;
XX
Alignment scores:
Pred. No.: 2,31e-45 Length: 8758
Score: 1016.50 Matches: 224
Percent Similarity: 59.52% Conservative: 101
Best Local Similarity: 41.03% Mismatches: 163
Query Match: 34.84% Indels: 60
DB: 24 Gaps: 10
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Db 3576 AAAAAACGATACATACATACATACATACATACATACATACATACATACATACATACAT 3518
QY 23 LysAlaGlnSerArgArgGly-----Arg 30
      :::: ::::
Db 3517 AAACCCACAAAAAATCTCAATATATCCCGCAGACTAAATCAACGATTAACCCCAAAA 3458
QY 31 ArgArgArgArgGlyArgAlaGlyArgAlaSerArgGlnArgAlaArgGlyArgProVal 50
      :::: ::::
Db 3457 AACCGACGCCCAAAAAACGCGCAGCAAAAAACGCAACTCGCAAAATTA-CGACCTTA 3399
QY 51 -----AlaLeuArgProAlaGlyValThrValProPro 61
      :::: ::::
Db 3398 CCTCCGCTACGCAACCGCAAAATATGAGACCTTACTCTCGCTACCAAAAAAATACACAGA 3339
QY 62 ProSerArgProSerArgProAlaGlyLeuPheTrpHisValThrProAspThrGlyHis 81
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Db 3338 CCTGACGACGCGCT---CCGAAACGAAAAAAAAAAGCATCCGCACTAAACAGC 3282
QY 82 ArgAlaGlyAlaAlaValGlyAlaThrArgArgPheAlaGlyArgArgGlyCysAlaArg 101
Db 3281 ATAAAAACCAACTCTAAACACGAGC-----TCCCTACAC 3246
QY 102 HisGlyAlaAlaValProAlaAlaProCysGlyCysGluArgLeuValLeuAsnVal 121
Db 3245 CAC-----CAACGCGTCACATCAACATC 3222
QY 122 AlaGlyLeuArgPheGlyThrArgAlaArgThrLeuGlyArgPheProAspThrLeu 141
Db 3221 TCGGAACCTACGCTTTAAACGCAACTAAACACCCCTAACCAATTTCCCAACACACTCTTA 3162
QY 142 GlyAspProAlaArgArgGlyArgPheTyAspAspAlaArgArgGlyArgPhePheAsp 161
Db 3161 AAAAACCAGCCCAACAGCCCTACGCTTACGACCCCTAAAAAAGCAATCTTCTTGAC 3102
QY 162 ArgHisArgProSerPheAspAlaValLeuTyTrpTyrGlnSerGlyArgLeuArg 181
Db 3101 CGCAACCGACCAACTTCGACGATTCCTCTACTACCAATCCGAAACCGCGCTACGA 3042
QY 182 ArgProAlaHisValProLeuAspValPheLeuGluGluValAlaPheTyGlyLeuGly 201
Db 3041 AAACCGATCAACGCTTCCTCCCTAAACGTAATTCGCAACGCAATTCCTACCAACTAAAA 2982
QY 202 AlaAlaAlaLeuAlaArgLeuArgGlyAspGluGlyCysProValProProGluArgPro 221
Db 2981 AACGAAACCTTAACACGCTTCGCGGAAATTAATAAACTTCATTAATAAAAAAAAAAACC 2922
QY 222 LeuProArgArgAlaPheAlaArgGlnLeuTrpLeuLeuPheGluPheProGluSerSer 241
Db 2921 CTACCCCGGACAGCAATTTCCAGCCCAATTAATTAATTAATTCGCAATTCGCAAAAACTCT 2862
QY 242 GlnAlaAlaArgValLeuAlaValSerValLeuValLeuValSerIleValVal 261
Db 2861 AAATCCGCGGAGCAATTCGCGATTCGATTCATTAATTCCTCATCTCCATCATCAACCC 2802
QY 262 PheCysLeuGluThrLeuProAspPheArgAspAspArgspGlyThrGlyLeuAlaAla 281
Db 2801 TTCTACTTAAACCCCTACTTAATTCATAATAATTAACGTAACCTACTCCGCCACCTCCG 2742
QY 282 AlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGlySerSerGlnMet----- 299
Db 2741 AGCCGCCACCAACCTCCCGG---CCGCGCCCTAAACCAACGACCAACCAATCATTAAC 2685
QY 300 ---ProGlyAsnPro-----ProArgLeuPro-----PheAsnAspProPhePhe 313
Db 2684 CCGCCCTCTAACCTCGATTAACACCGCTCTACCCCAAAACCTTAACCGACCCCTTCTTC 2625
QY 314 ValValGluThrLeuCysIleCysTrpPheSerPheGluLeuValArgLeuLeuVal 333
Db 2624 ATGCTTAATAACCGCATACGATTAATCACTTCGAACTACTCGACGCTTCTTCGCC 2565
QY 334 CysProSerIleValIlePhePheValMetAsnValMetAsnLeuIleAspPheValAlaIle 353
Db 2564 TACCCCAACAAAACAAATTCCTCCGAAACATCAATAACATCAATTAATAAACAATC 2505
QY 354 LeuProTyPheValAlaLeuGlyThrGluLeuAlaArgGlnArgGlyValGly----- 371
Db 2504 TTCCCTACTTCAACCCCTAACACCGCAACCAACCAACCAACCAACCAACCAACCAAC 2445
QY 372 -----GlnGlnAlaMetSerLeuAlaIleLeuArgValIleArgLeuVal 386
Db 2444 AACGACCAAAATTAACACCAACCAATATTCCTTAACCATCTCCGAAATCAATCCGCTAATC 2385
QY 387 ArgValPheArgIlePheValLeuSerArgHisSerIleGlyLeuGlnIleLeuGlyGln 406
Db 2384 CGAATATTCGCAATCTTCAAAATCTCCCGCACTCCCAAAAAACCTACAAATCTTAACAA 2325
QY 407 ThrLeuArgAlaSerMetArgGluLeuGlyLeuLeuIlePhePheLeuPheIleGlyVal 426
Db 2324 ACCTTACAAACCTTCATTAATAAAACCTAATCACTCATCTTCTCCCTCATCGAATC 2265

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QY 427 ValLeuPheSerSerAlaValTyrPheAlaGluValAspArgValAspSerHisPheThr 446
Db 2264 ATCTCTTCTCCATACCGCTACTACTTGCAGAAAACTAACCAACCAACCAACCAATTCCT 2205
QY 447 SerIleProGluSerPheTrpTrpAlaValAlaThrMetThrValGlyTyrGlyAsp 466
Db 2204 AACATCCCTAACCGCTTCTAATAAACCAATATATACCATTAACCACTTAACCAACCA 2145
QY 467 MetAlaProValThrValGlyGlyIleValGlySerLeuCysAlaIleAlaGlyVal 486
Db 2144 ATAAACCCATCACTATTAATAAACCAATATCTGTAATATACCATTCGCGCAATC 2085
QY 487 LeuThrIleSerLeuProValProValIleValSerAsnPheSerTyTrpPheTyHisArg 506
Db 2084 CTACACCTTAACCTACTATACCGGTATACCGGTATGCTGTCCCACTTCAACTACTTACACCGA 2025
QY 507 GluThrGluGluGlu 512
Db 2024 AAACGAATCAGCAAAA 2007

RESULT 15
AAD28734 standard; DNA: 691 BP.
ID AAD28734;
AC AAD28734;
DT 07-MAY-2002 (first entry)
DE Human ion channel gene, Ion-166.
XX
XX Human: ion channel; neurological disorder; psychiatric disorder;
KW schizophrenia; attention deficit hyperactivity disorder; depression;
KW proliferation disease; migraine; ischaemia; neurodegenerative disease;
KW macular degeneration; Alzheimer's disease; congestive heart failure;
KW glaucoma; Parkinson's disease; cardiovascular disease; arrhythmia;
KW high blood pressure; restenosis; metabolic disease; neuroprotective;
KW obesity; hormonal disorder; polycystic ovarian syndrome; gene therapy;
KW alopecia; anxiety; stroke; neuroleptic; nootropic; cancer; diabetes; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 566..658
FT CDS
FT /tag= a
FT /product= "Human ion channel Ion-166"
FT /note= "CDS does not include start and stop codon"
FT /partial
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XX WO200192303-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US16967.
XX
XX 26-MAY-2000; 2000US-207119P.
XX 26-MAY-2000; 2000US-207152P.
XX 26-MAY-2000; 2000US-207257P.
XX
XX (PHEA ) PHARMACIA & UPJOHN CO.
XX
XX Benjamin CW, Roberds SL, Karnovsky AM, Ruble CL, Gotow LF;
XX WPI; 2002-147617/19.
XX P-PDB; AAEL8034.
XX
XX New human ion channel polypeptides and nucleic acids, useful for
XX treating or diagnosing neurological, psychiatric or neurodegenerative
XX diseases, e.g. depression, anxiety, stroke, ischemia, or Alzheimer's or
XX Parkinson's disease
XX
XX Claim 1; Page 76; 126pp; English.
XX

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Job time : 400 secs

CC The invention relates to ion channel polypeptides designated as ion-x
CC (where x is 157-175) and their corresponding nucleic acids. The ion-x
CC sequences and their modulators are useful for the treatment of human
CC diseases and conditions such as neurological or psychiatric disorders.
CC These compounds are useful for treating schizophrenia, attention deficit
CC hyperactivity disorder, depression, anxiety, stroke, migraine, ischaemia
CC or neurodegenerative disease (e.g. macular degeneration, Alzheimer's
CC disease, glaucoma, or Parkinson's disease). The compounds that modulate
CC ion channels can be used for treating of cardiovascular diseases (e.g.
CC congestive heart failure, arrhythmia, high blood pressure or stenosis),
CC metabolic diseases and disorders (e.g. diabetes or obesity), hormonal
CC disorders (e.g. polycystic ovarian syndrome or alopecia) and
CC proliferation diseases and cancers. The ion channels are also useful as
CC targets for discovering ligands or drugs to treat many diverse disorders
CC and defects. The ion-x sequences and their modulators may also be used
CC in diagnostic assays for such diseases or conditions. Ion-x nucleic
CC acids are used in gene therapy. The present sequence is a DNA encoding
CC human ion channel designated as ion-166.

XX Sequence 691 BP; 113 A; 207 C; 185 G; 186 T; 0 other;

Alignment Scores:

Pred. No.:	2.6e-46	Length:	691
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Percent Similarity:	99.50%	Conservative:	0
Best Local Similarity:	99.50%	Mismatches:	1
Query Match:	34.75%	Indels:	0
DB:	24	Gaps:	0

US-09-804-014A-8 (1-559) x AAD28734 (1-691)

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Db	152	AATGACCCGTTCTCGTGGTGAGACGCTGTAATTGTGTCTCTTGTGAGCTGCTG	211
Qy	329	ValArgLeuLeuValCysProSerLysAlaIlePhePheLysAsnValMetAsnLeuIle	348
Db	212	GTAGCGCTCCGTCGTCCAGACAGGCTATCTTTCAGAACGTGATACCTCATC	271
Qy	349	AspPheValAlaIleLeuProTyrPheValAlaLeuGlyThrGluLeuAlaArgGlnArg	368
Db	272	GATTTGTGGCTATCTTCCTTACTTGTGGCACTGGGACCGAGCTGGCCGGCAGCGA	331
Qy	369	GlyValGlyGlnGlnAlaMetSerLeuAlaIleLeuArgValIleArgLeuValArgVal	388
Db	332	GGGGTGGGCCAGGCGCATGTCACCTGCCATCTCTGAGAGTCATCCGATTGGTGGTCTC	391
Qy	389	PheArgIlePheLysLeuSerArgHisSerLysGlyLeuGlnIleLeuGlyGlnThrLeu	408
Db	392	TTCGCAATCTTCAGCTGTCCCGCACTCAAGGGCTCGCAATCTTGGGCCAGACGCTT	451
Qy	409	ArgAlaSerMetArgGluLeuGlyLeuLeuIlePhePheLeuPheIleGlyValValLeu	428
Db	452	CGGGCCCTCCATGCTGAGCTGGGGCTCTCATCTTTTCTCTTCATCGGTGGTCTCTC	511
Qy	429	PheSerSerAlaValTyrPheAlaGluValAspArgValAspSerHisPheThrSerIle	448
Db	512	TTTTCCAGCCCGCTACTTGGCCGAAGTGCAGCGGGGTGACTCCCATTTCTACTAGCATC	571
Qy	449	ProGluSerPheTrpPAlaValAlaValThrMetThrThrValGlyTyrGlyAspMetAla	468
Db	572	CTTGAGTCTTCTGTGGGGGTAGTACCATGCTACAGTGGCTATGGAGACATGGCA	631
Qy	469	ProValThrValGlyGlyLysIleValGlySerLeuCysAlaIleAlaGlyValLeuThr	488
Db	632	CCGCTCACTGTGGGTGCAGATAGTGGGCTCTCTGTGTGCATTTGGGGGCTGCTGACT	691

Search completed: February 20, 2003, 12:18:51

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2003, 06:33:10 : Search time 64 Seconds
(without alignments)
2678.630 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	737.5	25.3	1805	1	US-07-955-916-6
5	732.5	25.1	1927	4	US-09-336-643A-3
6	728	24.9	2064	4	US-09-178-109-3
7	728	24.9	2121	4	US-09-178-109-1
8	721	24.7	2072	4	US-09-142-791A-3
9	721	24.7	2104	4	US-09-142-791A-1
10	709	24.3	2104	4	US-09-142-791A-5
11	696	23.9	3102	4	US-09-336-643A-17
12	649.5	22.3	2483	1	US-08-464-340A-3

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14	611.5	21.0	2127	1	US-08-464-340A-1	Sequence 1, Appli
15	611.5	21.0	2127	5	PCT-US94-08449A-1	Sequence 1, Appli
16	598.5	20.5	2293	4	US-09-336-643A-5	Sequence 5, Appli
17	593	20.3	3080	4	US-09-336-643A-7	Sequence 7, Appli
18	541	18.5	696	1	US-07-955-916-5	Sequence 5, Appli
19	334	11.4	271	1	US-08-288-405A-19	Sequence 19, Appli
20	296	10.1	3181	3	US-09-135-021-1	Sequence 1, Appli
21	296	10.1	3181	4	US-09-135-020-1	Sequence 1, Appli
22	296	10.1	3181	4	US-09-135-010A-1	Sequence 1, Appli
23	296	10.1	3181	4	US-09-444-871-1	Sequence 1, Appli
24	296	10.1	3181	4	US-09-597-735-1	Sequence 1, Appli
25	296	10.1	3181	4	US-09-444-295-1	Sequence 1, Appli
26	296	10.1	3181	4	US-09-597-732-1	Sequence 1, Appli
27	285	9.8	3182	3	US-09-135-021-5	Sequence 5, Appli
28	278.5	9.5	2028	4	US-09-634-920-1	Sequence 1, Appli
29	249	8.5	3232	4	US-09-177-650-1	Sequence 1, Appli
30	249	8.5	3237	4	US-09-177-650-95	Sequence 95, Appli
31	248.5	8.5	2814	4	US-09-177-650-90	Sequence 90, Appli
32	247	8.5	2734	3	US-09-135-021-79	Sequence 79, Appli
33	247	8.5	2821	4	US-09-135-010A-115	Sequence 115, App
34	247	8.5	2821	4	US-09-597-735-115	Sequence 115, App
35	247	8.5	2821	4	US-09-597-732-115	Sequence 115, App
36	246	8.4	2914	4	US-09-177-650-6	Sequence 6, Appli
37	236.5	8.1	3287	4	US-09-105-058C-19	Sequence 19, Appli
38	228	7.8	2169	4	US-09-105-058C-22	Sequence 22, Appli
39	226	7.7	900	4	US-09-105-058C-3	Sequence 3, Appli
40	226	7.7	2273	4	US-09-177-650-88	Sequence 88, Appli
41	220.5	7.6	900	4	US-09-105-058C-5	Sequence 5, Appli
42	216	7.4	735	4	US-09-105-058C-7	Sequence 7, Appli
43	215	7.4	196	1	US-08-288-405A-18	Sequence 18, Appli
44	215	7.4	2565	4	US-09-105-058C-26	Sequence 26, Appli
45	198	6.8	139	1	US-07-961-268-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-288-405A-9
Sequence 9, Application US/08288405A
Patent No. 5559009
GENERAL INFORMATION:
APPLICANT: Chandy, Kanianthara G.
APPLICANT: Kalman, Katalin
APPLICANT: Chandy, Grisca A.
APPLICANT: Gutman, George A.
TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
ADDRESSEE: Altin, Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,405A
FILING DATE: 10-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,431
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-59844-1/WHD

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1599
; US-08-288-405a-9

Alignment Scores:
Pred. No.: 2, 01e-153 Length: 1599
Score: 2203.00 Matches: 452
Percent Similarity: 84.938 Conserva: 10
Best Local Similarity: 83.098 Mismatches: 61
Query Match: 75.508 Indels: 22
DB: Gaps: 8

US-09-804-014a-8 (1-559) x US-08-288-405a-9 (1-1599)

QY 22 GlyLysAlaGlnSerArgArgGlyArgArgArgGlyArgAlaSer 41
DB 11 GGGAAAGCTCAAGATCCAGGAAAGCGCGGTGGCAGTGTTCACAGGTGGAA 70
QY 42 ArgGlnArgAlaArgGlyArgProValAlaLeuArgProAlaGlyValThrValProPro 61
DB 71 CGGCAAGAGGCG-----CCCTTAAG-CCGCGGGGGTAACACCGCCCTT 114
QY 62 ProSerArgProSerArgProAlaGlyLeuPheTyrAla-----Arg 75
DB 115 CCCCCCGCCCTGGCCGG-----ACTTTCATGCTATTTTACCCGCCACACCGG 165
QY 76 ThrProAspThrGlyHisArgAlaGlyAlaValAlaGlyAlaThrArgPheAlaGly 95
DB 166 ACACCCGACGAGGAGT-----GGCTGGCGGCTGGGGCCACACGTCGCTCACCGGT 216
QY 96 ArgArgGlyCysAlaArgHisGlyAlaAlaValProAlaAlaProCysGlyCysGly 115
DB 217 CGCGCGGCTGTGGCGCATGGAGCGGTCGCCGCCGCGC---CTGCGCTGCTCGAG 273
QY 116 ArgLeuValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGlyArg 135
DB 274 CGGCTGTGCTCAACTGGCGCGGTTGCGCTTGAAGACCGCGCGCACGCTCGGCGCG 333
QY 136 PheProAspThrLeuLeuGlyAspProAlaArgArgGlyArgPheTyrAspAlaArg 155
DB 334 TTCGCCGACACGCTGTGGGGGACCGCGGTGCGCGCACGCGCTTACGACGCGCGCG 393
QY 156 ArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyrGln 175
DB 394 GCCGATATTATTCTTCAACGACACCGCGCATGCTGATGGTGTCTACTACTACCA 453
QY 176 SerGlyGlyArgLeuArgArgProAlaHisValProLeuAspValPheLeuGluGluVal 195
DB 454 TGGGGGGCGCGCTGAGAGCGCGCGGACGTCGCCCTCGACGCTTCTTCGGAGAGG 513
QY 196 AlaPheTyrGlyLeuGlyAlaAlaAlaLeuAlaArgLeuArgGluAspGluGlyCysPro 215
DB 514 TCCCTCTACAGGCTGGGG---CGGCGGCTGGCGCGGCTGGGAGAGGAGGCGCGCG 570
QY 216 ValProProGluArgProLeuProAlaArgAlaPheAlaArgGlnLeuThrPheLeuPhe 235
DB 571 GTC---GCCGAGGCGCGCTGGCC---CGGCCCTTGGCGGTGAGCTGTGGCTGCTTC 624
QY 236 GluPheProGluSerSerGlnAlaAlaArgValLeuAlaValAlaSerValLeuValIle 255
DB 625 GAATTTCCTGAGAGCTCGCAGGCTGGCGCGGCTGCTGCGCTGCTCCGACTGCTCATC 664

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QY 256 LeuValSerIleValValPheCysLeuGluThrLeuProAspPheArgAspAspArg 275
DB 685 CTGCTCTCCATCGTGGCTTTTCCCTCGACACTGCCACACTTCCGCGACGCCGAT 744
QY 276 GlyThrGlyLeuAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGly 295
DB 745 GACCCGGGCTCGCGCGGTAGCGGCTGCTACTGCGCTTCTCGCTCGCTCAATGGC 804
QY 296 SerSerGlnMetProGluAsnProArgLeuProPheAsnAspProPheValVal 315
DB 805 TCCAGTCCCATGTCAGAGAGCCCTCCCGACACCCCTTCAAGCATCATCTTTGGTGG 864
QY 316 GluThrLeuCysIleCysTyrPheSerPheGluLeuLeuValArgLeuValCysPro 335
DB 865 GAGACCTGTGTATCTGCTGGTCTCTCTTGGACCTGCTGTCATCTGTGGGCTCCCT 924
QY 336 SerLysAlaIlePhePheLysAsnValMetAsnLeuIleAspPheValAlaIleLeuPro 355
DB 925 AGCAAGCTGTGTCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 984
QY 356 TyrPheValAlaLeuGlyThrGluLeuAlaArgGlyArgGlyValGlyGlnAlaMet 375
DB 985 TACTTGTGGCCCTGGGCAAGGATTAGCCCGGACAGCGGCTGTGGGCCAGCGCGCTATG 1044
QY 376 SerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIlePheLysLeuSer 395
DB 1045 TCCCTGGCCATCTTAAGGATCATCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1104
QY 396 ArgHisSerLysGlyLeuGlnIleLeuGlyGlnThrLeuArgLysSerLeuArgLys 415
DB 1105 AGCAATTCGAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1164
QY 416 GlyLeuLeuIlePhePheLeuPheIleGlyValValLeuPheSerSerAlaValTyrPhe 435
DB 1165 GGTCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1224
QY 436 AlaGluValAspArgValAspSerHisPheThrSerIleProGluSerPheTyrPala 455
DB 1225 GCTGAGTGTGACCGGCTGGACACCATTCACACGATCCGCGAGTCTTTGGTGCGCA 1284
QY 456 ValValThrMetThrThrValGlyTyrGlyAspMetAlaProValThrValGlyLys 475
DB 1285 GTGGTACCATGACCAAGGCTGATGGGATGATGATGATGATGATGATGATGATGATGAT 1344
QY 476 IleValGlySerLeuCysAlaIleAlaGlyValLeuThrIleSerLeuProValProVal 495
DB 1345 ATGCTGGCTCTGTGTGTCATTCAGAGTGTCTACCATCTCTGCTGCTGCTGCTGCTG 1404
QY 496 IleValSerAsnPheSerTyrPheTyrHisArgGluThrGluGlyGluAlaGlyMet 515
DB 1405 ATTGCTCTTAACCTTGTAGCTTATACCAACCGGAGACAGAGGCGACAGAGGAGGATG 1464
QY 516 PheSerHisValAspMetGlnProCysGlyProLeuGluGlyLysAlaAsnGlyLysLeu 535
DB 1465 TACAGCATGTGGACACACAGCCCTGCGGATCCCTGAGGAGGAGGATGAGGAGGAGG 1524
QY 536 ValAspGlyGluValProGluLeuProProIleThrAlaProProArgGluHisLeu 555
DB 1525 GTGACATCTGAGAGTGTGCTGACTCTCCACACACTGTGGCCCTGAGGAAACACATG 1584
QY 556 ValThrGluVal 559
DB 1585 GTGACTGAGGTG 1596

RESULT 2
US-08-527-152-1
; Sequence 1, Application US/08527152
; Patent No. 5827655
; GENERAL INFORMATION:
; APPLICANT: Chandu, Kanianthara G.
; APPLICANT: Cabalan, Michael D.
; APPLICANT: Grissmer, Stephan
; APPLICANT: Goldin, Alan L.

```



```

QY 397 sSerLysGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgGluLeuGlyLe 417
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Db 1180 CTCACAGGCGCTTGAGATCTGGCTACACACTCAAGACCTGTGCCTGGAGCTGGGCTT 1239
QY 417 uLeuIlePhePheLeuPheIleGlyValLeuPheSerSerAlaValTyrPheAlaG 437
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1240 TCTCCTCTTTCCTCAACCATGGCCATCATCTTGGCCACTGTCATCTTTATGCTGA 1299
QY 437 uAlaAspArgValAspSerHisPheThrSerIleProGlnUserPheIleProAlaVal 457
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1300 GAAGGCGCACAAACAGACCACTTTACAGCATCCCTGGCGCTTCTGTATACCATTT 1359
QY 457 lThrMetThrThrValGlyTyrGlyAspMetAlaProValThrValGlyLysIleVal 477
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1360 CACATGACACGCTTGGCTAGCGAGACATGTGTGGCCACACACATGTGTGGCAAGTTT 1419
QY 477 lGlySerLeuGlyAlaIleAlaGlyValLeuThrIleSerLeuProValIleVal 497
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1420 CGGGTCCATCTGCTACGTAGGGGCTTGTGTGTCATTCCTGCTGCTGCTGCTGCT 1479
QY 497 lSerAspPheSerTyrPheTyrHisArg-----GluThrGluGlyValGlu 512
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1480 GTCCACTTTTACCGCATCTACACACAGACAGCGGCTGACAAAGCGCCAGACAGCA 1539
QY 512 uAlaGlyMetPheSerHisValAspMetGlnProCysGlyPro-----LeuG 528
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1540 GAAGTGGCGCTTGGCAAGATCCGATTTGGCAAAAGATGTTACACCAATGCTTCTGCA 1599
QY 528 uGlyLysAlaAsnGlyGlyLeuValAsp 537
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Db 1600 GTACAAGCAGAAATGGGCGCTTAGAGAC 1627

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RESULT 4

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US-07-955-916-6
Sequence 6, Application US/07955916
Patent No. 5397702

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GENERAL INFORMATION:

```

APPLICANT: CAHALAN, Michael D.
APPLICANT: CHANDY, Kamalanthara G.
APPLICANT: GRISMER, Stephen
APPLICANT: GHANSHANI, Sanjiv
APPLICANT: GUTMAN, George A.
TITLE OF INVENTION: ASSAY FOR AND TREATMENT OF AUTOIMMUNE
DISEASES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111

```

COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/955,916
FILING DATE: 19921002
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:

```

```

NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-54474-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1805 base pairs
TYPE: NUCLEIC ACID

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-07-955-916-6

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Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
737,50	1805	189	67	138	128	16
Percent Similarity:	49.04%					
Best Local Similarity:	36.21%					
Query Match:	25.27%					

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US-09-804-014A-8 (1-559) x US-07-955-916-6 (1-1805)

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QY 60 PROPTOPROSerArgProSerArgProAlaGlyLeuPheTyrAlaArgThrProAspThr 79
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Db 55 CCCCCCTCCCGCTGGCAACTCCCTGGCGC-----AGC 90
QY 80 GLYHISARGALAGLYAlaAlaValProAlaAlaProCysGlyCys-CysGluArgLeuVal 99
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 91 TCCCATGGGTGTGCTGGGCGCGCCATGCTAAG-----GGCGCGCGCAT 138
QY 100 AlaArgHisGlyAlaAlaValProAlaAlaProCysGlyCys-CysGluArgLeuVal 119
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 139 -----GGCCAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 171
QY 119 uAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGlyArgPheProAspThr 139
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 CAACGTGGGCGCACCGCCACAGACGTACCGCTGACGTGCGACGCTGCGACGCTGCGGCGAC 231
QY 139 r-----LeuLeuGlyAspProAlaArgArgGlyArgPhe---TyrAspAspAla 155
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 GCGGCTTGGCTGGCTGGAGAGCGCGGAGCGCCAGACCACTTGCATATGACCGCGCTGC 291
QY 155 gArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyrG 175
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 292 CGACGAGTCTCTTCTTGACCGCCAGCCCGGCGCTTCTGCTGACATCTGACATATTACCG 351
QY 175 nSerGlyValArgLeuArgPheAlaHisValProLeuAspValPheLeuGluGluVal 195
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 352 CACC---GGCAGACCTTCACCTGCGCGCGCGAGCGTGGCGGCGCTGTACGAGAGAGCT 408
QY 195 lAlaPheTyrGlyLeu-----GlyAlaAlaAlaLeuAlaArgLeu 200
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 409 GGCCTTCTGGGCAATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 468
QY 201 -----GlyAlaAlaAlaLeuAlaArgLeu 209
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 469 GCACCGAGACGCTGAGAGAGCGGTGACAGCTTTGGCGGTGGCGCTGACAAAGCGCGC 528
QY 209 gGluAspGluGlyCysProValPro----- 217
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 529 CGACGAGCGGAGCGCGAGCGCGCGGCTGCGGCGAGCGAGCGAGAGAGAGAGAGAGAT 588
QY 218 -----ProGluArgProLeuProArg-----ArgAl 226
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 589 GACCAAGAGATTGGCAGTCACTGACCTCCCAAGATGGCGCGCGCTTCTGGCGCGCG 648
QY 226 aPheAlaArgGlnLeuThrPheLeuPheGluPheProGlnUserSerGlnAlaAlaArgVal 246
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 649 CTGGCAACCGCGCATGTGGCGCTGTGTGAGAGACCCCTACTCATCCCGCTAGCGCGGTA 708
QY 246 lLeuAlaValSerValLeuValIleLeuValSerIleValValPheCysLeuGluTh 266
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 709 TGTGGCTTGGCTGCTCTCTTTCATCTGCTGCTCATCAACACTTGTCTGTGAGAC 768
QY 266 rLeuProAspPhe-----ArgAspAspArgAspGlyTh 277
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 769 TCACGAGCGCTTCAACCCCATGCTGACAAAGACCGAAATCGAAGAGCTTCAAGAGCGGAC 828
QY 277 rGlyLeuAlaAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGlySer 297
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```


Db 940 -CGGGCTTCCTCCGCTTCAGGATCTTCAAGTTTCCCGCCACTCCAGGCGCTCGGAGT 998
 QY 403 eLeuGlyGlnThrLeuArgAlaSerMetArgLLeuGlyLeuLeuIlePhePheLeuPh 423
 Db 999 CCGTGGCTACACATGAGAGCTGTGCTCCGCAACTGGGCTTCTCTCTCCCTCAC 1058
 QY 423 eLeuGlyValLeuPheSerSerAlaValTyrPheAlaGlyAlaAspValAspSe 443
 Db 1059 CATGGCCATCATCTTTGCCACTGTGTATGTTCGCGGAGGAGGCTCTCCGCGCAG 1118
 QY 443 HisPheThrSerIleProGlySerPheTrpTrpAlaValAlaThrMetThrValG 463
 Db 1119 CAAGTACAAACATCTCCGCTGTTGGTACACACATGTTCACCATGACCACTGGG 1178
 QY 463 YTrpTrpLysMetAlaProValThrValGlyLysIleValGlySerLeuGlyAla 483
 Db 1179 ATACGAGACATGCTGCTACAGCATTCGAGGAAGATCTTCATCTGCTCCCTT 1238
 QY 483 eAlaGlyValLeuThrIleSerLeuProValProValIleValSerAsnPheSerTyrPh 503
 Db 1239 GAGTGGCGCTCGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1298
 QY 503 eTyrHisArg-----GluThrIleGlyLysIleValGlyMetPheSerH 518
 Db 1299 TTACCAACGAGATCAGAGAGCTGTATAACGAGGACAAAGAGCGCCGCTTGCAG 1358
 QY 518 sValAspMetGlnProCysGlyPro-----LeuGlyLysValAlaAsnGly 534
 Db 1359 GATTCGCTGGCCAAACAGCGAGTTGCAATGATACCTGACAGACGAGCGAGCGGT 1418
 QY 534 YLeuValAspGlyLysValProGlyLeuProProPheLeuTrpAlaProProArgGly 554
 Db 1419 CCTC-----AACGAGCGCCCTGAGCTG-----ACGGGACACCCCAAGAGAGCA 1463
 QY 554 sLeu 555
 Db 1464 CATG 1467

RESULT 8

US-09-142-791A-3
 : Sequence 3, Application US/09142791A
 : Patent No. 6368823
 : GENERAL INFORMATION:
 : APPLICANT: Antoine Michel Alain Brill
 : APPLICANT: Thierry Paul Gerard Calmels
 : APPLICANT: Jean-Francois Simon Pierre Faivre
 : APPLICANT: Jean-Luc Javie
 : APPLICANT: Sabine Rouanel
 : TITLE OF INVENTION: NOVEL COMPOUNDS
 : FILE REFERENCE: GH-30012
 : CURRENT APPLICATION NUMBER: US/09/142,791A
 : CURRENT FILING DATE: 1999-02-02
 : PRIOR APPLICATION NUMBER: PCT/EP98/01901
 : PRIOR FILING DATE: 1998-03-23
 : PRIOR APPLICATION NUMBER: UK 9706377.0
 : PRIOR FILING DATE: 1997-03-27
 : PRIOR APPLICATION NUMBER: EP 97402971.2
 : PRIOR FILING DATE: 1997-12-09
 : PRIOR APPLICATION NUMBER: EP 97403007.4
 : PRIOR FILING DATE: 1997-12-11
 : NUMBER OF SEQ ID NOS: 14
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 3
 : LENGTH: 2072
 : TYPE: DNA
 : ORGANISM: HOMO SAPIENS
 US-09-142-791A-3

Alignment Scores:

Pred. No.: 3,17e-44 Length: 2072
 Score: 721.00 Matches: 176
 Percent Similarity: 53.70% Conservative: 85
 Best Local Similarity: 36.21% Mismatches: 153

Query Match: 24.71% Indels: 73
 DB: 4 Gaps: 14
 US-09-804-014a-8 (1-559) x US-09-142-791A-3 (1-2072)
 QY 103 GLYAlaAlaValProAlaAlaProCys-----GlyCys 113
 Db 56 GGATGGCGGTGGGCAACCTGCCCATGCCCTGGCGCCGCGCAGAACAGAGCGGCAC- 114
 QY 114 CysGluArgLeuValLeuAsnValAlaGlyLeuArgPheGlyThrArgAlaArgThrLeu 133
 Db 115 GATGACCTATTGTCTCTCAACGAGTGGCGGAGGTTCCAGACCTGGAGAGCAAGCTG 174
 QY 134 GlyArgPheProPheThrLeuGlyAspProAlaArgGlyLysArgPheTyrAsp 153
 Db 175 GAGCGCTACCCGAGACCCCTGCTGGGAGC--ACGAGAGAGAGTTCCTTCAACAGAG 231
 QY 154 AlaArgArgLysTrpPhePheAspArgHisArgProSerPheAspAlaValLeuTyr 173
 Db 232 GACACCAAGAGAGTCTTTCGACCGGAGACCCGAGAGTGTCCGCTGCTGCATCACTTC 291
 QY 174 YTrpGlnSerGlyLysArgLeuArgArgProAlaHisValProLeuAspValPheLeuGlu 193
 Db 292 TACCGCAGC---GGGAGCTGCACATACCCGCGCTACGAGTGCATCTGCTACGAGCAG 348
 QY 194 GluValAlaPheThrGlyLeuGlyAlaAlaAlaLeuAla----- 206
 Db 349 GAGCTGGCTTCTACGGCATCTCCCGAGATCATCGGGAGCTGCTACGAGAGACTAC 408
 QY 207 -----ArgLeuArgLys-----AspGlyGlyCysProValProPro 218
 Db 409 AAGGACCGCAAGAGGAGAGAACCGCGAGGCTCATGTGACAGACAGACATCGGAGAACAC 468
 QY 219 GluArgProLeuProArgArgAlaPheAlaArgGlnLeuTrpLeuPheGluPhePro 238
 Db 469 CAGAGTCCATGCTCGCTCGCTCAGCTTCCGACAGACATGTGGCGGCTTCGAGAACCC 528
 QY 239 GluSerSerGlnAlaAlaArgValLeuAlaValSerValLeuValIleLeuValSer 258
 Db 529 CACACCGACAGCGTGGCGCTGCTTCTTACTACGTAGCTGCTTCTTCACTGCTGTCTG 588
 QY 259 IleValAlaPheCysLeuGlnThrLeuProAspPheArgAspAspArgAspGlyThrGly 278
 Db 589 GTCATCAACACAGTGTGTGAGAGCGTCCG-----TGGCGCAGC--- 627
 QY 279 LeuAlaAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGlySerSerGln 298
 Db 628 -----GTCCCGGCGACAGCAGAG 645
 QY 299 MetProGlyAsnProProArgLeuProPheAsnAspProPheValValGluThrLeu 318
 Db 646 CTCCCTCGCGCGGAG-----CCCTACTCGCGTCTCTTCCCTGCGACAGCGCG 696
 QY 319 CysIleCysTrpPheSerPheGlnLeuLeuValArgLeuLeuValLysProSerLysAla 338
 Db 697 TGGGTATGATCTTACCGCGAGGATCTCTCGGGCTCTTCCGCGGCTCCACGCGCTAC 756
 QY 339 IlePhePheLysAsnValMetAsnLeuIleAspPheValAlaIleLeuProTyrPheVal 358
 Db 757 CGCTTCATCCGCGAGCGTCAATGACATGACAGCTGTGTGCGCTCATGCTCTACTATC 816
 QY 359 AlaLeuGlyThrGluLeuAlaArgGlnArgGlyValGlyGlnIleMetSerLeuAla 378
 Db 817 -----GTCGTGCTATGACCAACAGAGAGCTGTCCGCGCTTCACAGCTC--- 867
 QY 379 IleLeuArgValIleArgLeuValArgValPheArgIlePheLysLeuSerArgHisSer 398
 Db 868 -----CGGCTCTCCGCGTCTTTCAGATCTTCAAGTTTCCCGCCACTCC 912
 QY 399 LysGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgGlyLeuGlyLeuLeu 418
 Db 913 CAGGCGCTCGGATCTCTGGCTACACATGAGAGCTGTGCTCCGCAACTGGGCTTCTT 972

DB 1033 GGCTCCTCGGCGACGACAAAGTTCACAAACATCCCTGCTGTTTGTATACCATTTGCACC 1092
QY 459 MetThrThrValGlyTyrGlyAspMetAlaProValThrValGlyLysIleValGly 478
DB 1093 ATGACCAACACTGGATATACGAGACATGTGCTTAAGACACGATTCGAGGAATCTTGCGC 1152
QY 479 SerLeuCYsAlaIleAlaIleValLeuThrIleSerLeuProValIleValSer 498
DB 1153 TCCATCTGCTCTGTAGTGGCGTCTGTCATATGCTGCACTCCCTGTGATGTTTTC 1212
QY 499 AsnPheserThrPheThrIleArg-----GluThrGluGlyGluAla 513
DB 1213 AACTTTAGCGCGATTTATACACGAATTCAGAGACTGATTAACGACGGCACAAAGAAC 1272
QY 514 GlyMetPheSerHisValAspMetGlnProCysGlyPro-----LeuGluGly 529
DB 1273 GCCCGCTTGGCCAGATCCGTGTGGCCAAACAGGCAAGTTCCGATACCTATCCGACACC 1332
QY 530 LysAlaAsnGlyLeuValAspGlyValProGluLeuProProLeuThrPala 549
DB 1333 AAGCGCAACGGGCTCTC-----AACGAGCGCGCTGGAGCTG-----ACGGGACCC 1377
QY 550 ProProArgGluHisLeu 555
DB 1378 CCAGAGAGGAGACACATG 1395
RESULT 10
US-09-142-791A-5
Sequence 5, Application US/09142791A
Patent No. 6368823
GENERAL INFORMATION:
APPLICANT: Antoine Michel Alain Brill
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Faivre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 2104
TYPE: DNA
ORGANISM: HOMO SAPIENS
US-09-142-791A-5
Alignment Scores:
Pred. No.: 2,47e-43 Length: 2104
Score: 709.00 Matches: 178
Percent Similarity: 51.76% Conservative: 86
Best Local Similarity: 34.90% Mismatches: 159
Query Match: 24.30% Indels: 87
DB: 4 Gaps: 15
US-09-804-014A-8 (1-559) x US-09-142-791A-5 (1-2104)
QY 77 ProAspThrGlyHisArgAlaGlyAlaValAlaIleThrArgArgPheAlaGlyArg 96
DB 36 CCGGGCTGGGGCATCGGGGTGGC----- 62
QY 97 ArgGlyCysAlaArgHisGlyAlaAlaValProAlaAlaPro-CysGlyCys----- 113
DB 63 -----GGTGGCCAACATGCCCCCATGCCCCCTGGCCCCCGCCGACAAAGAA 104

QY 114 -----CysGluArgLeuValLeuAsnValAlaGlyLeuArgPheGluThrArgAl 130
DB 105 CAAGCGGAGAGATAGACTGATTTGCTCAACGATGAGTGGGCGGAGGTCCAGACCTGGAG 164
QY 130 ArgThrLeuGlyArgPheProAspThrLeuLeuGlyAspProAlaArgArgGlyArgph 150
DB 165 GACACAGCTGAGACCGTACCCGACACACCTGTGGGAGC---ACGAGAAAGAGTTCTT 221
QY 150 eTyrAspAspAlaArgArgGluTyrPhePheAspArgHisArgProSerPheAspAlaVa 170
DB 222 CTTCACAGAGACACCAAGAGATCTTCGACCGGAGCCGAGGCTGTTCGCTGCT 281
QY 170 LleuTyrTyrGlnSerIleGlyArgLeuAlaArgArgProAlaHisValProLeuAspVa 190
DB 282 GCTCAACTTACCGACG---GGAAAGCTGCACTACACCGCTACGAGTGCATCTCTGC 338
QY 190 IPhleuGluGluValAlaPheTyrGlyLeuGlyAlaAlaAlaLeuAla----- 206
DB 339 CTACGACGACGAGCTGCTTACGCGCATCTCCGAGATCATCGGGAGTGTCTGCTA 398
QY 207 -----ArgLeuArgGlu-----AspGluGlyCysPr 215
DB 399 CGAGAGTACAGAGACCGCAAGAGGAGAACGCCGAGCTCATGACACACACATC 458
QY 215 oValProProGluArgProLeuProArgArgAlaPheAlaArgGluLeuThrLeuPh 235
DB 459 GGAGAACACACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 518
QY 235 eGluPheProGluSerSerGlnAlaAlaArgValLeuAlaValAlaSerValLeuValI 255
DB 519 CGAAGACCCCGACACGACGCGTGGCCGTGCTTCTACTAGTGCATGCTGCTTCTCAT 578
QY 255 eLeuValSerIleValAlaPheCysLeuGluThrLeuProAspPheArgAspArgAs 275
DB 579 CGCTGTCGCTCATCATCAACAGCTGTGGAGAGCGTCCG-----TG 620
QY 275 pGlyThrGlyLeuAlaAlaAlaAlaAlaIleGlyProValPheProAlaProLeuAsnG 295
DB 621 CGGCACG-----GTCCCGGG 635
QY 295 ySerSerGlnMetProGlyAsnProProArgLeuProPheAsnAspProPhePheValVa 315
DB 636 CACCAAGAGACTGCCCGCGGGAG-----CGTACTCGGTGGCCTTCTTCTGCT 686
QY 315 lGluThrLeuCysIleCysThrPheSerPheGluLeuLeuValArgLeuValCysPr 335
DB 687 GGACACGGCGGTGCTCATGTTCACCGGTGAGTACTCTCGGCTCTTCCGCGCTCC 746
QY 335 oSerLysAlaIlePhePheLysAsnValMetAsnLeuIleAspPheValAlaIleLeuPr 355
DB 747 CAGCGCTACCGCTCATCCGACGCTCATGACATCATGAGTGGTGCATCATAGCC 806
QY 355 oTyrPheValAlaLeuGlyThrGluLeuAlaArgGlnArgGlyValGlyGlnGlnAlaMe 375
DB 807 CTACTACATC-----GTTGTGCTATGACCAACACAGAGAGCTGTCCGCCCTTCT 860
QY 375 tSerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIlePheLysLeuSe 395
DB 861 CACGCTC-----CGGCTTCCCGCTTCAGATCTCCAAAGTTTTC 902
QY 395 rArgHisSerLysGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgGluLe 415
DB 903 CCGCCACTCCAGAGCGCTGGGATCTGGGCTACACACTGAAGAGCTGTCCCTCCGACAT 962
QY 415 uGlyLeuLeuIlePhePhePheIleGlyValValLeuPheSerSerAlaValYrph 435
DB 963 GGGCTTCTTCTCTCTCCCTCAACAGGACATCATCTTTGCCACTGTGATTTTA 1022
QY 435 eAlaGluValAspArgValAspSerHisPheThrSerIleProGluSerPheThrPala 455
DB 1023 TGCCGAGAAAGGCTCCGCGCGACAGATTCACAAAGATCCGTCGTTTGTATACAC 1082

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QY 455 aValaThMetThrThrValGlyTyrglyAspMetAlaProValThrValGlyGly 475
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Db 1083 CATGTGACCATGACCATGCGATGAGACATGCTGCTTAAGATTCAGAGGAA 1142
QY 475 sTleValGlySerLeuGlyAlaIleAlaGlyValLeuThrIleSerLeuProValProVa 495
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1143 GATCTTCGCTCATCTGCTCTGAGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1202
QY 495 lIleValSerAspPheSerTyrrPheThrHisArg-----GluThrGluG1 510
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1203 GATTGTTCCAACTTTAGCCGATTTACCCAGAACAAACAGAGCTGATTAAGCCAGGCG 1262
QY 510 yGluGluAlaGlyMetPheSerHisValAspMetGlnProCysGlyPro----- 526
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1263 ACAAAAGAACGCCCGCTTCCAGATCCGCTGCGCCAAACAGGAGGAGTTCGATGCGATA 1322
QY 527 -leuGluGlyLysAlaAsnGlyGlyLeuValAspGlyGlyValProGluLeuProProPr 546
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1323 CCGTCACAGCAGCAGCGGAGCGCTCTC-----AACGAGCGCTGAGGCTG----- 1368
QY 546 oleuTPAlaProProArgGluHisLeu 555
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1369 -ACGGGACCCCGACAGAGAGACATG 1395

RESULT 11
US-09-336-643A-17
; Sequence 17, Application us/0933643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: MILLER, Andrew P.
; APPLICANT: CURTAN, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rulter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 03/826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 3102
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (274)...(1705)
; OTHER INFORMATION: K+hnov11
US-09-336-643A-17

Alignment Scores:
Pred. No.: 3,74e-42 Length: 3102
Score: 696.00 Matches: 202
Percent Similarity: 44.53% Conservative: 87
Best Local Similarity: 31.12% Mismatches: 172
Query Match: 23.85% Indels: 190
Gaps: 22

US-09-804-014A-8 (1-559) x US-09-336-643A-17 (1-3102)
QY 8 SerArgArgGlnLysAspGlyGlyLysGlyAspProGlyThrGlyLysAlaGlnSer--- 26
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 124 AGACACCCAAAGACCCAGAGGCGCTGCGCCCGCCAGTAATGCTAGAGAGGAGGCGCC 183
QY 27 ArgArgGlyArgArgArgArgGlyArgAlaGly-ArgAlaSerArgGlnArgAla-- 45
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 184 CGCAGGCGCCAGCGCGCTCTCGCCAGCGCTTCCCTCCGCTTCAGGTTGAGCGCC 243

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QY 46 -----ArgGlyArgProValAlaLeuArgProAlaGlyValThrValProProSe 63
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 244 CCGCGCGCGCGCGCGCGCGCG-----CCTCCAGC 273
QY 63 rArgProSerArgProAlaGlyLeuPheTyrrAlaArgThrProAspThrGlyHisArgAl 83
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 274 ATGACCGCGCAGA----- 286
QY 83 aGlyAlaAlaValGlyLarThrArgArgPheAlaGlyArgArgGlyCysAlaArgHisG1 103
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 287 -----GCCGTGGGACGTGTGAGGCTTACCTCGACGAGAGGAG-ATCCGC----- 333
QY 103 yAlaAlaValProAlaAlaProCysGlyCysGlyArgLeuValLeuAsnValAlaG1 123
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 334 -----ATCATGTGGGCGG 347
QY 123 yLeuArgPheGluThrArgAlaArgThrLeuGlyArgPheProAspThrLeuLeuGlyAs 143
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 348 CTTCAAGAGAGGCGCTGCGCTCGACACGTGCTGCTGCCGAGAGC----- 396
QY 143 proAlaArgArgGlyArgPhe----- 150
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 397 -----CGCCTGGCGCGCTTCTGCTGCTGCTGCGCTGCGGAGCCATTCTGAGCTCTG 449
QY 151 -----TyrAspAspAlaArgArgGlyArgPheAspArgHisArgProSerPheAs 168
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 450 CGATGACTACGACGACGCTCCAGCGGAGGTTCTACTTCCGACCGCAACCTGAGCTCTCC 509
QY 168 pAlaValLeuTyrrTyrrGlnSerGlyArgLeuArgArgProAlaHisValProLe 188
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Db 510 CTAGCTGCTGCTCATTTATACACCC--GGCAACCTTCACGTCATGCTGCTGCTGCTGCT 566
QY 188 uAspValPheLeuGluGluValAlaPheTyrrGlyLeuGlyAlaAlaAlaLeuAlaArgLe 208
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 567 CTTCTCTTACGACGACGATCGATGCTGGGATCAAGAGCTTCTCATTT----- 618
QY 208 uArgGlyAspGluGlyGys-----ProValProProGluArgPr 221
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 619 -----GACTCTGCTGACGTACAGCTACATGAGCGCGCAAGTATAGCCCGAGCAGA 671
QY 221 o----- 221
Db 672 GAAGTGGAGCAGCAGAGTGACGACGAGCAGCAGCAGCTTCTTCATGATGATCTTGC 731
QY 222 -----LeuProArgArgAlaPheAlaArgGlnLe 231
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 732 CTTCTACAGACGACCTCCAAAGTTGATGGGACAGCCCTCGCAACTTCGAGGACAGCT 791
QY 231 uTPLeuLeuPheGluPheProGluSerSerGlnAlaAlaArgValLeuAlaValAlaSe 251
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 792 GTGCTGCGCTGACCAACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851
QY 251 rValLeuValIleLeuValSerIleValValPheCysLeuGluThrLeuProAspPheAr 271
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 852 CATCTGTGTGTGATGAGGAGGCTCATCACCAGTGTCTCAATGACCTGCGCGATTTTCCA 911
QY 271 gAspAspArgAspGlyThrGlyLeuAlaAlaAlaAlaAlaGlyProValPheProAl 291
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 912 A----- 912
QY 912 A----- 912
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 913 -----ATCCCTGACAGCAGGAGCAACCTGCGAGGAGCCTTAG----- 951
QY 913 oPhePheValValGluThrLeuGlyIleCysTrpPheSerPheGluLeuLeuValArgLe 331
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 952 -TTTGAATCATCGAGACATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1010
QY 331 uLeuValCysProSerLysAlaIlePhePheLysAsnValMetAsnLeuLeuAspPheVa 351
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Db 1011 TGCTGTGGCCCTGACTTCTCTCAAGTTCTTCAAGATGCGCTTAACCTTATTTGACCCAT 1070

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OY 351 lAlaIleuProTyrPheValAlaLeuGlyThrGluLeuAlaArgGlnArgGlyValG1 371
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Db 1071 GTTCATCGTCCCTTACATCATCTGTGTGAACCTG-----GTGGT 1115
OY 371 yGlnGlnAlaMetSerLeuAla-----lIleuArgValAlIleArgLeuValAr 387
    :::::::::::::::::::: |||
Db 1116 GGAGAGCACACCTACTACTTGAACACTTGGCAGGAGTGCCAGGCTCTGAGGCTGTATGG 1175
OY 387 gValPheArgIlePheLeuSerArgHisSerLysGlyLeuGlnIleLeuGlyGlnTh 407
    :::::::::::::::::::: |||
Db 1176 GATCTTCGCCATCTTAAGACTG6CCAGGACATCCAGCTG6CCTCCCTG6GGG6CCAC 1235
OY 407 rLeuArgAlaSerMetArgGluLeuGlyLeuLeuIlePheLeuPheIleGlyValAr 427
    :::::::::::::::::::: |||
Db 1236 TTTGAATACAGCTACAAGAAGTAGGGCTGCTGCTGCTACCTGCTGCTGCTGCTGCTG 1295
OY 427 lIlePheSerSerAlaValTyrPheAlaGluValAspArgValAspSerHisPheThr 447
    :::::::::::::::::::: |||
Db 1296 CATCTCTCTCGTGCGCTACACCATTTGAAAAGAGAGAG---AACGAGG6CCTG6CCAC 1352
OY 447 rIleProGluSerPheIlePheIleValAlaValAlaIleThrMetIleThrValGlyTyrGlyAsp 467
    :::::::::::::::::::: |||
Db 1353 CATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1412
OY 467 lAlaProValIleThrValGlyGlyLysIleValGlySerLeuCysAlaIleAlaGlyValLe 487
    :::::::::::::::::::: |||
Db 1413 GGTCCAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1472
OY 487 uThrIleSerLeuProValIleValIleValSerAsnPheSerTyrPheTyrHisArgG1 507
    :::::::::::::::::::: |||
Db 1473 CGTGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1532
OY 507 uThrGluGlyGluGluAla-----GlyMet----- 515
    :::::::::::::::::::: |||
Db 1533 AAAGCAACTTGAAGAGTGCATGCGCAGCTGTGAGATGTGAGATGAAGAGAGGTCCC 1592
OY 516 -----PheSerHis----- 519
    :::::::::::::::::::: |||
Db 1593 TTCGGCATTTAAGGAGCATATATGATGATGATGATGATGATGATGATGATGATGATG 1652
OY 519 lAspMetGlnProCysGlyProLeuGluGlyLysAlaAsn-----G1 533
    :::::::::::::::::::: |||
Db 1653 GAACATGAGCAGAGAGCTCCCAAGTGAATGATGATGATGATGATGATGATGATGATG 1712
OY 533 yGlyLeuVal-----AspGlyGluValProGluLeuProProProLeuIleThrAlaProP 551
    :::::::::::::::::::: |||
Db 1713 AGGACTTGTACCTCCACCC-CACATTCGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1771
OY 551 cArgGluHisLeuValIleThrGluVal 559
    :::::::::::::::::::: |||
Db 1772 CAGG---CACCTTATGATTATGTG 1793

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RESULT 12
US-08-464-340A-3
: Sequence 3, Application US/08464340A
: Patent No. 5710019
: GENERAL INFORMATION:
: APPLICANT: LI, ET AL.
: TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
: ADDRESSEE: CECCHI, STEWART & OLSTEIN
: STREET: 6 BECKER FARM ROAD
: CITY: ROSELAND
: STATE: NEW JERSEY
: COUNTRY: USA
: ZIP: 07068
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 INCH DISKETTE
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WORD PERFECT 5.1

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464,340A
: FILING DATE: June 5, 1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/08449
: FILING DATE: 28 JUL 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: FERRARO, GREGORY D.
: REGISTRATION NUMBER: 36,134
: REFERENCE/DOCKET NUMBER: 325800-415
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-994-1700
: TELEFAX: 201-994-1744
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2483 BASE PAIRS
: TYPE: NUCLEIC ACID
: STRANDEDNESS: SINGLE
: TOPOLOGY: LINEAR
: MOLECULE TYPE: CDNA
: US-08-464-340A-3

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Alignment Scores:
Pred. No.: 7.35e-39 Length: 2483
Score: 649.50 Matches: 204
Percent Similarity: 44.05% Conservative: 81
Best Local Similarity: 31.53% Mismatches: 208
Query Match: 22.26% Indels: 156
Gaps: 19
US-09-804-014a-8 (1-559) x US-08-464-340A-3 (1-2483)

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OY 3 ArgArgArgThr-----GlySerArgArgGlnLysAspGlyLysGlyAsp 18
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OY 19 ProGlyThrGlyLysAlaGlnSerArgArgGlyArgArgArgArgArgGly 38
    :::::::::::::::::::: |||
Db 417 GCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 476
OY 39 ArgAlaSerArgGlnArgAlaArgGlyArgProValAlaLeuArgProAlaGlyValThr 58
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Db 477 CGAGCGCGG-----CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 500
OY 59 ValPro-----ProPro-----SerArgProSerArgProAla 69
    :::::::::::::::::::: |||
Db 501 CTCGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 560
OY 70 GlyLeuPheTyrAlaArgThrProAspThrGlyHis----- 81
    :::::::::::::::::::: |||
Db 561 GGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 620
OY 82 -----ArgAlaGlyAlaAlaValAlaGlyAlaThrArg 91
    :::::::::::::::::::: |||
Db 621 CGACAACGCGGCGGAGCTGTGCAAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 680
OY 92 ArgPheAlaGlyArgArgGlyCysAlaArgHisGlyAlaAlaValAlaProAlaProCys 111
    :::::::::::::::::::: |||
Db 681 GAGAGTGAAGGCGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 740
OY 112 GlyCysCysGluArg-LeuValLeuAsnValAlaGlyLeuAlaPheGluThrArgAlaAr 131
    :::::::::::::::::::: |||
Db 741 CAGCGAGCAGATAGATAGATGCTCAACGATGGGGGCGGCGGCGGCGGCGGCGGCGGCGG 800
OY 131 gThrLeuGlyArgPheProAspThrLeuLeuGlyAsp-----ProAlaArgArgGlyAr 149
    :::::::::::::::::::: |||
Db 801 CCTCTCAGTCACTACCTGAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 860
OY 149 gPhe-----TyrAspAspAlaArgArgGlyLysThrPhePh 160
    :::::::::::::::::::: |||
Db 861 CTACGACACCACTTCTCCTGTGCGAGCAGCATACGACCGGCGGCGGCGGCGGCGGCGGCGG 920

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QY 402 GlnIleLeuGlyClnThrLeuArgAlaSerMetArgGluLeuGlyLeuLeuIlePhePhe 421
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Db 1371 CAGACGCTGGGGCTCACAGGCGCCGCTGCACCCGCGAGTTCGGGCTCTGCTCTTC 1430
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 422 LeuPheIleGlyValValLeuPheSerSerAlaValTyrPheAlaGluValAspArgVal 441
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1431 CTCTGGGTGGCCATCGCCCTCTTGGCGCCCTGCTCTACGTCAACGAGAGATGGCC 1490
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QY 442 AspSer--HisPheThrSerIleProGluSerPheTrpPalaValValThrMetThr 460
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Db 1491 GACAGCGCCGAGTTCACACGACATCCCTGCGCTACTGCTGGGCTGTGCATCACCATGACG 1550
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QY 461 ThrValGlyTyrGlyAspMetAlaProValThrValGlyGlyLysIleValGlySerLeu 480
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Db 1551 ACGGTGGACTATGGCAGCATGTGCCAGAGGACCCCGGGCCAGTGTGGCCCTGAGC 1610
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QY 481 CysAlaIleAlaGlyValLeuThrIleSerLeuProValProValIleValSerAsnPhe 500
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1611 AGCATCCTGAGCGGACATCCTGCTCATGGCCCTTCCAGTCCATCCTTCCACACCTTC 1670
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QY 501 SerTyrPheTyrHisArgGluThrGluGlyGluAlaGlyMetPhe 516
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1671 TCCCCCTCTACCTCGAGCTCAACAGAGACAGAGAGAGGTGATGTTC 1718
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Search completed: February 20, 2003, 12:12:51
Job time : 120 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OW protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2003, 11:49:51 : Search time 2234 Seconds
(without alignments)
4052.496 Million cell updates/sec

Title: US-09-804-014A-8
Perfect score: 2918
Sequence: 1 MERRRSGSRKQDEKGDGPG.....VPELPPLMAPPREHLVTEV 559

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 segs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2.1/USPTO_spool/US09804014/runat_10022003.161449.27221/app.query.fasta.1.711
-DB=IST -QFMT=fastap -SUFFIX=1st -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blonsum62 -TRANS=human40.cdi -LIST=45
-DOCLIN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09804014.qcgn.1.1.813 &runat_10022003.161449.27221 -NCRU=6 -ICRU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONLOG -DEV=TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1107	37.9	1085	17	CNS035KP
2	986.5	33.8	1058	14	BM924998
3	983.5	33.7	900	17	CNS02R3D3
4	896	30.7	839	17	CNS03DKC
5	892	30.6	876	13	BM117089
6	853	29.2	745	14	BM963332
7	815	27.9	636	17	AZ339279
8	794	27.2	954	14	BQ714749
9	765	26.2	2146	11	BC023222
10	760.5	26.1	1060	17	CNS058RO
11	744	25.5	559	12	BC812963
12	743	25.5	629	17	AG163977
13	736	25.2	575	13	BM128683
14	732	25.1	593	13	BM128211
15	729	25.0	963	17	CNS0215Y
16	719.5	24.7	1109	17	CNS045OM
17	700	24.0	697	10	BM541281
18	693.5	23.8	640	13	BC973314
19	693	23.7	772	13	B1764377
20	690	23.6	628	14	B0807519
21	676	23.2	443	17	AQ939702
22	649.5	22.3	468	9	A1324179
23	638	21.9	522	9	A1322534
24	634	21.7	900	14	BQ938497
25	633.5	21.7	2265	11	BC019010
26	625	21.4	1054	17	CNS05DBK
27	616.5	21.1	927	14	BQ930283
28	613	21.0	506	13	B1467889
29	606	20.8	434	10	BE654741
30	589.5	20.2	434	9	BE654741
31	574	19.7	687	13	B1295790
32	567	19.4	457	9	A1694783
33	566.5	19.4	457	11	A1694783
34	564.5	19.3	631	10	BB622001
35	559	19.2	990	17	CNS04EVP
36	557.5	19.1	990	17	CNS04EVP
37	554.5	19.0	770	12	BR530500
38	553.5	19.0	1087	17	CNS02H90
39	549	18.8	526	13	B1339926
40	521	17.9	526	10	B1339926
41	519.5	17.8	637	10	BR250655
42	519	17.8	637	17	BR250655
43	517	17.7	668	14	BQ187015
44	515	17.6	400	12	BF108522
45	510	17.5	437	12	BE865003

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CNS035KP/c	CNS035KP	Tetradon nigroviridis genome survey sequence PUC-ori end of clone 214T01 of library G from Tetradon nigroviridis, genomic survey sequence.	AL228850.1	GI:7887843	GSS: genome survey sequence.	Tetradon nigroviridis.	Tetradon nigroviridis
			AL228850				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

REFERENCE	1 (bases 1 to 1085)			
AUTHORS	Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Winkler,P., Brolier,P., Queller,F., Saurin,W. and Weissenbach,J.			
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 1085)			
AUTHORS	Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Queller,F., Saurin,W., Bernot,A. and Weissenbach,J.			
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis			
JOURNAL	Unpublished			
REFERENCE	3 (bases 1 to 1085)			
AUTHORS	Genoscope.			
TITLE	Direct Submission			
JOURNAL	Submitted (12-APR-2000)			
COMMENT	This sequence is a single read and was generated as part of a larger scale clone-and-sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon .			
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	/clone="214101"			
	/clone_11b="G"			
	/note="Genoscope sequence ID : C0AK214AE01SP1-end : pUC-Or1"			
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ORIGIN	6 others			
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Score:	1107.00	Matches:	222	
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Best Local Similarity:	63.43%	Mismatches:	64	
Query Match:	17.94%	Indels:	22	
DB:		Gaps:	3	
US-09-804-014A-8 (1-559) x CNS035KP (1-1085)				
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Db	1012	TGCTGCGAGCGCGGKTTTCATCAACATYTCAGGCTCGCCTTGGAAACCCAGCTGAAGCC	953	
Oy	133	LeuGly-ArgPheProAspThrLeuLeuGlyAspProAlaArgGlyArgPheThrAs	152	
Db	952	CTGGGCCCAAGTTCGCCGAGACCCCTCTGTGGGAACCCCCAGAGAGAGATCGCTACTTCCA	893	
Oy	152	PAspAlaArgArgGlyArgPhePheAspArgHisArgProSerPheAspAlaValLeuTy	172	
Db	892	CCCCGTCGGGAACGAGTACTTCTTCGACCGGAACCGGCCACAGCTTCGACGCGCATCTCTCA	833	
Oy	172	TYTYTyrGlnSerGlyGlyArgLeuArgArgProAlaHisValProLeuAspValPhe	192	
Db	832	CTACACCAAGTCGGCGGGCGGCTAGGCGGGCGGTCAACGTCCCGCTGGACATGTTCTC	773	
Oy	192	uGluGluValAlaPheTyArgGlyLeuGlyAlaAlaAlaLeuAlaLeuAlaArgLeuArgL	212	
Db	772	GGAGGAGATCAAAATTCACGACCTGGGCGCATGTGAGGCCATGTGAGAGGTTCCCGGAA	713	
Oy	212	uGlyCysProValProProGluArgProLeuProArgArgAlaPheAlaArgGlnLeuTr	232	
Db	712	GGGCTTCATCCGGGAGGAGGAGCGGCCCTCGCCGGAACGAGTTCACAGCGGCGAGCTCG	653	
Oy	232	PleuLeuPheGluPheProGluSerSerGlnAlaAlaArgValAlaValSerVa	252	
Db	652	GCT-CTCTTCGAGCACCCGAGAGAGCTCGGGTCCGGGCGGCGCATCGCATGCTCTGT	594	
Oy	252	lLeuValAlaValSerIleValAlaValPheCysLeuGluThrLeuProAspPheArg	272	

[illegible]

Alignment Scores:

Pred. No.: 3,58e-66 Length: 900
 Score: 983.50 Matches: 199
 Percent Similarity: 80.77% Conservative: 32
 Best Local Similarity: 69.58% Mismatches: 40
 Query Match: 33.70% Indels: 17
 DB: 17 Gaps: 2

US-09-804-014a-8 (1-559) x CNS02RD3 (1-900)

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QY 247 LeuAlaValValSerValLeuValIleLeuValSerIleValValPheCysLeuGluThr 266
Db 835 ATCCGGGTGGTCTCCCTCCGTGTCATCTCATCTGCATCTTCTGCTGGAGACG 776
QY 267 LeuProAspPheArgAspArgAspGlyThrGlyLeuAlaAlaAlaAlaGly 286
Db 775 CTGCGGAGATTCAAGGAGAGAGAG----- 749
QY 287 ProValPheProAlaProLeuAlaGlnGlySerSerGlnMetProGlyAsnProProArgLeu 306
Db 748 -----TACCTGCAGCGCGGGGCACTCCAGCGA-----GCCGACACGAGATTACG 701
QY 307 ProPheAsnAspProPhePheValValGluThrLeuCysIleGlySTPPhSerPheGlu 326
Db 700 CCTTCAACAGACCCCTTTTCATCTGTCAGACGCTGCATCATCTGTTCTCTTTCAG 641
QY 327 LeuLeuValArgLeuLeuValCysProSerLysAlaIlePhePheLysAsnValMetAsn 346
Db 640 ATTATATTGCTGCTTCTGCGCACGCCCAAGACCGGCTTCTTAAACATCATGAC 581
QY 347 LeuIleAspPheValAlaIleLeuProTyrPheValAlaLeuGlyThrGluLeuAlaArg 366
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QY 407 ThrLeuArgAlaSerMetArgGluLeuGlyLeuLeuIlePhePheLeuPheIleGlyVal 426
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QY 427 ValLeuPheSerSerAlaValTyrPheAlaGluValAspArgValAspSerHisPheThr 446
Db 341 ATCTCTCTTCCAGCGGGGTACTTCCGCGAGGGGAGCGAGCCACTCCCACTTCACC 282
QY 447 SerIleProGluSerPheTyrTPrAlaValValIleThrMetThrThrValGlyTyrGlyAsp 466
Db 281 AGCATCCCGCGCGGTCTGCTGGCTGTGTACCATGACAGAGGTCGCTACGGCGAT 222
QY 467 MetAlaProValThrValGlyGlyIleValGlySerLeuCysAlaIleAlaGlyVal 486
Db 221 ATGAAGCCTATACGAGTGGGGAGAGATCTGGGCTCCCTCGGCTGCGGAGTGGGGGCTG 162
QY 487 LeuThrIleSerLeuProValIleValSerAsnPheSerTyrPheTyrHisArg 506
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QY 507 GluThrGluGluGluGlu 512
Db 102 GAGACGATTAACGAAGAC 85

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RESULT 4
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 LOCUS CNS03DKC 839 bp DNA linear GSS 15-MAY-2000

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DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
ACCESSION 017A20 of library G from Tetraodon nigroviridis, genomic survey
VERSION AL239205
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis.
REFERENCE 1 (bases 1 to 839)
AUTHORS Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
HUMAN gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
TITILE Unpublished
JOURNAL 2 (bases 1 to 839)
REFERENCE Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
AUTHORS Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITILE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL 3 (bases 1 to 839)
REFERENCE Genoscope.
AUTHORS Submitted (12-APR-2000)
JOURNAL This sequence is a single read and was generated as part of a large
COMMENT scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
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Alignment Scores:
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Score: 896.00 Matches: 176
Percent Similarity: 73.63% Conservative: 39
Best Local Similarity: 60.27% Mismatches: 57
Query Match: 30.71% Indels: 20
DB: 17 Gaps: 3
US-09-804-014a-8 (1-559) x CNS03DKC (1-839)
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Db 778 GAGACCCCTCTGGGGAAACCCAGGAAAGAGATGCGCTTCTGACCCGCTGGAGACAG 719
QY 158 TyrPhePheAspArgAlaArgProSerPheAspAlaValLeuTyrTyrGlnSerGly 177
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QY 178 GlyArgLeuArgArgProAlaHisValProLeuAspValPheLeuGluGluValAlaPhe 197
Db 658 GGCCGGCTGAGGGGCGGCGTCACAGCTCCGCTGACATGTTCTGAGAGAGATCAATTC 599
QY 198 TyrGlyLeuGlyAlaAlaLeuAlaArgLeuArgGluAspGluGlyCysProValPro 217
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Qy	218	ProglutAqPProLeuPArGAlgaIphaeIAalvgnLnuETxPLeuLeuPhelUhe	237
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Qy	238	ProGlusSerSergInIAaIAalArgValLeuaIAvalISerValLeuValIIleuVal	257
Db	478	CCGAGACTTGGGNCGCCGGGAGCATGCCATCGTCTGTGATGATCACTTCATC	419
Qy	258	SerIleValIAIPhecysLeuGIuThrIleuProAspPheaIrgAspAspArgspLythr	277
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Qy	278	GLyeuIAaIAaIAaIAaIAaIaglyProValPheProAlaproLeuAAnglyserSer	297
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Qy	298	glnMetProGIyAsnProProArgIleuProPheAsnAspProPhePheValIAgluThr	317
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Db	100	GAGCAGGCGACCTGCTGCTGGCATCTCAGGGGTCATCCGCTGGTCCGCTTCGCAATC	41
Qy	392	PheIyLSerArGIhisSerIySGIyLeuGlnIle	403
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ACCESSION	B1117089		
VERSION	B1117089.1	GI:14567990	
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SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	NIH-MGC http://mgi.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: rgs@bbs-research.nih.gov Tissue Procurement: DCTD/DTP cDNA Library Preparation: Lung Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov Plate: LCM1026 row: d column: 21 High quality sequence stop: 830. Location/Qualifiers		
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		adaptor: GGCACGAG(G). Size-selected >500bp for average	
		insert size 1.8kb. Library constructed by Ling Hong in	
		the laboratory of Gerald M. Rubin (University of	
		California, Berkeley) using ZAP-cDNA synthesis kit	
		(Stratagene) and superscript II RT (Life Technologies)."	
		(Stratagene) and superscript II RT (Life Technologies)."	
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Query Match:	30.57%	Indels:	22
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QY	219 GluArgProLeuProAlaArgAlaPheAlaArgLnuEnturPleuleuPheglunPhePro	238	
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QY	359 AlaLeuGlyThrGluLeuAlaArgGln-ArgGly-----ValGlyGlnAlaMetSe	376	
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Qy 434 yrrPheAlaGlyValAspArgValAspSerHis-PheThrSerIleProGlyUserPheTrp 453
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Qy 454 TrpAlaValVal 457
Db 865 TGGCGGTGCTG 876
RESULT 6
BM963332 745 bp mRNA linear EST 18-MAR-2002
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IMAGE:5697484.5', mRNA sequence.
ACCESSION BM963332
VERSION BM963332.1 GI:19546752
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL 1 (bases 1 to 745)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pyx-5
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Location/Qualifiers
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/tissue_type="whole brain"
/dev_host="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/note="Organ: brain; Vector: pYX-asc; Site: 1: EcoR I;
Site: 2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
sequenced directionally into pYX-asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CAGCCAGCAGC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP). 'Gene discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemlin Chin, Ph.D., program coordinator."

BASE COUNT 139 a 216 c 202 g 188 t
ORIGIN
Alignment Scores: 3,43e-56 Length: 745
Pred. No.: 1

Score: 853.00 Matches: 176
Percent Similarity: 77.91% Conservative: 18
Best Local Similarity: 70.68% Mismatches: 29
Query Match: 29.23% Indels: 26
DB: 14 Gaps: 5
US-09-804-014a-8 (1-559) x BM963332 (1-745)
Qy 319 CysIleCysTrpPheSerPheGlyLeuValAlaArgLeuValCysProSerLysAla 338
Db 3 TGTATCGTCGTGTTCAAGCTTTGAGCTCTGCTGGCTTCTCGCTGCTCCAGCAAGGCG 62
Qy 339 IlePhePheLysAsnValMetAsnLeuIleAspPheAlaIleLeuProTyrPheVal 358
Db 63 GCCTCTTTTGGCAATATCATGAAATCATGACTTGTGGTCCATTTCCTTATTC 122
Qy 359 AlaLeuGlyThrGlyLeuAlaArg-----GlnArgGlyVal----- 370
Db 123 ACCTTGGGCAACCGAGCTAGTGCACAGCTACGACGACGAGCTGTGAGTGGTGCAGTGT 182
Qy 371 -----GlyGlnGlnAlaMetSerLeuAlaIleLeuArgValIleArgLeuValArgVal 388
Db 183 CAGATGGGCGACGAGCGCATGTCCTTACCATCTCCTGAGGTGATCCGCGTGGTCCGGGTG 242
Qy 389 PheArgIlePheLysLeuSerArgHisSerLysGlyLeuGlnIleLeuGlyGlnThrLeu 408
Db 243 TTCCGATCTTTCACAGCTCTCCGCCCATTCACAGGGGCTGAGATCCCTGGTAAAGCTTA 302
Qy 409 ArgAlaSerLeuArgGlyLeuGlyLeuIleIlePhePheLeuHelIleGlyValIleLeu 428
Db 303 CAGCGCTCCATGGGCGGAGCTGCGCTCTCATCTTCTCTTCATCGGAGCATCTC 362
Qy 429 PheSerSerAlaValTyrPheAlaGlyValAspArgValAspSerHisPheThrIle 448
Db 363 TTTTTCAGCGCTGTCTACTCTCGCAGAGCGTGAAGATGTTGATCGCTTCCCTAGATC 422
Qy 449 ProGlySerPheTrpIleValValIleMetThrThrValIleGlyGlyAspMetAla 468
Db 423 CCAGATGCTCTTCTGCTGGCTGTGTACCAATACACACGCTAGATGATGGGACATGTAC 482
Qy 469 ProValThrValGlyGlyLysIleValGlySerLeuCysAlaIleAlaGlyValIleThr 488
Db 483 CCATGACGCTAGGGGCGAGATGTGGCTCACTGCGCCCATGCTGGGCTCCTAC 542
Qy 489 IleSerLeuProValProValIleValIleAsnPheSerTrpPheTrpHisArgGlyThr 508
Db 543 ATTGCATTTACGGGTACCGGTCATTTCTCCATTTTCAACTTTCATACACGAGAGAG 602
Qy 509 GlyGlyGlyGlyAlaGlyLysPheSerHisValAspMet-----GlnProCysGlyProLeu 527
Db 603 GACGAGAGAGGAGGAGGAGCCAGTATACCCACGCTACTTGTGGCAGCCACTCCGAGACTTG 662
Qy 528 GluGlyLysAlaGlnGlyGlyLeuValAspGlyGlyValProGlyLeuProProProLeu 547
Db 663 AAGGCAACGAGCAATGG-----CTT 683
Qy 548 Trp-----AlaProProArgGlyHis 554
Db 684 TGGCACTGACTTGGCGAGAGCTTTCAC 710
RESULT 7
A2339279/c 636 bp DNA linear GSS 29-SEP-2000
LOCUS A2339279
DEFINITION IM0070M07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0070M07 R, DNA sequence.
ACCESSION A2339279
VERSION A2339279.1 GI:10413383
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 636)

Alignment Scores:

Pred. No.:	1,59e-51	Length:	954
Score:	794.00	Matches:	176
Percent Similarity:	69.74%	Conservative:	36
Best local Similarity:	27.89%	Mismatches:	68
Query Match:	27.21%	Indels:	24
DB:	14	Gaps:	7

US-09-804-014a-8 (1-559) x B0714749 (1-954)

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QY 123 GlyLeuAArgHegLurHrArgAlaArgThLeuArgPheProAspThrLeuGly 142
    |||||.....
DB 2 GGTTCGGCTTTGAGACGACGTGGCACCCTGGCGAGTTTCCCAACACCCTCTGGG 61

QY 143 AspProAlaArgArgGlyArgPheTyAspAspAlaArgArgLurGlyPhePheAspArg 162
    |||||.....
DB 62 GACCCAGTCAACGCCCGCTACTTGATCCCTGGAATGATGACTTCTTGACACCG 121

QY 163 HisArgProSerPheAspAlaValLeuTyTrpTyrGlnSerGlyArgLeuArgArg 182
    .....
DB 122 AACCGGCTGATTCGATGACATTTTACTACTACAGTCTGGGGCCGCTGCGAGG 181

QY 183 ProAlaHisValProLeuAspValPheLeuGluGluValAlaPheTyArgGlyLeuGlyAla 202
    |||||.....
DB 182 CCGGTCAATGTCCTCCGATGATGTTGACAGATGATCCGCTTACAGCTGGGGAC 241

QY 203 AlaAlaLeuAlaArgLeuArgGluAspGluGlyCysProValProProGluArgProLeu 222
    |||||.....
DB 242 GAGGCCATGAGACGCCCTCCGGAGATGAAGGCTTCATCAAGAGAGAGAACCCCTG 301

QY 223 ProArgArgAlaPheAlaArgGlnLeuTrpLeuPheGluPheProGluSerSerGln 242
    |||||.....
DB 302 CCCCAGTAATGATTCACGCGAGGTGGCTTATCTTCATATCCAGAAAGCTCTGGG 361

QY 243 AlaAlaArgValLeuAlaValSerValLeuValIleLeuValSerIleValValPhe 262
    .....
DB 362 TCAGCAAGACCCATGCGCATCGTCGTGTCATCTCATCTCATCATCACCCTTC 421

QY 263 CysLeuGluThrLeuProAspPheArgAspAspArgAspGlyThrGlyLeuAlaAla 282
    |||||.....
DB 422 TCGCTGAGACTCGCTGAGTTCAGGATGAACGAGGAG-----CTGTTACGCCAC 472

QY 283 AlaAlaAlaGlyProValPheProAlaPro-----LeuAsnGlySer----- 296
    |||||.....
DB 473 CCCCAGTGGCGCGCCAGCCCGCCAGCCCGCCAGGAGCAATGAGGAGGCTGTGT 532

QY 297 -----SerGlnMetProGlyAsnProProArgLeuPro-----PheAsnAspProPhe 312
    |||||.....
DB 533 GTCCCTTTCCTGCGCCACAGTGGCTCGCTGCTAGGACACTGGCTGACCCATTC 592

QY 313 PheValValGluThrLeuCysIleCysTrpPheSerPheGluLeuValArgLeuLeu 332
    |||||.....
DB 593 TTCATCGTGGAGAACACATGTGATCTGTGCTACTTTGAGCTGCTGGCGCTTCTTT 652

QY 333 ValCysProSerLysAlaIlePhePheLysAsnValIleCysLeuIleAspPheValAla 352
    |||||.....
DB 653 GCTTGGCCCGCAAGAGAGATTCCTCTCGGAATATTATGAACATCATTTGATGTGCC 712

QY 353 IleLeuProTyrrPheValAlaLeuGlyThrGluLeuAlaArg-----GlnArgGly--- 369
    |||||.....
DB 713 ATCTCCCTACTTTATCACTGGGCGCCAGGAGCTGGCAGAGCAAAAGGGGGTGG 772

QY 370 -----ValGlyGlnGlnAlaMetSerLeuAla-IleLeuArgValIleArg-LeuV 386
    .....
DB 773 GGGGTCAAAATGGGCAACAGGCGCATTCCTCAAGCAATCTCTAGGGTGTGATCCGCCCTGG 832

QY 386 alaArgValPheArgIle-Phe-LysLeuSerArgHisSerLysGly---LeuGlnIleLe 404
    |||||.....
DB 833 CCGGGGTGTTCACAAATCTTCACAGGTTTCCCGCCCTTTCAAGGAAACTTGCAAAATCTCT 892

QY 404 uGly 405
    |||||

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```

DB 893 CCGG 896

RESULT 9
BC023222/c
LOCUS
DEFINITION
5', mRNA sequence.
ACCESSION
B0714749
VERSION
B0714749.1 GI:21853648
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 954)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: Resgen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13731 row: 1 column: 17
High quality sequence stop: 576.
Location/Qualifiers
1.954
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:6310048"
/clone_1ib="NIH-MGC_129"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Olfactory epithelium; Vector:
pcwv-SPOK6.1.ccd; Site_1: EcoRV; Site_2: NotI; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
2.2 kb. Constructed by Resgen, Invitrogen Corp. Note: this
is a NIH-MGC Library."
BASE COUNT
179 a 284 c 254 g 237 t
ORIGIN

Alignment Scores:
Pred. No.: 6.51e-49 Length: 2146
Score: 765.00 Matches: 18
Percent Similarity: 56.25% Conservative: 9
Best local Similarity: 37.50% Mismatches: 19
Query Match: 26.22% Indels: 2
DB: 11 Gaps: 1

US-09-804-014a-8 (1-559) x BC023222 (1-2146)

QY 3 ArgArgArgThrGlySerArgArgGlnLys-----AspGlyGluLysGlyAspProGly 20
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DB 1702 AAGAAAGCGACAGAGAAACGAGAAAGACGAGAGAGCGAGAGAGAGAGAGAGAGAG 1643

QY 21 ThrGlyLysAlaGlnSerArgArgGlyArgArgArgArgArgGlyArgGlyArgGlyAla 40
    |||||.....
DB 1642 AAAGGAGAAACGAGAAACGAGAAAGAGACGAGAGAAACGAGAGAAAGAGAGAGAGAG 1583

QY 41 SerArgGlnArgAlaArgGlyArg 48
    .....
DB 1582 AACAGACAGAGAAAGAAACGAGAG 1559

RESULT 10
CNS058RO
LOCUS
DEFINITION
Tetradon nigroviridis genome survey sequence T7 end of clone
02019 of library A from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION
AL326301

```


KEYWORDS	AL326301.1	GI:8219890
REVISIONS	GSS: genome survey sequence.	
SOURCE	Tetraodon nigroviridis.	
ORGANISM	Tetraodon nigroviridis	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.	
AUTHORS	1 (bases 1 to 1060) Roest-Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Mincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.	
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 1060) Roest-Crolius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.	
AUTHORS	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis	
TITLE	Unpublished	
JOURNAL	3 (bases 1 to 1060) Genoscope.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (12-APR-2000)	
TITLE	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon .	
COMMENT	Location/Qualifiers	
FEATURES	1..1060 /organism="Tetraodon nigroviridis" /db_xref="taxon:99883" /clone="020L19" /clone_lib="A" /note="Genoscope sequence ID : CONA020CF10C1-end : T7"	
SOURCE	BASE COUNT 238 a 239 c 231 g 309 t 43 others	
ORIGIN		
Alignment Scores:		
Pred. NO.:	6.84e-49	Length: 1060.
Score:	760.50	Matches: 151
Percent Similarity:	82.55%	Conservative: 24
Best Local Similarity:	71.23%	Mismatches: 34
Query Match:	26.06%	Indels: 4
DB:	17 Gaps:	2
US-09-804-014A-8 (1-559) x CNS058RO (1-1060)		
OY	303 PROProAArgLeuProPheAsnAspProPhePheValAlaGluThrLeuCysIleCysTrp	322
Db	15 CCATCTCCNNGAAGCATCTCCNATCCCTTCTTCATCTCGAGACCGCTTGATTCCTGG	74
OY	323 PheSerPheGluLeuLeuValAlaArgLeuLeuValCysProSerLysAlaIlePhePheLys	342
Db	75 TTCCTTTTGGAGCTGTGTGTGATTTTGGGTCTCTCTACAGAAAGATTCTTCCAC	134
OY	343 AsnValMetAnLeuIleAspPheValAlaIleLeuProTyrrPheValAlaLeuGlyThr	362
Db	135 AACCTCATGACATATTGATATCTCATTCATCATCATCTTATTTTGTAAACCGGTGACA	194
OY	363 GluLeu-----AlaArgGlnArgGlyAlaGlyGlnGlnAlaMetSerLeuAlaIleLeu	380
Db	195 GAAATCTTCACAAACCGGAGAGAGAGCTCAGAGACAGAAC---ATGTCTTTGGCCATTCTG	251
OY	381 ArgValIleLeuGluLeuValAlaArgAlaPheArgIlePheLysLeuSerArgHisSerLysGly	400
Db	252 CGCATCATTCGCTCGCTGTAGAGTATTCGTTATTTTCAACACTCTCCAGCATTTCCAAAGGT	311
OY	401 LeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgGluLeuGlyLeuLeuIlePhe	420
Db	312 CTGCAGATCTCTGGACACACCCCTGAAGGAAAGACATGCGTGA-NTTGATTTGGCTCATTTT	370

Oy	421	PheuuPheilleglYvalValluehpserSerlaValTyPhpeAlagluValAsparg	440
Dd	371	TTCCTCTTCAACGGGAGGTATCCTCTTCCACAGTGTACTACTTTGCCGAGGTGCAGAG	430
Oy	441	ValasSerHisphrThSerlleProgluSerPherIPTRPalAvalValThmetThr	460
Dd	431	CCAACACGAGATTGTTAGCATACCAGTGCTCTGTGGCGCGCTGTAACCATGACT	490
Oy	461	ThraValglyTYRglYaspMetalaProValIthrValJlglyIghysIlleValIglySerIue	480
Dd	491	ACTGTCGGTTATGGGACATGTGTCCTCACACCTTGGGAGGCAAATAATGTGGGACGCTG	550
Oy	481	CysAlallealaglValIueThrlleserIueProValIProValIIeValSeranPhe	500
Dd	551	TGCGCATCGCTGGAGTGTACTAACCTTGTCTGTGCTGTGCCGTGCCGTCATTTGCCACTTT	610
Oy	501	SerTYrPhetyrHIsArvgluThrgluIglugluIu	512
Dd	611	AACCTACTCTACACAGAGACAGAACTGTGAGC	646
RESULT 11			
BG812963			
LOCUS	BG812963	559 bp	mRNA linear EST 22-MAY-2001
DEFINITION	da3f3603.y1 NICHD XGC Brn1 Xenopus laevis cDNA clone IMAGE:4740197		
KEYWORDS	5' similar to TR:070259 070259 VOLTAGE-GATED POTASSIUM CHANNEL		
ACCESSION	BG812963		
VERSION	BG812963.1	GI:14183943	
KEYWORDS	EST.		
ORGANISM	Xenopus laevis		
SOURCE	African clawed frog.		
REFERENCE	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;		
AUTHORS	Xenopodinae; Xenopus.		
JOURNAL	1 (bases 1 to 559)		
COMMENT	Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.		
	WashU Xenopus EST project, 1999		
	Unpublished (1999)		
	Contact: Sandy Clifton, Ph.D.		
	WashU Xenopus EST Project, 1999		
	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: est@watson.wustl.edu		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA Sequencing by: Washington University Genome Sequencing Center		
	clone distribution: Xenopus clones from this library are available		
	through the I.M.A.G.E. Consortium/LNLN at: info@image.lnl.gov		
	High quality sequence stop: 420.		
FEATURES	Location/Qualifiers		
SOURCE	1..559		
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	/db_xref="taxon:8355"		
	/clone="IMAGE:4740197"		
	/clone_id="NICHD XGC Brn1"		
	/dev_stage="adult"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: brain; Vector: PCMV-SPORT6; Site_1: NotI;		
	Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.		
	Average insert size 1.5 kb. Constructed by Life		
	Technologies. Note: This is a Xenopus Gene Collection (XGC		
) library."		
BASE COUNT	135 a	133 g	171 t
ORIGIN	120 c		
Alignment Scores:	6.5e-48	Length:	559
Pred. No.:			

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL.3 ; mRNA sequence.

ACCESSION BM128683

VERSION BM128683.1 GI:17122327

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 575)

AUTHORS

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Maria, M., Pape, D., Wylie, T., Martin, J., Blistein, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y., and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brownjefas.harvard.edu) This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov

High quality sequence stop: 429.

FEATURES

source

Location/Qualifiers

1..575

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5676446"

/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"

/sex="Both"

/tissue_type="Islets of Langerhans"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Organ: Pancreas; Vector: pSPOR1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using

SuperScript Plasmid library kit (Life Technologies). cDNA

made by oligo-dT priming. Size-selected by column

fractionation; average insert size 1.08 kb. Library was

amplified once on solid support and plasmid DNA from

library was prepared. The library DNA was normalized by

method #4 from Bonaldo, Lennon, and Soares 1996 Genome

Research 6:791-806; 0.5 microgram single-stranded library

plasmid DNA was mixed with 5 micrograms PCR product

representing library inserts and hybridized to an EcoT of

20. Single-stranded (unhybridized) plasmids were isolated

by hydroxyapatite chromatography and used to make this

library."

library"

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|||||

62 GGACAGCAGCCATGCTCTGCGCCATCGAGCGTCATCGCTCGTAAGGCTTCCCG 121

QY 391 IIEpHelylsuSerArghsSerlysglyleuGlnlleuenglylnhrleuAga1a 410

Db 122 ATCTTCAAGCTGTGCGCCATCTCAAGGGCTCAGATCTCGGGAACGCTGAAGGCG 181

QY 411 SerMetArgIuLeuGlyLeuLeuIlePhePheLeuPheIleGlyValValLeuPheSer 430

Db 182 TCCATCGGAGCTGGATGATGTCATCTTCTTATTTGGGTCATCTTTCTTC 241

QY 431 SerAlaValTyrPheAlaGlyValAspArgValAspSerHisPheThrSerIleProGlu 450

Db 242 AGCGCGCTACTTTCGCCGAGCAGACCCACCTTCAAGTTTCAGACGATCCCGAT 301

QY 451 SerPheTyrPheAlaValTyrMetThrValGlyTyrGlyAspMetAlaProVal 470

Db 302 GCTTCTGTGGGCGATGTGATACCATGACACAGTGGTACGCGATATGACCCAGTG 361

QY 471 ThrValGlyTyrIleValGlySerLeuGlyAlaIleAlaGlyValLeuThrIleSer 490

Db 362 ACCATAGGGGCGAGATGTGGGATCTCTGTGCGCATGCGGCTGTGACCATCGCA 421

QY 491 LeuProValProValIleValSerAsnPheSerTyrPheTyrHisArgIuThrGlyGly 510

Db 422 TTGCGATTCGCGGTATGTTTCCACTTCACTTACACCGGAGACAGAAAGG 481

QY 511 GluGlnAlaGlyMetPheSerHisValAspMetGlnProGlyProLeuGlyGly 530

Db 482 GAAGACCAATCCCATGATGACAGGGAAGTGGCAGCACTCTCTTCAACCGGAG 541

QY 530 salaaSn 532

Db 542 GAGCTCC 548

RESULT 14

BM128211

LOCUS

DEFINITION

BM128211 593 bp mRNA linear EST 12-MAR-2002

1 f10h09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens

CDNA clone IMAGE:5676160 5' similar to SW:CIK3_HUMAN P22001

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL.3 ; mRNA sequence.

ACCESSION BM128211

VERSION BM128211.1 GI:17122763

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 593)

AUTHORS Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,

Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Maria, M., Pape, D., Wylie, T., Martin, J., Blistein, A.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas,

M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,

Jackson, Y., and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Juliana Brown

(brownjefas.harvard.edu) This sequence now available from the IMAGE

consortium, for clone orders contact: info@image.llnl.gov

High quality sequence stop: 438.

Location/Qualifiers

1..593

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5676160"
/clone.lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/Note="Organ: Pancreas; Vector: pSPORT1; Site: 1; Not 1; Site: 2: Sal 1: Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldi, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
BASE COUNT      125 a      164 c      162 g      142 t
ORIGIN
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Best Local Similarity: 78.69%      Mismatches: 18
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DB:             13      Gaps:        0

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QY 431 SerAlaValTyrrPheAlaGluValaAspArgValaAspSerHisPheThrSerIleProGlu 450
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LOCUS
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sequence.
ACCESSION
AL198511.1 GI:7836662
VERSION
GSS: genome survey sequence.
KEYWORDS
Tetradodon nigroviridis.
SOURCE
Tetradodon nigroviridis.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetradontiformes;
Tetraodontidae; Tetradodon.
1 (bases 1 to 963)
REFERENCE
1 Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
Roest-Crolius,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetradodon nigroviridis DNA sequence
JOURNAL
Unpublished
2 (bases 1 to 963)
REFERENCE
1 Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradodon nigroviridis
Unpublished
3 (bases 1 to 963)
REFERENCE
Genoscope.
Direct Submission
Submitted (12-APR-2000)
JOURNAL
TITL
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradodon.
location/Qualifiers
1.963
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DB:             17      Gaps:        4

US-09-804-014a-8 (1-559) x CNS0215Y (1-963)
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QY 69 AlaGlyLeuPheTyrrAlaArgThrProAspThrGlyHisArgAlaGlyAlaValaGly 88
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Db 785 GCAGA-ATGACTGTGGM--ACAGGCGACCCCTGACGAGCGGCGACACCCAGGG 730
QY 89 AlaThrArgArgPheAlaGlyArgArgGlyCysAlaArgHisGlyAlaAlaValaProAla 108
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Db 729 CACCCGACGACGACGAT-----CCGAG 706
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Db 585 GCGGATTTTCGATCCGCGAGAGAAATGATATTTTTCGATAGGAACAGACCGAGTTTCA 526
Qy 168 PALaValLeuTyTYrTYrGlnSerGlyGlyArgLeuArgArgProAlaHisValProLe 188
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Qy 208 uArgGluAspGluGlyCysProValProGluArgProLeuProArgArgAlaPheAl 228
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Qy 228 aArgGlnLeuTrpLeuLeuPheGluPheProGlnSerSerGlnAlaAlaArgValLeuAl 248
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Qy 288 lPheProAlaProLeuAsnGlySerSerGlnMetProGlyAsnProProArgLeuPro-- 307
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Qy 308 -----PheAsnAspProPhePheValValGluThrLeuGlyIleCysTrpPh 323
Db 141 TACAGCCACATACCTTACCGACCACTCTTATVCTTAGAGACACTCTGCATCATATAGTT 82
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Qy 343 nValMetAsnLeuIleasp 349
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Job time : 2250 secs

GenCore version 5.1.3
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Run on: February 20, 2003, 04:22:08 ; Search time 682.436 Seconds
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Title: US-09-804-014A-7_COPY_382_631

Perfect score: 250

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
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- 6: gb_pat.*
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- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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3	250	100.0	1747	6	AX268121	AX268121 Sequence
4	250	100.0	4372	9	HS310479	HS310479 Homo sapi
c	250	100.0	157633	9	AC008687	AC008687 Homo sapi
5	216.4	86.6	91668	2	AC095540	AC095540 Rattus no
6	216.4	86.6	172671	2	AC128792	AC128792 Rattus no
c	216.4	86.6	208632	2	AC073711	AC073711 Mus muscu
7	213.2	85.3	1075	10	MMKNC1	AF032100 Mus muscu
8	213.2	85.3	1599	6	I26643	I26643 Sequence 9
9	213.2	85.3	1599	6	I26643	AF032099 Mus muscu
10	162.2	64.9	445	10	MMU409348	AF032099 Mus muscu
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13	155	62.0	780	9	HS3337055	AJ337055 Homo sapi
14	153.4	61.4	444	9	HS336845	AJ336845 Homo sapi
15	150.2	60.1	609	9	HS337128	AJ337128 Homo sapi
16	146	58.4	1780	4	CFU08596	U08596 Canis fami
17	145	58.0	2098	10	RATKV2AA	M27159 Rat potassi
18	145	58.0	2743	10	RRCK2	X17621 Rat RCK2 mR
19	145	58.0	191664	2	AC125751	AC125751 Rattus no
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23	140.2	56.1	3219	10	MUSMURINE	M95688 Mus musculu
24	140.2	56.1	259159	2	AC124756	AC124756 Mus muscu
25	139.8	55.9	2755	9	HUMPOTCH	M83254 Human card
26	139.8	55.9	185952	9	AC005906	AC005906 Homo sapi
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27	139.6	55.8	1836	9	HUMPOCH	L23499 Homo sapien
28	139.6	55.8	2397	9	HUMKCHN	M38217 Homo sapien
29	139.6	55.8	90458	2	AL513469	AL513469 Homo sapi
30	139.6	55.8	150001	9	AC006063	AC006063 Homo sapi
31	139.6	55.8	155343	9	AL365361	AL365361 Human DNA
c	138	55.2	1551	4	OCU38240	U38240 Oryctolagus
32	138	55.2	1883	10	RATRGK5	M30312 Rat voltage
33	136.4	54.6	1994	6	AR050270	AR050270 Sequence
34	136.4	54.6	1994	6	AR050270	M30441 Mouse intro
35	136.4	54.6	2264	10	MUSMK3A	M31744 Rat potassi
36	136.4	54.6	2956	10	RNRCK3	X16001 Rat mRNA fo
37	136.4	54.6	3004	9	HUMKCHAN	M85217 H.sapiens K
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39	134.2	53.7	752	9	HS3327766	AJ327766 Homo sapi
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ALIGNMENTS

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LOCUS AX352535
DEFINITION Sequence 7 from Patent WO0194390.
ACCESSION AX352535
VERSION AX352535.1 GI:18617765
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Curtis, R.A.
TITLE 52906, 33408, and 12189, potassium channel family members and uses thereof

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JOURNAL Patent: WO 0194390-A 7 13-DEC-2001;
FEATURES Millennium Pharmaceuticals, Inc. (US)
source Location/Qualifiers
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BASE COUNT 190 a 443 c 411 g 297 t
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Best Local Similarity 100.0%; Pred. No. 2.1e-31;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS Homo sapiens voltage-gated potassium channel KCNA7 mRNA, complete
DEFINITION cds.
ACCESSION AF315818
VERSION AF315818.1 GI:14485554
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1447)
AUTHORS Bardenkruger,S., Wulff,H., Arleff,H., Brink,P., Chandy,K.G. and Corfield,V.
TITLE Characterization of the human voltage-gated potassium channel gene, KCNA7, a candidate gene for inherited cardiac disorders, and its exclusion as cause of progressive familial heart block I (PFHBI)
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1447)
Bardenkruger,S., Wulff,H., Arleff,H., Brink,P., Chandy,K.G. and Corfield,V.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2000) SANBI, University of Western Cape, Modderdam Road, Cape Town 7535, South Africa
FEATURES Location/Qualifiers
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DB 196 CCGGAGTATTCTTCGACCGGACCGCGCGCGCGCGCTTCTACTACTACTACCA 255
QY 181 GTCGGTGGCGGCTGGCGGCGCGCGCGCGCGCTGCGCTGCGAGCTCTTCCTGGAAGAGGT 240
DB 256 GTCGGTGGCGGCTGGCGGCGCGCGCGCGCGCTGCGCTGCGAGCTCTTCCTGGAAGAGGT 315
QY 241 GGCCTTCTAC 250
DB 316 GGCCTTCTAC 325
RESULT 3
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LOCUS Sequence 7 from Patent WO0168851.
DEFINITION AX268121
ACCESSION AX268121
VERSION AX268121.1 GI:16516622
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Padigaru,M., Vernet,C.A., Fernandes,E., Shinkets,R.A., Spaderna,S.K., Majumder,K. and Li,L.
TITLE Polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0168851-A 7 20-SEP-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2e-31; Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 442 CTTCCGGGACACTCTGCTAGGAGACCCAGCGCGCGCGCGCTTCTAGCAGACGCGCG 501
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QY 121 CCGCGAGTATTTCTCGACCGGACCGCGCGCGCGCGCTTCGAGCGCGGCTCTACTACCA 180
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QY 181 GTCCGGTGGCGGCTGCGCGCGCGCGCGCACGCTGCGCGCTTCCTGGAAGAGT 240
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Db 562 GTCCGGTGGCGGCTGCGCGCGCGCGCGCACGCTGCGCGCTTCCTGGAAGAGT 621
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QY 241 GGCTTCTAC 250
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Db 622 GGCTTCTAC 631
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RESULT 4
HSA310479
LOCUS
DEFINITION
Homo sapiens mRNA for potassium voltage-gated channel,
shaker-related subfamily, member 7 (KCNA7 gene).
ACCESSION
AJ310479.1 GI:12830376
VERSION
KCN7 gene; Kv1.7 gene; potassium voltage-gated channel,
shaker-related subfamily, member*.
KEYWORDS
human.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 4372)
Kashuba,V.I., Kvasha,S.M., Protodopov,A.I., Gizatullin,R.2.,
Rynditch,A.V., Wahlestedt,C., Wasserman,W.W. and Zabarovsky,E.R.
Initial isolation and analysis of the human Kv1.7 (KCN7) gene, a
member of the voltage-gated potassium channel gene family
Gene 268 (1-2), 115-122 (2001)
MEDLINE
21261947
PUBMED
11368907
REFERENCE
2 (bases 1 to 4372)
Kashuba,V.
Direct Submission
AUTHORS
Submitted (09-FEB-2001) Kashuba V., Microbiology and Tumorbiology
Center, Karolinska Institute, Box 280, 171 77, SWEDEN
JOURNAL
Location/Qualifiers
FEATURES
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1. 4372
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/codon_start=1
/product="potassium voltage-gated channel, shaker-related
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/db_xref="GI:12830377"
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CLETLPDFRDRDDGTGLAAAGAAGFPAPLNGSSQMPGNPRLPNDFPFFVETLIC
WFSFELLVRLVCPSKAIFFXNMNLDVAILPYFVALGTALARQGVGGQMSLA
LRLVRLVRFRIKLSRHSKGLIQLIGQTLRASMRELGLLFIFFLFGVVLFSVAVFAE

VDRVDSHTSIPSEFWAVTMTTVGYGDMAPVTVGGKIVGSLCAIAGVLTISLPVPV
IVNSFYTHRETEGEAGMFSHVDTPCGPLEGRKANGLVDEVPFPPPLWAPPKG
HLVTEV"

BASE COUNT 930 a 1117 c 1408 g 917 t
ORIGIN

Query Match 100.0%; Score 250; DB 9; Length 4372;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCTGGTGCCTCAAGCTGGCGGGCTGGCTTCGAGACGGCGGCGCACGCTGGGCG 60
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Db 395 GCGGCTGGTGCCTCAAGCTGGCGGGCTGGCTTCGAGACGGCGGCGCACGCTGGGCG 454
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QY 61 CTTCCGGGACACTCTGCTAGGAGACCCAGCGCGCGCGCGCTTCTAGCAGACGCGCG 120
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Db 455 CTTCCGGGACACTCTGCTAGGAGACCCAGCGCGCGCGCGCTTCTAGCAGACGCGCG 514
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QY 121 CCGCGAGTATTTCTTCGACCGGACCGCGCGCGCGCTTCGAGCGCGGCTCTACTACCA 180
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Db 515 CCGCGAGTATTTCTTCGACCGGACCGCGCGCGCGCTTCGAGCGCGGCTCTACTACCA 574
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QY 181 GTCCGGTGGCGGCTGCGCGCGCGCGCGCACGCTGCGCGCTTCCTGGAAGAGT 240
|||||
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... QY 241 GGCTTCTAC 250
|||||
Db 635 GGCTTCTAC 644
|||||

RESULT 5
AC008687/c
LOCUS
DEFINITION
Homo sapiens chromosome 19 clone CTB-60B18, complete sequence.
ACCESSION
AC008687.5 GI:15887249
VERSION
HTG.
KEYWORDS
Homo sapiens.
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 157633)
DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS
Direct Submission
TITLE
Unpublished
JOURNAL
2 (bases 1 to 157633)
REFERENCE
2 (bases 1 to 157633)
DOE Joint Genome Institute.
AUTHORS
Direct Submission
TITLE
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
JOURNAL
3 (bases 1 to 157633)
DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
3 (bases 1 to 157633)
DOE Joint Genome Institute.
AUTHORS
Direct Submission
TITLE
Submitted (27-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
JOURNAL
4 (bases 1 to 157633)
DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
4 (bases 1 to 157633)
DOE Joint Genome Institute.
AUTHORS
Direct Submission
TITLE
Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
JOURNAL
COMMENT
On Oct 3, 2001 this sequence version replaced gi:10312243.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
STS Content:
SHGC-15869 G15229
SHGC-15864 G15225
SHGC-5822 G14090
SHGC-58615 G42524.


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* 16063 16162: gap of unknown length
* 16163 17546: contig of 1384 bp in length
* 17547 17646: gap of unknown length
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* 22037 22136: gap of unknown length
* 22137 23484: contig of 1348 bp in length
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* 27128 27227: gap of unknown length
* 27228 29339: contig of 2112 bp in length
* 29340 29439: gap of unknown length
* 29440 30983: contig of 1544 bp in length
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* 33046 34553: contig of 1508 bp in length
* 34554 34653: gap of unknown length
* 34654 36212: contig of 1559 bp in length
* 36213 36312: gap of unknown length
* 36313 38343: contig of 2031 bp in length
* 38344 38443: gap of unknown length
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* 39957 40056: gap of unknown length
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* 41781 43601: contig of 1821 bp in length
* 43602 43701: gap of unknown length
* 43702 45106: contig of 1405 bp in length
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* 47378 49203: contig of 1826 bp in length
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* 82813 82912: gap of unknown length
* 82913 85429: contig of 2517 bp in length
* 85430 85529: gap of unknown length
* 85530 88068: contig of 2539 bp in length
* 88069 88168: gap of unknown length

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/db_xref="taxon:10116"
/clone="CH230-8F24"
BASE COUNT 20713 a 21006 c 21177 g 21287 t 7485 others
ORIGIN
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Best Local Similarity 91.6%; Pred. No. 2.3e-26;
Matches 229; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 GGGGCTGGTGCACACGTGGCGGGCTGCGCTTCGAGACGCGGCGCGCACGCTGGGCGG 60
DB 75282 GCGGCTGGTGCACACGTGGCGGGTGGCTTCGAGACCGCGCGCGCACGCTCGGCGG 75341
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QY 181 GTCCGCTGGCGGCTGCGCGCGCGCGCACGCTGCGCGCTCGACGCTTCTCTGGAAGAGGT 240
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QY 241 GGCCTTCTAC 250
DB 75522 GTCCTTCTAC 75531

RESULT 7
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LOCUS Rattus norvegicus clone CH230-262A9, *** SEQUENCING IN PROGRESS
DEFINITION *** 55 unordered pieces.
ACCESSION AC128792.1 GI:21952595
VERSION AC128792.1
KEYWORDS HTG; HTGS-PHASE1.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 172671)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Haviak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsy,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlssohn,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louiseged,H.,
Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
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Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, L., Sodergren, E., Sonaite, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, F., Wu, F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Unpublished
2 (bases 1 to 172671)
Direct Submission
Worley, K.C.

Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KAJM
Center clone name: CH230-262A9
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 108496 bases at least Q40
Consensus quality: 114733 bases at least Q30
Consensus quality: 119570 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 55 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 3041 3140: gap of unknown length
* 3141 4347: contig of 1207 bp in length
* 4348 4447: gap of unknown length
* 4448 5658: contig of 1211 bp in length
* 5659 5758: gap of unknown length
* 5759 7065: contig of 1307 bp in length
* 7066 7165: gap of unknown length
* 7166 8912: contig of 1747 bp in length
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* 9013 10121: contig of 1109 bp in length
* 10122 10221: gap of unknown length
* 10222 11495: contig of 1274 bp in length
* 11496 11595: gap of unknown length
* 11596 12895: contig of 1300 bp in length
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* 16337 16436: gap of unknown length
* 16437 18286: contig of 1850 bp in length
* 18287 18386: gap of unknown length

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23103: contig of 1180 bp in length
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24338: contig of 1035 bp in length
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26341: contig of 1903 bp in length
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28299: contig of 1958 bp in length
28399: gap of unknown length
29886: contig of 1487 bp in length
29886: gap of unknown length
31191: contig of 1205 bp in length
31191: gap of unknown length
33131: contig of 1840 bp in length
33331: gap of unknown length
35206: contig of 1975 bp in length
35306: gap of unknown length
38250: contig of 2844 bp in length
38250: gap of unknown length
39679: contig of 1429 bp in length
39779: gap of unknown length
43111: contig of 3332 bp in length
43211: gap of unknown length
45028: contig of 1817 bp in length
45128: gap of unknown length
46530: contig of 1402 bp in length
46630: gap of unknown length
49509: contig of 2879 bp in length
49509: gap of unknown length
51389: contig of 1780 bp in length
51489: gap of unknown length
53715: contig of 2226 bp in length
53815: gap of unknown length
57135: contig of 3320 bp in length
57235: gap of unknown length
59889: contig of 2654 bp in length
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62234: contig of 2245 bp in length
62334: gap of unknown length
66086: contig of 3752 bp in length
66186: gap of unknown length
70673: contig of 4487 bp in length
70773: gap of unknown length
73088: contig of 2315 bp in length
73188: gap of unknown length
75049: contig of 1861 bp in length
75149: gap of unknown length
78164: contig of 3015 bp in length
78264: gap of unknown length
81938: contig of 3674 bp in length
82038: gap of unknown length
85018: contig of 2980 bp in length
85118: gap of unknown length
89432: contig of 4314 bp in length
89532: gap of unknown length
93510: contig of 3978 bp in length
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97371: contig of 3961 bp in length
97571: gap of unknown length
102274: contig of 4603 bp in length
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105519: contig of 3145 bp in length
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108265: contig of 2646 bp in length
108365: gap of unknown length
113533: contig of 5168 bp in length
113633: gap of unknown length
117825: contig of 4192 bp in length
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124230: contig of 6305 bp in length

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* 124231 124330: gap of unknown length
* 124331 129365: contig of 5035 bp in length
* 129366 129465: gap of unknown length
* 129466 136317: contig of 6852 bp in length
* 136318 136417: gap of unknown length
* 136418 144084: contig of 7667 bp in length
* 144085 144184: gap of unknown length
* 144185 151956: contig of 7772 bp in length
* 151957 152056: gap of unknown length
* 152057 159994: contig of 7938 bp in length
* 159995 160094: gap of unknown length
* 160095 172671: contig of 12577 bp in length.

FEATURES
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            /db_xref="taxon:10116"
            /clone="CH230-262A9"

Query Match      86.6%; Score 216.4; DB 2; Length 172671;
Best Local Similarity 91.6%; Pred. No. 2.1e-26;
Matches 229; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 GCGGCTGGTCTCAAGTCGCGCGGCTGCGCTTCGAGACGCGGCGCGACGCTGGCGCG 60
Db 86020 GCGGCTGGTCTCAAGTCGCGCGGTTGCGCTTCGAGACCGCGCGCGACGCTCGGCGG 86079

QY 61 CTTCCCGGACACTCTCTAGGGGACCCAGCGCGCGCGCGCTTCTACGAGCAGCGCGG 120
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Db 86140 CCGCGAGTATTCTTCGACCGACACCGGCCCGACGCTTCGATGCGGTCTCTACTACTACCA 86199

QY 181 GTCGCTGGCGGCTGCGCGCGCGCGCGCGCTGCGCTTCGAGCTTCTTCTTGAAGAGT 240
Db 86200 GTCAGCGCGCGGCTGAGACGCGCGCGCGCGCGCTGCGCTTCGAGCTTCTTCTTGAAGAGT 86259

QY 241 GGCCTTCTAC 250
Db 86260 GTCCTTCTAC 86269

RESULT 8
AC037371/c
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DEFINITION
AC037371
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 208632)
DOE Joint Genome Institute.
Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:8810328.
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 1810994
Center clone name: RPCI-23_193A10
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Summary Statistics
Consensus quality: 204234 bases at least Q40
Consensus quality: 207322 bases at least Q30
Consensus quality: 207805 bases at least Q20
Estimated insert size: 221930; agarose-fp estimation
Estimated insert size: 208382; sum-of-contigs estimation
Quality coverage: 8.77 in Q20 bases; agarose-fp estimation
Quality coverage: 9.34 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 93558: contig of 93558 bp in length
* 93559 93658: gap of unknown length
* 93659 94751: contig of 1093 bp in length
* 94752 94851: gap of unknown length
* 94852 118285: contig of 23434 bp in length
* 118286 118385: gap of unknown length
* 118386 157043: contig of 38658 bp in length
* 157044 157143: gap of unknown length
* 157144 164561: contig of 7418 bp in length
* 164562 164661: gap of unknown length
* 164662 176791: contig of 12130 bp in length
* 176792 176891: gap of unknown length
* 176892 208632: contig of 31741 bp in length.

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            /db_xref="taxon:10090"
            /clone="RP23-193A10"
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BASE COUNT 48823 a 51932 c 52697 g 54580 t 600 others
ORIGIN

Query Match      86.6%; Score 216.4; DB 2; Length 208632;
Best Local Similarity 91.6%; Pred. No. 2e-26;
Matches 229; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 GCGGCTGGTCTCAAGTCGCGCGGCTGCGCTTCGAGACGCGGCGCGACGCTGGCGCG 60
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QY 61 CTTCCCGGACACTCTCTAGGGGACCCAGCGCGCGCGCGCTTCTACGAGCAGCGCGG 120
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QY 121 CCGCGAGTATTCTTCGACCGGACCGGCCCGACGCTTCGAGCGCGGCTCTACTACTACCA 180
Db 74468 CCGCGAGTATTCTTCGACCGACACCGGCCCGACGCTTCGATGCGGTGCTCTACTACTACCA 74409

QY 181 GTCGCTGGCGGCTGCGCGCGCGCGCGCGCTGCGCTTCGAGCTTCTTCTTGAAGAGT 240
Db 74408 GTCGCGCGCGGCTGAGACGCGCGCGCGCGCTTCTTCTTGAAGAGT 74349

QY 241 GGCCTTCTAC 250
Db 74348 GTCCTTCTAC 74339

RESULT 9
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LOCUS
DEFINITION
AC037371/c
VERSION
KEYWORDS
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PROJECT
CLONE
CENTER CLONE NAME
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SEGMENT 1 of 2
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1075)
AUTHORS Kalman,K., Nguyen,A., Tseng-Crank,J., Dukes,I.D., Chandy,G.,
Hustad,C.M., Copeland,N.G., Jenkins,N.A., Mohrenweiser,H.M.,
Brandriff,B., Cahalan,M.D., Gutman,G.A. and Chandy,K.G.
TITLE Genomic organization, chromosomal localization, tissue
distribution, and biophysical characterization of a novel mammalian
Shaker-related voltage-gated potassium channel, Kv1.7
J. Biol. Chem. 273 (10), 5851-5857 (1998)
JOURNAL 9488722
MEDLINE
PUBMED
REFERENCE 2 (bases 1 to 1075)
AUTHORS Kalman,K., Nguyen,A., Tseng-Crank,J., Dukes,I.D., Chandy,G.,
Hustad,C.M., Copeland,N.G., Jenkins,N.A., Mohrenweiser,H.M.,
Brandriff,B., Cahalan,M.D., Gutman,G.A. and Chandy,K.G.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-1997) Physiology and Biophysics, University of
California, Irvine, CA 92697, USA
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genes"
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BASE COUNT 190 a 343 g 351 g 191 t
ORIGIN
Query Match 85.3%; Score 213.2; DB 10; Length 1075;
Best Local Similarity 90.8%; Pred. No. 1.9e-25;
Matches 227; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 GCGGCTGGTCTCAACGTGGCGGGTTCGCTTCGAGACGGCGCGCGACGCTGGGCCG 60
Db 534 GCGGCTGGTCTCAACGTGGCGGGTTCGCTTCGAGACCGCGCGCGACGCTGGGCCG 593
QY 61 CTTCCCGGACACTCTGCTAGGACCGCCAGCTTCGACGCGCGCGCTTCTACGACGCGCG 120
Db 594 CTTCCCGGACACTCTGCTAGGACCGCCAGCTTCGACGCGCGCGCTTCTACGACGCGCG 653
QY 121 CCGCGAGTATTCTTCGACGCGCGCGCGCGCGCGCTTCGCTCTACTACTACCA 180
Db 654 CCGCGAGTATTCTTCGACGCGCGCGCGCGCGCGCTTCGCTCTACTACTACCA 713
QY 181 GTCGGTGGCGGCTGGCGGCGCGCGCGCGCGCGCTTCCTCTGGAAGAGGT 240
Db 714 GTCGGGCGCGCGCTGAGACGCGCGCGCGCGCGCGCTTCCTCTGGAAGAGGT 773
QY 241 GGCCTTCTAC 250
Db 774 GTCCTTCTAC 783
RESULT 10
I26643
LOCUS I26643
DEFINITION Sequence 9 from patent US 5559009.
ACCESSION I26643
VERSION I26643.1 GI:1606513
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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```
Unclassified.
1 (bases 1 to 1599)
Chandy,K.G., Kalman,K., Chandy,G. and Gutman,G.A.
Voltage-gated potassium channel gene, Kv1.7, vectors and host cells
comprising the same, and recombinant methods of making potassium
channel proteins
Patent: US 5559009-A 9 24-SEP-1996;
FEATURES
source Location/Qualifiers
1..1599
/organism="unknown"
BASE COUNT 233 a 521 c 502 g 343 t
ORIGIN
Query Match 85.3%; Score 213.2; DB 6; Length 1599;
Best Local Similarity 90.8%; Pred. No. 1.8e-25;
Matches 227; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 GCGGCTGGTCTCAACGTGGCGGGTTCGCTTCGAGACGGCGCGCGCGCTGGGCCG 60
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QY 61 CTTCCCGGACACTCTGCTAGGACCGCCAGCTTCGACGCGCGCGCTTCTACGACGCGCG 120
Db 333 CTTCCCGGACACTCTGCTAGGACCGCCAGCTTCGCGCGCGCGCTTCTACGACGCGCG 392
QY 121 CCGCGAGTATTCTTCGACGCGCGCGCGCGCGCGCTTCGCTCTACTACTACCA 180
Db 393 CCGCGAGTATTCTTCGACGCGCGCGCGCGCGCGCTTCGCTCTACTACTACCA 452
QY 181 GTCGGTGGCGGCTGGCGGCGCGCGCGCGCGCGCTTCGCTCTGGAAGAGGT 240
Db 453 GTCGGGCGCGCGCTGAGACGCGCGCGCGCGCGCTTCGCTCTGGAAGAGGT 512
QY 241 GGCCTTCTAC 250
Db 513 GTCCTTCTAC 522
RESULT 11
AF032099
LOCUS AF032099
DEFINITION Mus musculus voltage-gated potassium channel Kv1.7 (Kcnc7) mRNA,
complete cds.
ACCESSION AF032099
VERSION AF032099
KEYWORDS
SOURCE AF032099.1 GI:3004906
ORGANISM Mus musculus.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Kalman,K., Nguyen,A., Tseng-Crank,J., Dukes,I.D., Chandy,G.,
Hustad,C.M., Copeland,N.G., Jenkins,N.A., Mohrenweiser,H.M.,
Brandriff,B., Cahalan,M.D., Gutman,G.A. and Chandy,K.G.
TITLE Genomic organization, chromosomal localization, tissue
distribution, and biophysical characterization of a novel mammalian
Shaker-related voltage-gated potassium channel, Kv1.7
J. Biol. Chem. 273 (10), 5851-5857 (1998)
JOURNAL 948722
MEDLINE
PUBMED
REFERENCE 2 (bases 1 to 1599)
AUTHORS Kalman,K., Nguyen,A., Tseng-Crank,J., Dukes,I.D., Chandy,G.,
Hustad,C.M., Copeland,N.G., Jenkins,N.A., Mohrenweiser,H.M.,
Brandriff,B., Cahalan,M.D., Gutman,G.A. and Chandy,K.G.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-1997) Physiology and Biophysics, University of
California at Irvine, Irvine, CA 92697, USA
FEATURES
source Location/Qualifiers
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gene
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HVPDLVLEEVSVYGLRRLARLREDECAVAERPLPPFARQLWLLFEFPESQAAR
VLAVSVLYLVSVYVFCLETLDFDRDRDDPLAPVAATGSLARUNGSPMPGAP
PLQVNPFFVETICWFSFELLVHLVACPSKAVFKNNMLIDFVAILPYFVALG
TELARQGVGPAMSLAILRILRVIRFVKLSHSGQLIQLGQTLRSMRELGLLI
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BASE COUNT 234 a 520 c 502 g 343 t
ORIGIN
Query Match 85.3%; Score 213.2; DB 10; Length 1599;
Best Local Similarity 90.8%; Pred. No. 1.8e-25;
Matches 227; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GCGGCTGGTCTCAACGTGGCGCGGCTTCGAGACGGCGCGCACGCTGGGCGG 60
DB 273 GCGGCTGGTCTCAACGTGGCGCGGCTTCGAGACCGCGCGCACGCTGGGCGG 332
QY 61 CTTCCGGGACACTCTCTAGGGACCCAGCGCGCGCGCGCTTCTAGCAGACGCGCG 120
DB 333 CTTCCGGGACACTCTCTAGGGACCCAGCGCGCGCGCGCTTCTAGCAGACGCGCG 392
QY 121 CCGCGAGTATTCTTCGACCGGCGCGCGCGCGCGCGCTTCTACTACTACCA 180
DB 393 CCGCGAGTATTCTTCGACCGGCGCGCGCGCGCGCGCTTCTACTACTACCA 452
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QY 241 GGCCTTCTAC 250
DB 513 GTCCCTTCTAC 522

RESULT 12
MMU409348
LOCUS
DEFINITION
Mus musculus partial Kcna7 gene for voltage-gated potassium channel
Kv1.7, exon 1.
ACCESSION
AJ409348
VERSION
AJ409348.1 GI:13508802
KEYWORDS
KCN7 gene; voltage-gated potassium channel Kv1.7.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 445)
AUTHORS
Kashuba,V.I., Kvasha,S.M., Protodopov,A.I., Gizatullin,R.Z.,
Rynditch,A.V., Wahlstedt,C., Wasserman,W.W. and Zabarovsky,E.R.
Initial isolation and analysis of the human Kv1.7 (KCN7) gene, a
member of the voltage-gated potassium channel gene family
Gene 268 (1-2), 115-122 (2001)
JOURNAL
21261947
MEDLINE
11368907
PUBMED
2 (bases 1 to 445)
AUTHORS
Kashuba,V.
TITLE
Direct Submission
JOURNAL
Submitted (23-MAR-2001) Kashuba V., Microbiology and Tumor Biology
Center, Karolinska Institute, Box 280, 171 77, SWEDEN
FEATURES
Location/Qualifiers
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/db_xref="GI:3004907"
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VLAVSVLYLVSVYVFCLETLDFDRDRDDPLAPVAATGSLARUNGSPMPGAP
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BASE COUNT 234 a 520 c 502 g 343 t
ORIGIN
Query Match 85.3%; Score 213.2; DB 10; Length 1599;
Best Local Similarity 90.8%; Pred. No. 1.8e-25;
Matches 227; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GCGGCTGGTCTCAACGTGGCGCGGCTTCGAGACGGCGCGCACGCTGGGCGG 60
DB 273 GCGGCTGGTCTCAACGTGGCGCGGCTTCGAGACCGCGCGCACGCTGGGCGG 332
QY 61 CTTCCGGGACACTCTCTAGGGACCCAGCGCGCGCGCGCTTCTAGCAGACGCGCG 120
DB 333 CTTCCGGGACACTCTCTAGGGACCCAGCGCGCGCGCGCTTCTAGCAGACGCGCG 392
QY 121 CCGCGAGTATTCTTCGACCGGCGCGCGCGCGCGCGCTTCTACTACTACCA 180
DB 393 CCGCGAGTATTCTTCGACCGGCGCGCGCGCGCGCGCTTCTACTACTACCA 452
QY 181 GTCCGGTGGCGGCTGGCGCGCGCGCGCGCGCGCTTCTCTGGAAGAGGT 240
DB 453 GTCCGGGCGCGGCTGAGACGGCGCGCGCGCGCGCGCTTCTCTGGAAGAGGT 512
QY 241 GGCCTTCTAC 250
DB 513 GTCCCTTCTAC 522

RESULT 13
HSHBK2
LOCUS
DEFINITION
Human HBK2 mRNA for potassium channel protein.
ACCESSION
X17522
VERSION
X17522.1 GI:32032
KEYWORDS
membrane protein; potassium channel protein.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 4234)
AUTHORS
Pongs,O.
TITLE
Direct Submission
JOURNAL
Submitted (23-NOV-1989) Pongs O., Ruhr Universitaet, Lehrstuhl fuer
Biochemie, Universitaetstr 150, D-4630 Bochum
2 (bases 1 to 4234)
AUTHORS
Grupe,A., Schroter,K.H., Ruppertsberg,J.P., Stocker,M., Drewes,T.,
Beckh,S. and Pongs,O.
Cloning and expression of a human voltage-gated potassium channel.
A novel member of the RCK potassium channel family
EMBO J. 9 (6), 1749-1756 (1990)
JOURNAL
90269208
MEDLINE
2347305
PUBMED
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CDS
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ELLVRESAPSKPAFRNIMLIDLVAIFPPIITGLTELVOQEQPASGGGQNGQQ
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BASE COUNT      851 a 1174 c 1227 g 982 t
ORIGIN

Query Match      62.9%; Score 157.2; DB 9; Length 4234;
Best Local Similarity 76.8%; Pred. No. 1.5e-16;
Matches 192; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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Db 985 GCGCGTGGTGAATATCTCTCGGCGTGGCTTTGAGACAAATTCGACACCTGTGCGT 1044
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QY 61 CTTCCGCGACACTCTCTAGGGACCGACGCGCGCGCGCTTCTAGCACGACGCGG 120
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Db 1045 GTTTCGGACACGCTGCTCGGACACCTGGCGCGGAGTCCGCTTCTCGACCCCTGAG 1104
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QY 121 CCGCGAGTATTTCTCGACGCGCACGCGGCCAGCTTCGACGCGGTCTCTACTACTACCA 180
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QY 181 GTCCGTTGGCGGCGTGGCGGCGCGCGCACGCTGCGCTTCGCTGAGGAGGT 240
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Db 1165 GTTGGGGCGCGCTCGGAGGCGGCTCAACGTCGCCCTGGACATTTTCTCTGGAGAGAT 1224
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RESULT 14
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LOCUS
DEFINITION Homo sapiens 12p13.3 BAC RPi11-234B24 (Roswell Park Cancer
Institute Human BAC Library) complete sequence.
ACCESSION AC005833
VERSION AC005833.1 GI:4165003
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 122903)
Muzny,D., Aronson,A.D., Bouck,J., Bunac,C., Chen,Z., Ding,Y.,
Dugan,S., Durbin,J., Forcum,J., Garcia,C., Gorrell,J.H.,
Gorrell,L.L., Hernandez,J.J., Issar,A., Jackson,L., Kneitz,S.,
Kondejewski,N., Lau,S., Leal,B., Lee,E., Lichtarge,O., Liu,W.,
Logan,O., Lu,J., Marondel,I., Martinez,C., Merscher,S., Miller,A.,
Montgomery,K., Oswal,G., Pampell,L.R., Parish,B.J., Perez,L.,
Rashid,N.D., Rives,C., Scherer,S.E., Shen,H., Shim,C., Simon,M.,
Vo,O., Williamson,A., Worley,K.C., Xiang,A.M., Yang,R., Yu,W.,
Zhou,X., Kucherlapati,R., Nelson,D. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 122903)
Worley,K.C.
Direct Submission
Submitted (20-OCT-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 122903)
```

AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Worley,K.C.
Direct Submission
Submitted (29-DEC-1998) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 122903)
Worley,K.C.
Direct Submission
Submitted (20-JAN-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 122903)
Worley,K.C.
Direct Submission
Submitted (30-JAN-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 122903)
Worley,K.C.
Direct Submission
Submitted (15-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jan 20, 1999 this sequence version replaced gi:4071009.
INFORMATION: <http://gc.bcm.tmc.edu:8088/home.html> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTSs, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished,) for Human and Mouse sequences.
Genes and region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.
SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----
----- Summary Statistics -----
Contig length: 122912
Phrap values in estimate: 121736
Average error rate (BCM-Phrap estimate): 9.84188e-05
Fraction of Phrap values less than 40 : 0.0170533
Number of consensus changing edits: 8
Number of N's in consensus : 0

Consensus changing edits			Edited+Context	
Position	Original+Context			
13624	gagaaataaa(c)ttgtcttgc		gagaaataaa(a)ttgtcttgc	
13769	ggagggggg(n)cgatagcat		ggagggggg(a)cgatagcat	
28984	cgagcgggg(n)gctcaagcct		cgagcgggg(g)gctcaagcct	
44274	gatgctctcg(n)aagacatc		gatgctctcg(g)aagacatc	
64600	gtgcaatgat(n)naaccagaat		gtgcaatgat(g)naaccagaat	
106923	gcctggggga(n)ccatggttct		gcctggggg(a)ccatggttct	
107127	caatggacat(n)actgocctgt		caatggacat(g)actgocctgt	

Bases with BCM-Phrap value < 20			Surrounding Sequence	
Quality	Position			
46			tttaacggag(t)ggatgggtg	
6	13718		ttatacagtc(t)gggacgtgt	
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7	37711		tagctactag(t)cacacatggc	
7	37712		agctactagt(c)acacatggct	
7	37728		tggtactta(a)atgtaaatta	
7	37729		ggctactta(a)tgtaaatata	
8	47		ttaacggagt(g)ggatgggtg	
8	48		taacggagt(g)gatgggtgga	
8	49		aacggagt(g)gatgggtgga	
8	13716		gattatacag(t)ctgggactgt	
8	13717		attatacagt(c)tgggactgt	
8	13720		atacagtctg(g)ggactgtgt	
8	13773		gggggacgg(a)tagcattagg	
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8	37702		tcaatatgat(a)gctactagtc	
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9	13775		gggggacgg(a)ctgtgtggg	
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10	37370		agctgtagca(c)atagaactta	
10	37379		acatagaact(t)acctatgtc	
10	37685		atctctgct(g)cactgttcaa	
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10	53176		attataaat(t)tttacctata	
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11	14274		taagtactgt(c)aaagatttga	
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11	14277		gtactgtcaa(g)attgtgcatc	
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12	37697		actgttcaat(a)tgatagctac	

12	ctgttcaata(t)gatagctact	37698	
12	tggtcaatat(g)atagctacta	37699	
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13	ggattattaa(a)tttttacctt	53174	
14	acggatgtggg(a)tggttgagtt	50	
14	caaagaagct(t)ccataaccgg	73	
14	aggcaaaaatg(g)ggaacaagg	164	
14	acagctctggg(g)actgtgtgg	13722	
14	gggacggata(g)cattaggaga	13776	
14	ataataataa(a)aaaagtcaaa	13912	
14	taaaaaaagt(c)aaacaaaaaa	13919	

Query Match	62.9%	Score 157.2	DB 9	Length 122903
Best Local Similarity	76.8%	Pred. No. 7.8e-17		
Matches 192	Conservative	0	Mismatches 58	Indels 0
Gaps	0			

QY	1	CGCGCTGGTGTCAACGTGGCGGGCTCGCTTCGAGACGCGGGCGCGCACGCTGGCGCG	60
Db	115266	GGCGCTGGTGATCAATATCTCGGGCTGCGCTTTGACACACAATTCGCACCCCTGTCGCT	115325

QY	61	CTTCCCGGACACTCTGTAGGGACCCAGCGCGCGCGCGCGCTTCTACGACGACGCGCG	120
Db	115326	GTTCGCGACACGCTGCTCGGAGACCCCTGGCGGGAGTCCGCTTCTCGACCCCTGAG	115385

QY	121	CGCGAGTATTCTTCGACGGCGCACCGCGCGCGCTTCGAGCGCGCTCTACTACTACCA	180
Db	115386	GAACGAGTATTCTTCGACGGCGCACCGCGCGCGCTTCGAGCGCGCTCTACTACTACCA	115445

QY	181	GTCCGGTGGCGGCTCGCGCGCGCGCGCGCTTCGAGCGCGCTCTCTCTGGAAGAGGT	240
Db	115446	GTCTGGGCGCGCGCTCGGAGGCGCGTCAACGTGCCCCCTGGACATTTCTCTGGAGGAGAT	115505

QY	241	GGCCTTCTAC	250
Db	115506	CGCCTTCTAC	115515

RESULT 15				
HSA337055				
LOCUS	HSA337055	780 bp	DNA	linear
DEFINITION	Homo sapiens genomic sequence surrounding NotI site, clone			
ACCESSION	NLI-YE2R			
VERSION	AJ337055			
KEYWORDS	AJ337055.1	GI:15881473		
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
	1 (bases 1 to 780)			
	Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,			
	Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V.,			
	Levitsky, V.G., Kolchanov, N.A., Protodopov, A.I., Kashuba, V.I.,			
	Kiselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.			
TITLE	NotI flanking sequences: a tool for gene discovery and verification			
JOURNAL	of the human genome			
MEDLINE	Nucleic Acids Res. 30 (14), 3163-3170 (2002)			
	22131767			

PUBMED 12136098
REFERENCE 2 (bases 1 to 780)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden

FEATURES
source Location/Qualifiers
1..780
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NL1-YE2R"
BASE COUNT 121 a 241 c 280 g 134 t 4 others
ORIGIN

Query Match 62.0%; Score 155; DB 9; Length 780;
Best Local Similarity 100.0%; Pred. No. 4.9e-16;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 GCGGCCGCTTCTACGACGACGCGCGCGAGTATTTCTCGACCGGCGCACCGGCCAGCT 155
|||||
Db 1 GCGGCCGCTTCTACGACGACGCGCGCGAGTATTTCTCGACCGGCGCACCGGCCAGCT 60
|||||

QY 156 TCGACGCCGTGCTCTACTACTACCACTCCGGTGGCGGCTGCGGCGCGCGCGCGCGTGC 215
|||||

Db 61 TCGACGCCGTGCTCTACTACTACCACTCCGGTGGCGGCTGCGGCGCGCGCGCGCGTGC 120
|||||

QY 216 CGCTCGACGCTTCTCTGGAAGAGGTGGCTTCTAC 250
|||||

Db 121 CGCTCGACGCTTCTCTGGAAGAGGTGGCTTCTAC 155
|||||

Search completed: February 20, 2003, 10:11:48
Job time : 1055.44 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2003, 05:50:07 ; Search time 413.95 Seconds
(without alignments)
9781.067 Million cell updates/sec

Title: US-09-804-014A-7_COPY_382_631
Perfect score: 250
Sequence: 1 gcggctgtgtcgaactgg.....tggagaggtgccttctac 250

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	214.8	85.9	468	9 AI324179	AI324179 mh83g06.x
2	192.8	77.1	687	13 BI295790	BI295790 UI-R-DK0-
3	191.6	76.6	522	9 AI322534	AI322534 mh83g06.y
4	177.8	71.1	477	9 AA021711	AA021711 mh83g06.r
5	157.2	62.9	770	12 BF530500	BF530500 602071745
6	155	62.0	443	17 AQ939702	AQ939702 NRS-028R

7	140.2	56.1	900	14	BQ938497	BQ938497	AGENCOURT
8	140.2	56.1	927	14	BQ930283	BQ930283	AGENCOURT
9	135.4	54.2	704	10	BB612634	BB612634	BB612634
c	10	135.2	54.1	839	17	CNS03DKC	Tetraodon
	11	134.4	53.8	414	9	AL843701	AL843701
	12	125	50.0	316	9	AL844004	AL844004
	13	123.6	49.4	537	17	FR0032804	AL015668 F.rubripe
c	14	121.8	48.7	1085	17	CNS03SKP	AL228850 Tetraodon
c	15	120.6	48.2	1023	17	CNS02A6D	AL188158 Tetraodon
c	16	116.2	46.5	433	17	DR17024S	AL732913 Danio rer
	17	112	44.8	665	13	BM492036	
	18	109.6	43.8	954	14	BQ714749	BQ714749
c	19	108.8	43.5	954	10	BQ714749	AGENCOURT
c	20	106.6	42.6	1109	17	CNS045OM	AL275647 Tetraodon
c	21	103.2	41.3	1109	10	CNS045OM	AL275647 Tetraodon
c	22	98.6	39.4	1109	13	CNS045OM	AL275647 Tetraodon
c	23	98.2	39.3	1058	14	BM924998	BM924998
c	24	96.6	38.6	1058	17	BM924998	AGENCOURT
c	25	92.8	37.1	1058	12	BM924998	AGENCOURT
c	26	90.6	36.2	1054	17	CNS03DBK	AL332201 Tetraodon
c	27	87.2	34.9	1054	9	CNS05DBK	AL332201 Tetraodon
c	28	84	33.6	640	13	CG973314	CG973314
c	29	83.4	33.4	963	17	CNS03F5Y	AL198511 Tetraodon
c	30	83	33.2	557	10	BE666693	BE666693
c	31	82.4	33.0	557	9	BE666693	150296 MA
c	32	80.4	32.2	876	13	BI117089	BI117089
c	33	78.2	31.3	876	13	BI117089	602867882
c	34	70	28.0	876	17	BI117089	602867882
c	35	69.4	27.8	876	10	BI117089	602867882
c	36	69.2	27.7	876	9	BI117089	602867882
c	37	69.2	27.7	876	9	BI117089	602867882
c	38	68.6	27.4	628	14	BQ807519	BQ807519
c	39	67.8	27.1	628	9	BQ807519	NISC_kk05
c	40	64.4	25.8	628	17	BQ807519	NISC_kk05
c	41	62.6	25.0	628	9	BQ807519	NISC_kk05
c	42	62.6	25.0	628	9	BQ807519	NISC_kk05
c	43	62.4	25.0	628	9	BQ807519	NISC_kk05
c	44	62.4	25.0	628	9	BQ807519	NISC_kk05
c	45	62.4	25.0	628	12	BQ807519	NISC_kk05

ALIGNMENTS

RESULT 1
AI324179/c
LOCUS
... DEFINITION
AI324179
mh83g06.x1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA
clone IMAGE:457594 3' similar to gb:X17622-cds1 POTASSIUM CHANNEL
PROTEIN KVI.6 (HUMAN); gb:Y00305 Mouse MBK1 mRNA for mouse brain
potassium channel (MOUSE);, mRNA sequence.
ACCESSION
AI324179
VERSION
AI324179.1 GI:4058608
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 468)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wyllie, T., Lennon, G., Soares, B., Willson, R. and
Waterston, R.
TITLE
The WashU-RHMI Mouse EST Project
JOURNAL
Unpublished (1996)
COMMENT
Contact: Marra M/Mouse EST Project
WashU-RHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LML ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:274482
This clone was previously sequenced on the 5' end only, this new data is from the 3' end
High quality sequence stop: 453.

FEATURES

source
1..468
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:457594"
/clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
/sex="unknown"
/tissue_type="placenta"
/lab_host="adult"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGAAGTGGGAGCGCGGAAATTTTTTTTTTTTTTTTTTTT
T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 75 a 166 c 176 g 51 t

Query Match 85.9%; Score 214.8; DB 9; Length 468;
Best Local Similarity 91.2%; Pred. No. 2.3e-36;
Matches 228; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 GCGCGTGGTCTCAAGCTGGCGGGTGGCTTCGAGACGCGCGCGCGCGCGCG 60
Db 288 GCGCGTGGTCTCAAGCTGGCGGGTGGCTTCGAGACGCGCGCGCGCGCGCG 229
QY 61 CTTCGCGGACACACTCTGTAGGGACCGACGCGCGCGCGCGCTTCTACGACGCGCG 120
Db 228 CTTCGCGGACACACTCTGTGGGGACCGCGGTGGCGCGCGCGCTTCTACGCGCGCG 169
QY 121 CCGCGAGTATTTCTGACGGCGACCGCGCCAGCTTCGAGCGCGTCTCTACTACTACCA 180
Db 168 CCGCGAGTATTTCTGACGGCGACCGCGCCAGCTTCGAGCGCGTCTCTACTACTACCA 109
QY 181 GTCGCGTGGCGGCTCGCGGGCGCGCGACGTCGCGCTCGACGCTCTCTGGAAGAGGT 240
Db 108 GTGCGGCGCGCGCTGAGACGCGCGCGCACCTGCCCTCGACGCTCTCTGGAAGAGGT 49
QY 241 GGCCTTCTAC 250
Db 48 GTCCTTCTAC 39

RESULT 2
BI295790
LOCUS
DEFINITION BI295790 687 bp mRNA linear EST 19-JUL-2001
UI-R-DK0-cfa-f-09-0-UI.s1 UI-R-DK0 Rattus norvegicus cDNA clone
UI-R-DK0-cfa-f-09-0-UI 3', mRNA sequence.
ACCESSION BI295790
VERSION BI295790.1 GI:14959590
KEYWORDS EST.
SOURCE Norway rat.
Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 687)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE COMMENT

97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized rat placenta pool library cDNA Library Preparation: M.B. Soares lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-41.
>AT-rich/Low-complexity 45-170, >BI_MM#SINE/Alu 264-317,
>GC-rich/Low-complexity
Seq primer: M13 Forward
POLYA=Yes.

FEATURES

Source
1..687
Location/Qualifiers
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-DK0-cfa-f-09-0-UI"
/clone_lib="UI-R-DK0"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DK0 library is a subtracted library derived from a mixture of five individually tagged normalized rat libraries: brain-nRBP (20%), heart-nRHP (20%), kidney-nRKP (20%), aorta-nRAP (20%), and placenta-nRPP (20%). Each original library was constructed from a mixture of equal amounts of RNA from seven different developmental time-points: embryonic day 17, embryonic day 19, embryonic day 21, adult day 1, adult day 12, adult day 75, and adult day 200. (Exception: the aorta pool does not contain embryonic day 17 RNA and the placenta pool contains only the three embryonic stages). Each library was normalized individually according to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the DK0 subtracted library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five non-normalized libraries of brain (CT0s), heart (CS0s), kidney (CU0s), aorta (CW0s), and placenta (CX0s). The resulting pool of approximately 5,000 clones represented about 33.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CT0), heart (CS0), kidney (CU0), aorta (CW0), and placenta (CX0). The resulting pool of about 10,000 clones represented about 66.6% of the final driver population.
TAG_LIB=UI-R-DK0
TAG_TISSUE=rat placenta pool
TAG_SEQ=TCACGACGT

BASE COUNT 140 a 217 c 203 g 126 t 1 others
ORIGIN
Query Match 77.1%; Score 192.8; DB 13; Length 687;
Best Local Similarity 90.0%; Pred. No. 1.1e-31;
Matches 206; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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QY 1 GCGGCTGGTCTCAACGTGGCCGGGCTGGCTTCGAGACGCGCGCGCACGCTGGCGCG 60
|||||
Db 459 GCGGCTGGTCTCAACGTGGCCGGGTTGGCTTCGAGACCGCGCGCACGCTGGCGCG 518
|||||

QY 61 CTTCCCGGACACCTCTAGGAGACCCAGCGCGCGCGCGCTTCTACGACACGCGCG 120
|||||
Db 519 CTTCCCGGACACCTCTAGGAGACCCAGCGCGCGCGCTTCTACGACACGCGCGCG 578
|||||

QY 121 CCAGGAGTATTTCTTCCAGCGGACCGCGCCAGCTTCGAGCGCGCTCTACTACTACCA 180
|||||
Db 579 CCAGGAGTATTTCTTCCAGCGGACCGCGCCAGCTTCGAGCGCGCTCTACTACTACCA 638
|||||

QY 181 GTCGGTGGCGGCTCGCGCGCGCGCGCGCGCTCGAGCGTCTTCTACTACTACTACCA 229
|||||
Db 639 ATCAGCGCGCGGCTGAAACGCGCGCGCGCGCGCGCTCGAGCTTCTTCTTCTTCTTCT 687
|||||

RESULT 3
AI322534 522 bp mRNA linear EST 23-DEC-1998
LOCUS mh83g06.y1 Soares mouse placenta 4NbMPL3.5 14.5 Mus musculus CDNA
DEFINITION clone IMAGE:457594 5' similar to gb:XI7622_cds1 POTASSIUM CHANNEL
PROTEIN KVI.6 (HUMAN);, mRNA sequence.
ACCESSION AI322534
VERSION AI322534.1 GI:4056963
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 522)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is a RESEQUENCE of a previously sequenced mouse clone
correct orientation)
This read has been verified (found to hit its original self in the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:274482
This read is a RESEQUENCE of a previously sequenced mouse clone
correct orientation)
This read has been verified (found to hit its original self in the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40RP from Gibco
High quality sequence stop: 367.
Location/Qualifiers
1..522
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:457594"
/lab_host="DH10B"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TCTTACCAATCTGAAGTGGGAGCGCGCGCGGAAATTTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library

```

```

BASE COUNT 58 a 192 c 188 g 84 t
ORIGIN
Query Match 76.6%; Score 191.6; DB 9; Length 522;
Best Local Similarity 87.7%; Pred. No. 2e-31;
Matches 221; Conservative 0; Mismatches 29; Indels 2; Gaps 1;

QY 1 GCGGCTGGTCTCAACGTGGCCGGGCTGGCTTCGAGACGCGCGCGCACGCTGGCGCG 60
|||||
Db 223 GCGGCTGGTCTCAACGTGGCCGGGTTGGCTTCGAGACCGCGCGCACGCTGGCGCG 282
|||||

QY 61 CTTCCCGGACACCTCTAGGAGACCCAGCGCGCGCGCGCTTCTACGACACGCGCG 120
|||||
Db 283 CTTCCCGGACACCTCTAGGAGACCCAGCGCGCGCGCTTCTACGACACGCGCGCG 342
|||||

QY 121 CCAGGAGTATTTCTTCCAGCGGACCGCGCCAGCTTCGAGCGCGCTCTACTACTACCA 180
|||||
Db 343 CCAGGAGTATTTCTTCCAGCGGACCGCGCCAGCTTCGAGCGCGCTCTACTACTACCA 402
|||||

QY 181 GTCGGTGGCGGCTCGCGCGCGCGCGCGCGCTCGAGCGTCTTCTACTACTACTACCA 238
|||||
Db 403 GTCGGCGCGCGGCTCGAGACCGCGCGCGCGCGCTTGGCCCTCGAGCGTCTTCTCTGGAGAG 462
|||||

QY 239 GTGGCCTTCTTAC 250
|||||
Db 463 GTGTCCTTCTTAC 474
|||||

RESULT 4
AA021711 477 bp mRNA linear EST 21-JAN-1997
LOCUS mh83g06.r1 Soares mouse placenta 4NbMPL3.5 14.5 Mus musculus CDNA
DEFINITION clone IMAGE:457594 5' similar to gb:XI7622_cds1 POTASSIUM CHANNEL
PROTEIN KVI.6 (HUMAN);, mRNA sequence.
ACCESSION AA021711
VERSION AA021711.1 GI:1485501
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 477)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:274482
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 263.
Location/Qualifiers
1..477
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:457594"
/lab_host="DH10B"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"

```

went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

/lab_host="DH10B"
/note="Organ: placenta; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTT
T 3'] ; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 55 a 177 c 161 g 84 t
ORIGIN

Query Match 71.1%; Score 177.8; DB 9; Length 477;
Best Local Similarity 88.2%; Pred. No. 1.7e-28;
Matches 216; Conservative 0; Mismatches 27; Indels 2; Gaps 2;
QY 1 GCGGCTGGTCTCAACGTGGCGGGCTGCGCTTCGAGACGGCGCGCGACGCTGGGCGG 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 223 GCGGCTGGTCTCAACGTGGCGGGTTCGCTTCGAGACCGCGCGCGCACGCTCGGCGG 282
QY 61 CTTCCCGGACACTCTGCTAGGGACCCAGCGCGCGCGCGCTTCTACGACGCGCGG 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 283 CTTCCCGGACACTCTGCTAGGGACCCAGCGCGCGCGCGCTTCTACGACGCGCGG 342
QY 121 CCGGAGTATTTCTTCGACCGGACCGCGCGCGCGCTTCGACGCGGCTGCTACTACTACCA 180
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Db 343 -CGGAGTATTTCTTCGACCGGACCGCGCTCAGCTTCGATGCGGTGCTACTACTACCA 401
QY 181 GTCCGGTGGCGGCTGGCGGCGCGCGCGCGCGCTTCGCGCTGCGCTTCCTGGAAGAGGT 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 402 GTCCGGGCGCGGCTGAGAGCGGCGCTC-TACCTGCCCTCGACGCTCTCTCTGGAGGAGGT 460
QY 241 GGCGT 245
Db 461 GTCTT 465

RESULT 5
BF530500
LOCUS BF530500 770 bp mRNA linear EST 11-DEC-2000
DEFINITION 60201745F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4214506
5', mRNA sequence.
ACCESSION BF530500
VERSION BF530500.1 GI:11617863
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 770)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9788 row: j column: 11
High quality sequence stop: 671.
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1. .770
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4214506"
/tissue_lib="NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with lp/19q

loss"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCWV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 135 a 231 c 228 g 176 t
ORIGIN
Query Match 62.9%; Score 157.2; DB 12; Length 770;
Best Local Similarity 76.8%; Pred. No. 4.2e-24;
Matches 192; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 1 GCGGCTGGTCTCAACGTGGCGGGTTCGCTTCGAGACGGCGCGCGACGCTGGGCGG 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GCGGCTGGTCAATATCTCCGGGCTGCGCTTCGAGACACAAATTCGCCACCTGTGCT 60
QY 61 CTTCCCGGACACTCTGCTAGGGACCCAGCGCGCGCGCGCTTCTACGACGACGCGG 120
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Db 61 GTTCCGGACACGCTGCTCGGAGACCTTCGCGCGCGAGTCCGCTTCTTCGACCCCTGAG 120
QY 121 CCGGAGTATTTCTTCGACCGGACCGCGCGCGCGCTTCGAGCCATCTCTACTACTACCA 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GACGAGTACTTCTTCGACCGGACCGCGCGCGCTTCGAGCCATCTCTACTACTACCA 180
QY 181 GTCCGGTGGCGGCTGGCGGCGCGCGCGCTTCGCGCTGCGAGCTCTTCTTCTGGAAGAGGT 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GTCTGGGCGCGCTGCGGAGCGCGTCAACGTCGCCCTTGACATTTTCTCTGGAGGAGAT 240
QY 241 GGCGTCTCTAC 250
Db 241 CGGCTTCTAC 250
RESULT 6
AQ939702
LOCUS AQ939702 443 bp DNA linear GSS 23-AUG-2000
DEFINITION NR5-028R Human NotI clones Homo sapiens genomic, DNA sequence.
ACCESSION AQ939702
VERSION AQ939702.1 GI:7216080
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 443)
AUTHORS Zabarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovska,V.V., Xie
J.L., Muravenko,O.V., Kozyrev,S., Petrenko,L., Skobeleva,N., Li,J.,
Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and Wahlestedt,C.
TITLE NotI clones in the analysis of the human genome
JOURNAL Nucleic Acids Res. 28 (7), 1635-1639 (2000)
MEDLINE 20175728
COMMENT Contact: Podowski RM
Center for Genomics Research
Karolinska Institute
17177 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-337983
Email: Raf.Podowski@cgr.ki.se
Class: NotI site.
FEATURES
source
1. .443
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human NotI clones"
/note="Organ: Lung; DNA was isolated from A549 cells after
sodium arsenite exposure for 4 weeks. This fragment was
differentially methylated relative to untreated controls
and was identified using methylation sensitive AP-PCR and
sequenced."
BASE COUNT 43 a 167 c 152 g 80 t 1 others
ORIGIN

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Query Match          62.0%; Score 155; DB 17; Length 443;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 GCGCGCGCTTCTACGACGCGCGCGCGAGTATTCTTCGACCGCGCGCCAGCT 155
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Db 1 GCGCGCGCTTCTACGACGCGCGCGCGAGTATTCTTCGACCGCGCGCCAGCT 60
      |||||

QY 156 TCGACCGCGTCTACTACTACAGTCCGGTGGCGGCTGCGCGCGCGCGCGCGTGC 215
      |||||
Db 61 TCGACCGCGTCTACTACTACAGTCCGGTGGCGGCTGCGCGCGCGCGCGCGTGC 120

QY 216 CGCTGACGCTTCTCTGGAAGAGGTGGCCTTCTAC 250
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Db 121 CGCTGACGCTTCTCTGGAAGAGGTGGCCTTCTAC 155

RESULT 7
BQ938497
LOCUS          BQ938497
DEFINITION    AGENCOURT_8930577 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6466414
              5', mRNA sequence.
ACCESSION     BQ938497
VERSION       BQ938497.1 GI:22353975
KEYWORDS      EST.
SOURCE        house mouse.
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE     1 (bases 1 to 900)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs@mail.nih.gov
              Tissue Procurement: The Cepko Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM13990 row: k column: 23
              High quality sequence stop: 663.
              Location/Qualifiers
                1..900
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                /db_xref="taxon:10090"
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                /clone_lib="NIH_MGC_94"
                /tissue_type="retina"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                Average insert size 3.3 kb. Library enriched for
                full-length clones and constructed by Life Technologies.
                Note: this is a NIH_MGC Library."
BASE COUNT      162 a 267 c 294 g 177 t
ORIGIN
Query Match          56.1%; Score 140.2; DB 14; Length 900;
Best Local Similarity 72.7%; Pred. No. 1.7e-20;
Matches 181; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GCGCGTGGTGCTCAAGTGGCGCGGCTGCGCTTCGAGACGCGCGCGCGCGTGGCGG 60
      |||||
Db 354 GAGGTGGTGATCAACATCTCCGGGTGCGCTTCGAGACGAGCTCGCACCCCTGTCGT 413
      |||||

QY 61 CTTCCCGGACACTCTGCTAGGCGCCAGCGCGCGCGCGCTTCTACGACGCGCGG 120
      |||||
Db 414 GTTCCCTGACACGCTGCTAGGACACCTGGCGCGAGAGTCCGTTCTTTGACCCCTTGAG 473
      |||||

QY 181 GTCGCGAGTATTCTTCGACGCGCGCGCGCGCGCTTCGAGCTTCCTACTACTACCA 180
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Db 474 GAACGAGTACTTCTTTGACCGCAACGACCGAGCTTCGAGCTATCCTTTATTACTATCA 533
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QY 181 GTCGCGTGGCGCGCTGCGCGCGCGCGCGAGTGGCGCTCTCTCTGGAAGAGGT 240
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Db 534 ATCTGGAGGTGCGCTGCGCAGGCGCTGTTAATGTGCCCTCGACATTTTATGGAAGAGAT 593
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QY 241 GCGCTTCTA 249
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Db 594 CCGCTTCTA 602
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RESULT 8
BQ930283
LOCUS          BQ930283
DEFINITION    AGENCOURT_8930593 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6466415
              5', mRNA sequence.
ACCESSION     BQ930283
VERSION       BQ930283.1 GI:22345314
KEYWORDS      EST.
SOURCE        house mouse.
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE     1 (bases 1 to 927)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs@mail.nih.gov
              Tissue Procurement: The Cepko Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM13990 row: k column: 24
              High quality sequence stop: 672.
              Location/Qualifiers
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                /organism="Mus musculus"
                /db_xref="taxon:10090"
                /clone="IMAGE:6466415"
                /clone_lib="NIH_MGC_94"
                /tissue_type="retina"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                Average insert size 3.3 kb. Library enriched for
                full-length clones and constructed by Life Technologies.
                Note: this is a NIH_MGC Library."
BASE COUNT      176 a 269 c 299 g 181 t
ORIGIN
Query Match          56.1%; Score 140.2; DB 14; Length 927;
Best Local Similarity 72.7%; Pred. No. 1.7e-20;
Matches 181; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GCGCGTGGTGCTCAAGTGGCGCGGCTGCGCTTCGAGACGCGCGCGCGCGTGGCGCG 60
      |||||
Db 354 GAGGTGGTGATCAACATCTCCGGGTGCGCTTCGAGACGAGCTCGCACCCCTGTCGT 413
      |||||

QY 61 CTTCCCGGACACTCTGCTAGGCGCCAGCGCGCGCGCGCTTCTACGACGCGCGG 120
      |||||
Db 414 GTTCCCTGACACGCTGCTAGGAGACCTGGCGCGAGAGTCCGTTCTTTGACCCCTTGAG 473
      |||||

QY 121 CCGCGAGTATTCTTCGACGCGCGCGCGCGCTTCGAGCTTCGCTACTACTACCA 180
      |||||
Db 474 GAACGAGTACTTCTTTGACCGCAACCGACCGAGCTTCGAGCTATCCTTTATTACTATCA 533
      |||||
QY 181 GTCGCGTGGCGCGCTGCGCGCGCGCGCGAGCTGCGCGCTCGACGCTTCCTTGGGAAGAGGT 240
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Db 534 ATCTGGAGGTGCGCTGCCAGCGCTGTATTATGTGCCCCCTCGACATTTTTTTATGGAAGAGAT 593
Qy 241 GGCGTTCTTA 249
Db 594 CCGCTTCTTA 602

RESULT 9
BB612634 704 bp mRNA linear EST 26-OCT-2001
LOCUS BB612634 RIKEN full-length enriched, 10 day neonate skin Mus
DEFINITION musculus cDNA clone 4732440K03 5', mRNA sequence.
ACCESSION BB612634
VERSION BB612634.1 GI:16453519
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 704)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Sakai
Okazaki,Y., Okido,T., Saito,K., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
FEATURES
Location/Qualifiers
1..704
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4732440K03"
/clone_lib="RIKEN full-length enriched, 10 day neonate
skin"
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/dev_stage="10 days neonate"
/lab_host="DH10B"
/note="Site_1: Salt; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAAGGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATTCTCGAGTTAATTAATTAATCCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I"
BASE COUNT 122 a 264 c 113 g 205 t
ORIGIN
Query Match 54.2%; Score 135.4; DB 10; Length 704;
Best Local Similarity 71.5%; Pred. NO. 1.8e-19;
Matches 178; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
... QY 2 CCGCTGCTCTCAAGTGGCGGCTGCGCTTCGAGACGGCGGCGCGCTGGCGCGC 61
Db 78 CGTGTGCTCAACTGGCGCGCTTGCCTTCTTTACCCCGCGCCACTCTTGGCCTA 137
QY 62 TTCGCGGACTCTGTAGGGACCCAGCGCGCGCGCTTCTTACGACGAGCGCGC 121
Db 138 TTTCGCGGACTCTGCTGGGGACCCCAACGACCTCATCCACTTTTACCACCGCCCTCGC 197
QY 122 CGCGAGTATTTCTTCGACCGCGCCCGCCAGCTTCGACCGCTGCTCTACTACAG 181
Db 198 CCAAAATTTTATTTTACCTCCACCTTCCCAACTTCAATGCGGTGCTCTACTACAC 257
QY 182 TCCGGTGGCGGCTGCGCGCGCGCGCGCTGCGCTGCGCTGCGTTCCTTGGAGAGGTG 241
Db 258 TCTGTCAGCGTTTGAACAGCGCGCCACATACCCCTACACTTCTTCTCTGAAGAAGTA 317
QY 242 GCCTTCTAC 250
Db 318 TCCTCTAC 326

RESULT 10
CNS03DKC/c
LOCUS CNS03DKC/c
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
017A20 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL239205
VERSION AL239205.1 GI:7898340
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 839)
Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
2 (bases 1 to 839)
Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
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TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL REFERENCE	unpublished
AUTHORS	3 (bases 1 to 839)
TITLE	Genoscope.
JOURNAL	Direct Submission
COMMENT	submitted (12-APR-2000) This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon .

	source
FEATURES	

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/clone_id= g
/note="Genoscope sequence ID : C0BG017BA10LP1-end : T7"
BASE COUNT
157 a 246 c 281 q 155 t

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RESULT 11	
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DEFINITION	F00M Takifugu rubripes cDNA clone F00M10aeE12, mRNA sequence.
ACCESSION	AL843701
VERSION	AL843701.1 GI:22021529
KEYWORDS	EST.
SOURCE	Takifugu rubripes.
ORGANISM	Takifugu rubripes.

REFERENCE	1 (bases 1 to 414)
AUTHORS	Clark, M.S.
TITLE	Takifugu rubripes ESTs
JOURNAL	Unpublished (2002)
COMMENT	Contact: Clark MS MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB, UK Email: biohelp@hgmp.mrc.ac.uk Vector: pME18S-FL3 V_type: phagemid PRIMER: ME-735FW Library created by Koichi Kawakami, Masahide Sasaki, Yutaka Suzuki, Sumio Sudano

The Institute of Medical Science, The University of Tokyo,
Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
and
Kiyoshi Kikuchi, Shugo Watabe
Laboratory of Aquatic Molecular Biology and Biotechnology, Graduate
School of Agricultural and Life Sciences, The University of Tokyo,
Bunkyo-ku, Tokyo 108-8639, Japan
Library sequenced by Melody S. Clark and Amanda Thompson MRC Human
Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10
1SB. UK.

FEATURES
source

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BASE COUNT      81 a 125 c 139 g 68 t 1 others
ORIGIN
/note="vector: pMEROS-FL3"

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RESULT	12
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LOCUS	316 bp mRNA linear EST 30-JUL-2002
DEFINITION	F00M Takifugu rubripes cDNA clone F00M15ae10, mRNA sequence.
ACCESSION	AL844004
VERSION	AL844004.1 GI:22021832
KEYWORDS	EST.
SOURCE	Takifugu rubripes.
ORGANISM	Takifugu rubripes.

REFERENCE	1 (bases 1 to 316)
AUTHORS	Clark, M.S.
TITLE	Takifugu rubripes ESTs
JOURNAL	Unpublished (2002)
COMMENT	Contact: Clark MS MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB, UK Email: biohelp@hgmp.mrc.ac.uk Vector: pME185-FL3 V_type: phagemid PRIMER: ME-735FW

Library created by Koichi Kawakami, Masahide Sasaki, Yutaka Suzuki, Sumio Sugano
The Institute of Medical Science, The University of Tokyo,
Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
and

Kiyoshi Kikuchi, Shugo Watabe
Laboratory of Aquatic Molecular Biology and Biotechnology, Graduate
School of Agricultural and Life Sciences, The University of Tokyo,
Bunkyo-ku, Tokyo 108-8639, Japan
Library sequenced by Melody S. Clark and Amanda Thompson MRC Human
Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10
1SB. UK.

FEATURES
source Location/Qualifiers
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/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone="F000M15aE10"
/clone_lib="F000M"
/sex="female"
/tissue_type="muscle"
/dev_stage="adult"
/notes="Vector: pME18S-FL3"
BASE COUNT 53 a 102 c 99 g 62 t
ORIGIN

Query Match 50.0%; Score 125; DB 9; Length 316;
Best Local Similarity 71.5%; Pred. No. 3e-17;
Matches 178; Conservative 0; Mismatches 70; Indels 1; Gaps 1;
QY 1 GCGGCTGGTCTCAACGTGCGGGGTCGCTTCGAGACGGCGCGGCGGTGGCGG 60
Db 26 GCGTCTGCCATCAACGTGTCGGGGATGCTTACGAGCTCAGCTGAGAACTCT-GGCC 84
QY 61 CTTCCCGACACACTCTGTAGGGACGACGCGCGCGCGCTTCTACGACGACGCGG 120
Db 85 AGTCCGGACTCCTGCTGGGGACCGCCCGCGTCCGCTCGACTTCGACCCCTACCAG 144
QY 121 CCGGAGTATTTCTCGACCGGACCGGCGCCAGCTTCGAGCGCGTCTCTACTACTACCA 180
Db 145 AAACGAGCTTTTCTCGACAGAGTGGCGTCTCTCGACGCGTCTCTACTACTACCA 204
QY 181 GTCGGTGGCGGCGCGCGCGCGCGTTCGCTCGCTCGCTCTCTCTGGAAGAGGT 240
Db 205 ATCCGGGGAGGCTGCGGGCGGCTGCCAACGTCCTTGGACGTGTCCTGGAGGAGCT 264
QY 241 GGCCTTCTA 249
Db 265 GCGCTTCTA 273

RESULT 13
LOCUS FR0022804
DEFINITION F rubripes GSS sequence, clone 081C09ad12, genomic survey sequence.
ACCESSION AL015668
VERSION AL015668.1 GI:2682036
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes
ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
REFERENCE 1 (bases 1 to 537)
AUTHORS Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrانيا,Y.,
Williams,G. and Brenner,S.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmrc.mrc.ac.uk
COMMENT V-type: phagemid
PRIMER: KS
DESCR:

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sequence.
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QY 242 GCCTTCTA 249
Db 282 NNTNTCTA 289
RESULT 14
LOCUS CNS035KP/C
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
214101 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL228850
VERSION AL228850.1 GI:7887843
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 1085)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1085)
TITLE Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
JOURNAL Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
AUTHORS 3 (bases 1 to 1085)
TITLE Genoscope.
JOURNAL Direct Submission
AUTHORS Submitted (12-APR-2000)
JOURNAL This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

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QY 120 GCGCGCAGTATTTCTCGACGGCAGCCGCCAGCTTCGACGCGTGCTCTACTATACC 179
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Db 884 GGAACGAGTACTTCTTCGACGGCAACCGCGCCAGCTTCGACGCCATCTCTACTACC 825
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Db 764 TCAATCTCTAC 754

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DEFINITION
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sequence.
ACCESSION
AL188158
VERSION
AL188158.1 GI:7826262
KEYWORDS
GSS: genome survey sequence.
SOURCE
Tetraodon nigroviridis.
ORGANISM
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 1023)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1023)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
JOURNAL
Unpublished
REFERENCE
3 (bases 1 to 1023)
Genoscope.
Direct Submission
TITLE
Submitted (12-APR-2000)
JOURNAL
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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Best Local Similarity 68.5%; Pred. No. 2.6e-16;
Matches 165; Conservative 1; Mismatches 75; Indels 0; Gaps 0;
QY 1 GCGGCTGGTCTCAAGCTGGCGGGCTGGCTTCGAGACGGCGCGCACGCTGGGCGG 60
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Db 319 GCGGCTGGTCTCAAGCTGGCGGGCTGAAGTTTGAACCCAGCTGAAGACCCCTCAGCCA 260
QY 61 CTTCCCGGACACTCTCTAGGGGACCCAGCGCGCGCGCTTCTACGACGACGCGCG 120
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QY 241 G 241
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Db 79 G 79

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Job time : 662.95 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2003, 04:22:08 ; Search time 1517.74 Seconds
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Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: gb_in.*
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- 7: gb_ph.*
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- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	556	100.0	1341	6	AX352535	AX352535 Sequence
2	556	100.0	1447	9	AF315818	AF315818 Homo sapi
3	556	100.0	1747	6	AX268121	AX268121 Sequence
c	556	100.0	157633	9	AC008687	AC008687 Homo sapi
5	554.4	99.7	4372	9	HS310479	HS310479 Homo sapi
6	532	95.7	691	6	AX354900	AX354900 Sequence
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8	438.2	78.8	1599	10	AF032099	AF032099 Mus muscu
9	438.2	78.8	2459	10	MMKNC2	AF032101 Mus muscu
10	436.6	78.5	1599	6	I26643	I26643 Sequence 9
11	430.8	77.5	172671	2	AC128792	AC128792 Rattus no
12	416.6	74.9	770	9	HS340320	HS340320 Homo sapi
13	357	64.2	664	9	HS338833	HS338833 Homo sapi
14	351	63.1	420	6	AX268139	AX268139 Sequence
15	351	63.1	420	6	AX268140	AX268140 Sequence
16	350.2	63.0	1551	4	OCU38240	UC38240 Oryctolagus
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20	339	61.0	90458	2	AL513469	AL513469 Homo sapi
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26	334.2	60.1	2867	6	AX333745	AX333745 Sequence
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33	327.8	59.0	1814	4	AF149787	AF149787 Oryctolag
34	327.8	59.0	1872	4	AF056943	AF056943 Oryctolag
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38	325.6	58.6	1780	4	CFU08596	U08596 Canis famli
39	324.8	58.4	760	9	HS329753	HS329753 Homo sapi
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41	324.6	58.4	2264	10	RATKV3AA	M31744 Rat potassi
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ALIGNMENTS

RESULT 1
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LOCUS AX352535
DEFINITION Sequence 7 from Patent WO0194390.
ACCESSION AX352535
VERSION AX352535.1 GI:18617765
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Curtis, R.A.
TITLE 52906, 33408, and 12189, potassium channel family members and uses thereof

AX352535. linear PAT 06-FEB-2002

JOURNAL	Patent: WO 0194390-A 7 13-DEC-2001;
FEATURES	Millennium Pharmaceuticals, Inc. (US)
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QY	1014 CTTCTGTGTGGCGGTAGTCACTAGTACAGTTGGCTATGGAGACATGCAACCCGTCAC 1073
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QY	1074 TGTGGGTGGCAAGTAGTGGGCTCTCTGTGTGCCATTGCGGGGTGCTGACTATTTCCT 1133
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DEFINITION	cds.
ACCESSION	AF315818
VERSION	AF315818.1 GI:14485554
KEYWORDS	Homo sapiens.
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1447)
AUTHORS	Bardien-Kruger,S., Wulff,H., Arleff,H., Brink,P., Chandy,K.G. and Corfield,V.
TITLE	Characterization of the human voltage-gated potassium channel gene, KCNA7, a candidate gene for inherited cardiac disorders, and its exclusion as cause of progressive familial heart block I (PFHBI)
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1447)
AUTHORS	Bardien-Kruger,S., Wulff,H., Arleff,H., Brink,P., Chandy,K.G. and Corfield,V.
TITLE	Direct Submission
JOURNAL	Submitted (23-OCT-2000) SANBI, University of Western Cape, Modderdam Road, Cape Town 7535, South Africa
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QY	721 CCTGGTCTGTCCAAAGCAAGCTATCTTCTTCAAGAAGCTGATGAACCTCATCGATTTTGT 780
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QY	241 CTTCAAGCTGTCCGGCACTCAAGGCGCTGCAAAATCTTGGCCAGACGCTTCGGGGCTC 300
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RESULT 3

LOCUS AX268121 1747 bp DNA linear PAT 26-OCT-2001

DEFINITION Sequence 7 from Patent WO0168851.

ACCESSION AX268121

VERSION AX268121.1 GI:16516622

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Padigaru,M., Vernet,C.A., Fernandes,E., Shinkets,R.A.,

TITLE Spaderna,S.K., Majumder,K. and Li,L.

JOURNAL Polypeptides and nucleic acids encoding same

Curagen Corporation (US)

Patent: WO 0168851-A 7 20-SEP-2001;

FEATURES

source

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/db_xref="taxon:9606"

BASE COUNT 255 a 582 c 575 g 335 t

ORIGIN

Query Match 100.0%; Score 556; DB 6; Length 1747;

Best Local Similarity 100.0%; Pred. No. 1.2e-122;

Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTCGTGGTGGAGACGCTGTGATTGTTGGTTCTCTTTGAGCTGCTGGTACGGCT 60

Db 970 GTTCTTCGTGGTGGAGACGCTGTGATTGTTGGTTCTCTTTGAGCTGCTGGTACGGCT 1029

QY 61 CTTGTCTGTCCAAGCAGGCTATCTTCTCAAGAACGTGATGAACCTCATCGATTTTGT 120

Db 1030 CTTGTCTGTCCAAGCAGGCTATCTTCTCAAGAACGTGATGAACCTCATCGATTTTGT 1089

QY 121 GGCTATCTCTCTACTTTGTGGCACTGGGACCGAGCTGGCCGCGAGAGGGGTGGG 180

Db 1090 GGCTATCTCTCTACTTTGTGGCACTGGGACCGAGCTGGCCGCGAGAGGGGTGGG 1149

QY 181 CCAGCAGGCCATGTCACTGGCCATCTTGAGATCATCGATTTGGTGGCTGCTTCGCGCAT 240

Db 1150 CCAGCAGGCCATGTCACTGGCCATCTTGAGATCATCGATTTGGTGGCTGCTTCGCGCAT 1209

QY 241 CTTCAAGCTGTCCCGGCACTCAAGGGCTGCAAAATCTTTGGGCCAGAGCTTCGGGCTTC 300

Db 1210 CTTCAAGCTGTCCCGGCACTCAAGGGCTGCAAAATCTTTGGGCCAGAGCTTCGGGCTTC 1269

QY 301 CATGGTGGAGCTGGCCCTCATCTTTTCTCTCTCTCATCGGTGGTCTCTTTTCCAG 360

Db 1270 CATGGTGGAGCTGGCCCTCATCTTTTCTCTCTCTCATCGGTGGTCTCTTTTCCAG 1329

QY 361 CGCGCTCTACTTTGGCGAAGTTGACCGGTGGACTTCCCATTTCTACTAGCATCCCTGAGTC 420

Db 1330 CGCGCTCTACTTTGGCGAAGTTGACCGGTGGACTTCCCATTTCTACTAGCATCCCTGAGTC 1389

QY 421 CTTCTGGTGGCGGTAGTCACCATGACTACAGTTGGCTATGAGACATGGCACCCGTCAC 480

Db 1390 CTTCTTCGTGGCGGTAGTCACCATGACTACAGTTGGCTATGGAGACATGGCACCCGTCAC 1449

QY 481 TGTGGTGGCAAGATAGTGGGCTCTCTGTGTGCCATTTGGGGCGTGTGCTGACTATTTCCCT 540

Db 1450 TGTGGTGGCAAGATAGTGGGCTCTCTGTGTGCCATTTGGGGCGTGTGCTGACTATTTCCCT 1509

QY 541 GCCAGTGGCCGTCATT 556

Db 1510 GCCAGTGGCCGTCATT 1525

RESULT 4

LOCUS AC008687/c

DEFINITION Homo sapiens chromosome 19 clone CTB-60B18, complete sequence.

ACCESSION AC008687

VERSION AC008687.5 GI:15887249

KEYWORDS HTG.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

JOURNAL 1 (bases 1 to 157633)

REFERENCE 2

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

2 (bases 1 to 157633)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

3 (bases 1 to 157633)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (27-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 4

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (03-OCT-2001)/DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On Oct 3, 2001 this sequence version replaced gi:10312243.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.9% of Sequence;

Estimated Total Number of Errors is 0.2.

STS Content:

SHGC-15869 G15229

SHGC-15864 G15225

SHGC-5822 G14090

SHGC-58615 G42524.

Location/Qualifiers

1. 157633

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="19"

/clone="CTB-60B18"

BASE COUNT 33926 a 43885 c 42816 g 37006 t

ORIGIN

Query Match 100.0%; Score 556; DB 9; Length 157633;

Best Local Similarity 100.0%; Pred. No. 1.5e-122;

Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CTTGTGCTGTCCAAGCAGGCTATCTTCTCAAGAACGTGATGAACCTCATCGATTTTGT 120

Db 82058 CTTGTGCTGTCCAAGCAGGCTATCTTCTCAAGAACGTGATGAACCTCATCGATTTTGT 81999

QY 121 GGCATATCTTCCCTACTTTGTGCACTGGGCACCGAGCTGGCCCGCAGCGAGGGGTGGG 180
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Db 81998 GGCATATCTTCCCTACTTTGTGCACTGGGCACCGAGCTGGCCCGCAGCGAGGGGTGGG 81939
QY 181 CCAGCAGGCCATGTCACTGGCCATCTGAGATCATCCCATGGTGGTCTTCCGCAT 240
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Db 81938 CCAGCAGGCCATGTCACTGGCCATCTGAGATCATCCCATGGTGGTCTTCCGCAT 81879
QY 241 CTTCAAGCTGTCCCGCACTCAAAGGCTGCAAAATCTTTGGGCCAGACGCTTCGGGCCCTC 300
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QY 301 CATCGCTGAGCTGGGCTCTCATCTTTTTCCTCTTCATCGGTGGTCTCTTTTCCAG 360
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QY 361 CGCGCTCTACTTTCGCGAAGTTGACCGGGTGGACTCCCATTTTCATAGATCCCTGAGTC 420
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Db 81758 CGCGCTCTACTTTCGCGAAGTTGACCGGGTGGACTCCCATTTTCATAGATCCCTGAGTC 81699
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Db 81698 CTTCTGGTGGGGTGTAGTCACATGACTACAGTTGGCTATGAGACATGSCACCGCTCAC 81639
QY 481 TGTGGTGGCAAGATAGTGGGCTCTCTGTGTCATTTGTCATCGGTGGTCTCTTTTCCCT 540
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Db 81638 TGTGGTGGCAAGATAGTGGGCTCTCTGTGTCATTTGTCATCGGTGGTCTCTTTTCCCT 81579
QY 541 GCCAGTGCCCGTCATT 556
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Db 81578 GCCAGTGCCCGTCATT 81563

RESULT 5
HSA310479
LOCUS
DEFINITION
Homo sapiens mRNA for potassium voltage-gated channel, shaker-related subfamily, member 7 (KCNA7 gene).
ACCESSION
AJ310479
VERSION
AJ310479.1 GI:12830376
KEYWORDS
KCNA7 gene; Kv1.7 gene; potassium voltage-gated channel, shaker-related subfamily, member*.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 4372)
AUTHORS
Kashuba,V.I., Kvasha,S.M., Protodopov,A.I., Gizatullin,R.Z., Rynditch,A.V., Wahlestedt,C., Wasserman,W.W. and Zabarovsky,E.R.
TITLE
Initial isolation and analysis of the human Kv1.7 (KCNA7) gene, a member of the voltage-gated potassium channel gene family
JOURNAL
Gene 268 (1-2), 115-122 (2001)
MEDLINE
21261947
PUBMED
11368907
REFERENCE
2 (bases 1 to 4372)
AUTHORS
Kashuba,V.
TITLE
Direct Submission
JOURNAL
Submitted (09-FEB-2001) Kashuba V., Microbiology and Tumorbiology Center, Karolinska Institute, Box 280, 171 77, SWEDEN
FEATURES
Location/Qualifiers
source
1..4372
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/db_xref="taxon:9606"
/chromosome="19"
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/codon_start=1

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BASE COUNT 930 a 1117 c 1408 g 917 t
Query Match 99.7%; Score 554.4; DB 9; Length 4372;
Best Local Similarity 99.8%; Pred. No. 3.1e-122;
Matches 555; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCTTCGTGGTGAGACGCTGTGTAATTTTGGTTCTCTCTTTGAGCTGCTGGTAGCCCT 60
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Db 980 GTTCTTCGTGGTGAGACGCTGTGTAATTTTGGTTCTCTCTTTGAGCTGCTGGTAGCCCT 1039
QY 61 CTTGCTCTCTCCAAAGCAAGGCTATCTTCTCAAGAACGTCATGAACCTCATCGATTTTGT 120
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Db 1040 CTTGCTCTCTCCAAAGCAAGGCTATCTTCTCAAGAACGTCATGAACCTCATCGATTTTGT 1099
QY 121 GCGTATCTTCCCTACTTTTGGCACTGGGCACCGAGCTGGCCCGCAGCGAGGGGTGGG 180
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Db 1100 GCGTATCTTCCCTACTTTTGGCACTGGGCACCGAGCTGGCCCGCAGCGAGGGGTGGG 1159
QY 181 CCAGCAGGCCATGTCACTGGCCATCTCTGAGAGTCATCCGATTTGGTGTCTTCCGCAT 240
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Db 1160 CCAGCAGGCCATGTCACTGGCCATCTCTGAGAGTCATCCGATTTGGTGTCTTCCGCAT 1219
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Db 1220 CTTCAAGCTGTCCCGCACTCAAAGGCTCGCAAAATCTTTGGGCCAGACGCTTCGGGCCCTC 1279
QY 301 CATCGTGAGCTGGGCTCTCTCATCTTTTCTCTTCATCGGTGGTGTCTTTTCCAG 360
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Db 1280 CATCGTGAGCTGGGCTCTCTCATCTTTTCTCTTCATCGGTGGTGTCTTTTCTAG 1339
QY 361 CGCGCTCTACTTTGCCAAGTTGACCGGCTGGACTCCCATTTCCATAGCATCCCTGAGTC 420
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Db 1340 CGCGCTCTACTTTGCCAAGTTGACCGGCTGGACTCCCATTTCCATAGCATCCCTGAGTC 1399
QY 421 CTTCTGGTGGGCGGTAGTCACCATGACTACAGTTGGCTATGGAGACATGGCACCCGCTCAC 480
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Db 1400 CTTCTGGTGGGCGGTAGTCACCATGACTACAGTTGGCTATGGAGACATGGCACCCGCTCAC 1459
QY 481 TGTGGTGCAAGATAGTGGGCTCTCTGTGCCATTTGGGGGCTGCTGACTATTTTCCCT 540
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Db 1460 TGTGGTGCAAGATAGTGGGCTCTCTGTGCCATTTGGGGGCTGCTGACTATTTTCCCT 1519
QY 541 GCCAGTGCCCGTCATT 556
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Db 1520 GCCAGTGCCCGTCATT 1535
RESULT 6
AX354900
LOCUS
DEFINITION
Sequence 10 from Patent WO0192303.
ACCESSION
AX354900
VERSION
AX354900.1 GI:18619603
KEYWORDS
human.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1

AUTHORS Benjamin,C.W., Roberds,S.L., Karnovsky,A.M., Ruble,C.L. and Gotow,L.F.
TITLE Human ion channels
JOURNAL Patent: WO 0192303-A 10 06-DEC-2001;
PHARMACIA & UPJOHN COMPANY (US)
FEATURES Location/Qualifiers
source
1..691
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 113 a 207 c 185 g 186 t
ORIGIN

Query Match 95.7%; Score 532; DB 6; Length 691;
Best Local Similarity 100.0%; Pred. No. 6.5e-117;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTTCGTCGTCGAGACGCTGTGATTTGTTGGTTCTCTTTGAGCTGCTGGTAGCCCT 60
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QY 61 CCTGGTCTCTCCAAAGCAAGGCTATCTTCTCAAGAACGTCATGAACCTCATCGATTTTCT 120
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Db 220 CCTGGTCTCTCCAAAGCAAGGCTATCTTCTCAAGAACGTCATGAACCTCATCGATTTTCT 279
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QY 121 GGTATCTTCCTACTTTGTGGCACTGGGCACCGAGTCGGCCGCGACGAGGGGTGGG 180
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Db 280 GGTATCTTCCTACTTTGTGGCACTGGGCACCGAGTCGGCCGCGACGAGGGGTGGG 339
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QY 181 CCAGAGGGCCATGTCACCTGGCCATCTGAGAGTCATCCGATTTGGTGGTGTCTTCGGCAT 240
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Db 340 CCAGAGGGCCATGTCACCTGGCCATCTGAGAGTCATCCGATTTGGTGGTGTCTTCGGCAT 399
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QY 241 CTTCAAGCTGTCCCGCACTCAAGGGCTCAAGGGCTGCAAAATCTTTGGCCAGACGCTTCGGGCCCTC 300
Db 400 CTTCAAGCTGTCCCGCACTCAAGGGCTGCAAAATCTTTGGCCAGACGCTTCGGGCCCTC 459
QY 301 CATGCGTAGCTGGGCTCCTCATCTTTTCCTTCATCTTCATCGTGGTGGTCTCTTTTCCAG 360
Db 460 CATGCGTAGCTGGGCTCCTCATCTTTTCCTTCATCTTCATCGTGGTGGTCTCTTTTCCAG 519
QY 361 CGCGCTACTTTGCGGAAGTTGACCGGTGGACCTCCATTTTCATAGCATCCCTGAGTC 420
Db 520 CGCGCTACTTTGCGGAAGTTGACCGGTGGACCTCCATTTTCATAGCATCCCTGAGTC 579
QY 421 CTTCTGTCGGCGGTAGTCACCATGACTACAGTTGGCTATGGAGATGGACATGGCACCCGCTCAC 480
Db 580 CTTCTGTCGGCGGTAGTCACCATGACTACAGTTGGCTATGGAGATGGCACCCGCTCAC 639
QY 481 TGTGGTGCAAGATAGTGGGCTCTCTGTGGCCATTGGCGGCGTGGTGACT 532
Db 640 TGTGGTGCAAGATAGTGGGCTCTCTGTGGCCATTGGCGGCGTGGTGACT 691

RESULT 7
AC073711/c 208632 bp DNA linear HTG 18-JUL-2000
LOCUS Mus musculus clone RP23-193A10, WORKING DRAFT SEQUENCE, 7 ordered
DEFINITION pieces.
ACCESSION AC073711
VERSION AC073711.2 GI:9256763
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 208632)
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Mouse
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 208632)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint

COMMENT

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:8810328.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1810994
Center clone name: RPI-23_193A10

Summary Statistics
Consensus quality: 204234 bases at least Q40
Consensus quality: 207322 bases at least Q30
Consensus quality: 207805 bases at least Q20
Estimated insert size: 221930; agarose-fp estimation
Estimated insert size: 208382; sum-of-ctnigs-estimation
Quality coverage: 8.77 in Q20 bases; agarose-fp estimation
Quality coverage: 9.34 in Q20 bases; sum-of-ctnigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 ctnigs. Gaps between the ctnigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 93558: contig of 93558 bp in length
* 93559 93658: gap of unknown length
* 93659 94751: contig of 1093 bp in length
* 94752 94851: gap of unknown length
* 94852 118285: contig of 23434 bp in length
* 118286 118385: gap of unknown length
* 118386 157043: contig of 38658 bp in length
* 157044 157143: gap of unknown length
* 157144 164561: contig of 7418 bp in length
* 164562 164661: gap of unknown length
* 164662 176791: contig of 12130 bp in length
* 176792 176891: gap of unknown length
* 176892 208632: contig of 31741 bp in length.
FEATURES
Location/Qualifiers
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/organism="Mus musculus"
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/clone_lib="RPI mouse BAC library 23"
BASE COUNT 48823 a 51932 c 52697 g 54580 t 600 others
ORIGIN

Query Match 79.1%; Score 439.8; DB 2; Length 208632;
Best Local Similarity 87.0%; Pred. No. 9.9e-95;
Matches 483; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 2 TTCTTCGTGTGAGACGCTGTGATTTGTTGGTTCTCTCTTTGAGCTGCTGGTAGCCCTC 61
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Db 72070 TTCTTTGTCGTGAGACCCCTGTGATCTGCTGCTTCTCTTTGAGCTGCTGGTGCCTG 72011
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QY 62 CTGGTCTGTCCAAAGCAAGGCTATCTTCTCAAGAACGTCATGAACCTCATCGATTTTGTG 121
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Db 72010 GTGGCCTGCCCTAGCAAGGCTGTGTTCTTCAAGAAATGTATGAACCTAATTGACTTCGTG 71951
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QY 122 GCTATCTTTCCTTACTTTTGTGGCACTGGCAGCGAGCTGGCCGGCAGGAGGGTGGGC 181
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Db 71950 GCATCTCTGCTTACTTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 71891
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QY 182 CAGCAGGCCATGTCTACTGGCCATCTCTGAGATCATCCGATTTGGTGGTGTCTTCCGCATC 241
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Db 71890 CAGCGGCTATGTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 71831
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QY 242 TTCAAGCTGTCCGGCGCACTCAAGAGGCCCTGCAAAATCTTGGGCGACAGCTTCCGGGCTCC 301
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Db 71830 TTCAAGCTGTCCAGGCAATTCGAAGGCTCTACAGATCTTGGGTTCAGACACTTCGCGGCTCC 71771

AUTHORS Kalman,K., Nguyen,A., Tseng-Crank,J., Dukes,I.D., Chandy,G.,
Hustad,C.M., Copeland,N.G., Jenkins,N.A., Mohrenweiser,H.M.,
Brandriff,B., Cahalan,M.D., Gutman,G.A. and Chandy,K.G.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-1997) Physiology and Biophysics, University of
California, Irvine, CA 92697, USA
FEATURES
source location/Qualifiers
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/db_xref="taxon:10090"
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/gene="Kcna7"
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847..>2459
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ORIGIN
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Best Local Similarity 86.8%; Pred. No. 1.9e-94;
Matches 482; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 2 TTCTTCGTGGTGAGACGCTGTGATTTTGTGGTTCTCCTTTGAGCTGCTGATCGCCTC 61
DB 100 TTCTTTGTGGTGAGACCCCTGTATCTGCTGGTTCTCCTTTGAGCTGCTGATCTG 159
QY 62 CTGGTCTGTCCAAGCAAGGCTATCTTCTTCAAGACGCTGATGAACCTCATCGATTTTGG 121
DB 160 GTGGCTGCGCCTAGCAAAAGCTGTGTTCTTCAAGAATGTGATGAACCTAATTCAC 219
QY 122 GCTATCTTCCCTACTTTGTGCACTGGGACCGGCTGGCCCGGCGAGGAGGGTGGCG 181
DB 220 GCATCTCTCCCTTACTTCTGTGGCCCTGGGACGGAGTTAGCCCGGCGAGGGGTGGGC 279
QY 182 CAGCAGGCCATGCTACATGGCCATCTCTGAGAGTCATCCGATTTGGTGGCTGTCTTCGCGCATC 241
DB 280 CAGCGGCTATGTCCCTGGCCATCTAAGGTCATCCGATTTGGTGGCTGTCTTCGCGCATC 339
QY 242 TTCAAGCTGTCCGGGACTCAAGGCCCTGCAAAATCTTGGGCCAGACGCTTCGGGCTCC 301
DB 340 TTCAAGCTCTCCAGGCAATTCGAAGGCTCTACAGATCTTTGGGTCAACACACTGGGGCTTCC 399
QY 302 ATGCGTGAGCTGGGCTCTCTATCTTTTCCCTTCATCGGTGGTGGCTCTTTTCCAGC 361
DB 400 ATGCGTGAGCTAGGTCTCTCTATCTTTTCCCTTCATCTTCAATTTGGGCTGGTCTCTTTCCAGC 459
QY 362 GCGGTCTACTTTGCGCAAGTTGACCGGGTGGACTGCCATTTCACTAGCATCCCTGAGTCC 421

DB 460 GCAGTCTACTTTGCTGAAGTGGACCGGGTGGACACCCATTTCACCAAGCATCCCGGAGTCC 519
QY 422 TTCTGTGTGGCGGTAGTCACTACCATGACTACAGTTGGCTATGGAGACATGCACCCGTCAC 481
DB 520 TTTTGTGGGCAAGTGGTCACTACCATGACCCAGGTTGGCTATGGGACATGCACCCGTCAC 579
QY 482 GTGGGTGGCAAGATAGTGGGCTCTCTGTGTGCCATTTCGCGGGGTGCTGACTATTTCCCTG 541
DB 580 GTGGGTGGCAAGATCGTGGGCTCTCTGTGTGCCATTTCGAGGTGTGCTCACCACATCTCTCTG 639
QY 542 CCAGTGCCCGCTCATTT 556
DB 640 CCTGTGCTGTTCATT 654
RESULT 10
I26643
LOCUS I26643
DEFINITION Sequence 9 from patent US 5559009.
ACCESSION I26643
VERSION I26643.1 GI:1606513
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Chandy,K.G., Kalman,K., Chandy,G. and Gutman,G.A.
TITLE Voltage-gated potassium channel gene, Kvl.7, vectors and host cells
comprising the same, and recombinant methods of making potassium
channel proteins
JOURNAL Patent: US 5559009-A 9 24-SEP-1996;
FEATURES
Location/Qualifiers
source 1..1599
BASE COUNT 233 a 521 c 502 g 343 t
ORIGIN
Query Match 78.5%; Score 436.6; DB 6; Length 1599;
Best Local Similarity 86.7%; Pred. No. 4.6e-94;
Matches 481; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 2 TTCTTCGTGGTGAGACGCTGTGATTTTGTGGTTCTCCTTTGAGCTGCTGTGATCGCCTC 61
DB 853 TTCTTTGTGGTGAGACCCCTGTATCTGCTGTTCTCCTTTGAGCTGCTGGTGATCTG 912
QY 62 CTGGTCTGTCCAAGCAAGGCTATCTTCTTCAAGACGCTGATGAACCTCATCGATTTTGG 121
DB 913 GTGGCTGCGCCTAGCAAAAGCTGTGTTCTTCAAGAATGTGATGAACCTAATTCAC 972
QY 122 GCTATCTTCCCTACTTTGTGCACTGGGACCGGCTGGCCCGGCGAGGAGGGTGGGC 181
DB 973 GCATCTCTCCCTTACTTCTGTGGCCCTGGGACGGAGTTAGCCCGGCGAGGGGTGGGC 1032
QY 182 CAGCAGGCCATGCTACTGGCCATCTCTGAGAGTCATCCGATTTGGTGGCTGTCTTCCGCATC 241
DB 1033 CAGCGGCTATGTCCCTGGCCATCTTAAGGTCATCCGATTTGGTGGCTGTCTTCCGCATC 1092
QY 242 TTCAAGCTGTCCGGGACTCAAGGCCCTGCAAAATCTTGGGCCAGACGCTTCGGGCTCC 301
DB 1093 TTCAAGCTCTCCAGGCAATTCGAAGGCTCTACAGATCTTGGGTCAACACACTGGGGCTTCC 1152
QY 302 ATGCGTGAGCTGGGCTCTCTGATCTTTTCCCTCTTCACTGGTGGTGGCTCTTTTCCAGC 361
DB 1153 ATGCGTGAGCTAGGTCTCTCTATCTTCTTCTTCAATTTGGGCTGGTGGCTCTTTTCCAGC 1212
QY 362 GCGGTCTACTTTGCGCAAGTTGACCGGGTGGACTGCCATTTCACTAGCATCCCTGAGTCC 421
DB 1213 GCAGTCTACTTTGCTGAAGTGGACCGGGTGGACACCCATTTCAACAGCATCCCGGAGTCC 1272
QY 422 TTCTGTGTGGGCGGTAGTCACTACATGACTACAGTTGGCTATGGAGACATGCACCCGTCAC 481
DB 1273 TTTTGTGGGCAAGTGGTCACTACCATGACACGGTTGGCTATGGGACATGCACCCGTCAC 1332

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QY 482 GTGGGTGGCAAGATAGTGGCTCTCTGTGTGCGCATTCGGGGCGTGTGCTGACATTTCCCTG 541
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|||||
QY 542 CCAGTGGCCCGTCATT 556
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Db 1393 CCGTGGCTGTCTATT 1407

RESULT 11
AC128792
LOCUS
DEFINITION
AC128792 172671 bp DNA linear HTG 24-JUL-2002
Rattus norvegicus clone CH230-262A9, *** SEQUENCING IN PROGRESS
***, 55 unordered pieces.
AC128792
VERSION
AC128792.1 GI:21952595
HTG: HTGS_PHASE1.
KEYWORDS
Rattus norvegicus.
SOURCE
Rattus norvegicus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 172671)
Muzny,D.M., Adams,C.C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayelle,M., Banks,T.,
Barberia,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,K., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davalila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,B., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
Homi,F., Howard,S., Huber,J., Hulyk,S., Hune,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
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Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
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Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Picken,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rivers,M., Rojas,A., Rojibokan,I., Roife,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vaquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wlarczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 172671)
Worley,K.C.
Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
```

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KAJM
Center clone name: CH230-262A9
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 108496 bases at least Q40
Consensus quality: 114733 bases at least Q30
Consensus quality: 119570 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 55 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1740: contig of 1740 bp in length
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* 1841 3040: contig of 1200 bp in length
* 3041 3140: gap of unknown length
* 3141 4347: contig of 1207 bp in length
* 4348 4447: gap of unknown length
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* 5659 5759: gap of unknown length
* 5759 7165: contig of 1307 bp in length
* 7166 8912: contig of 1747 bp in length
* 8913 9012: gap of unknown length
* 9012 10121: contig of 1109 bp in length
* 10122 10221: gap of unknown length
* 10222 11495: contig of 1274 bp in length
* 11496 11595: gap of unknown length
* 11596 12895: contig of 1300 bp in length
* 12896 12995: gap of unknown length
* 12996 14935: contig of 1940 bp in length
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* 18287 18386: gap of unknown length
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* 20382 21823: contig of 1342 bp in length
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* 21924 23103: contig of 1180 bp in length
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* 26342 28299: contig of 1958 bp in length
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* 31292 33131: contig of 1840 bp in length
* 33132 33231: gap of unknown length
* 33232 35206: contig of 1975 bp in length
* 35207 35306: gap of unknown length
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* 39779: gap of unknown length

ORIGIN

Query Match 74.9%; Score 416.6; DB 9; Length 770;
Best Local Similarity 94.0%; Pred. No. 2.7e-89;
Matches 453; Conservative 0; Mismatches 27; Indels 2; Gaps 2;

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QY 61 CTTGGTCTGTCCCAAGCAAGCTATCTTCTTCAAGAAGCTGATGAACCTCATCGATTTGT 120
DB 350 CTTGGTCTGTCCCAAGCAAGCTATCTTCTTCAAGAAGCTGATGAACCTCATCGATTTGT 409
QY 121 GGCTATCTTCCCTACTTTTGTGGCACTGGCACCAGCTGGCCGGCAGCGAGGGGTGGG 180
DB 410 GGCTATCTTCCCTACTTTTGTGGCACTGGCACCAGCTGGCCGGCAGCGAGGGGTGGG 469
QY 181 CCAGCAGCCATGTCACCTGCGCATCTCTGAGATCATCCGATTTGGTGGTGTCTTCCGCAT 240
DB 470 CCAGCAGCCATGTCACCTGCGCATCTCTGAGATCATCCGATTTGGTGGTGTCTTCCGCAT 529
QY 241 CTTCAAGCTGTCCGGCAGCTCAAGGGCCTGCAAAATCTTGGCCAGACGCTTCGGGCCTC 300
DB 530 CTTCAAGCTGTCCGGCAGCTCAAGGGCCTGCAAAATCTTGGCCAGACGCTTCGGGCCTC 589
QY 301 CATGCGTGAGCTGGCCCTCCTCATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 360
DB 590 CATGCGTGAGCTGGCCCTCCTCATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 648
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DB 709 TTTTGTGGGGCGGAAG-CACCATGACTACAGTGGCTATGGAAACATGACCCCTTACT 767
QY 481 TG 482
DB 768 TG 769

RESULT 13
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LOCUS
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
ACCESSION AJ338833
VERSION AJ338833.1 GI:15883251
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 664)
AUTHORS Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M., Podowsky, R.M., Matshkin, Y.G., Gyanchandani, A., Muravenko, O.V., Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I., Kiselev, L.I., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.
TITLE NotI flanking sequences: a tool for gene discovery and verification of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PUBMED 12136098
REFERENCE 2 (bases 1 to 664)
AUTHORS Zabarovsky, E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre, Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77, Sweden
FEATURES
source Location/Qualifiers
1. .664

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ORIGIN

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Best Local Similarity 97.1%; Pred. No. 4.9e-75;
Matches 363; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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QY 241 CTTCAAGCTGTCCGGCAGCTCAAGGGCCTGCAAAATCTTGGCCAGACGCTTCGGGCCTC 300
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RESULT 14
AX268139
LOCUS
DEFINITION Sequence 25 from Patent WO0168851.
ACCESSION AX268139
VERSION AX268139.1 GI:16516630
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Padigaru, M., Vernet, C.A., Fernandes, E., Shimkets, R.A., Spaderna, S.K., Majumder, K. and Li, L.
TITLE Polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0168851-A 25 20-SEP-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
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RESULT 15
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LOCUS AX268140 420 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 26 from Patent WO0168851.
ACCESSION AX268140
VERSION AX268140.1 GI:16516631
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Padigaru, M., Vernet, C.A., Fernandes, E., Shinkets, R.A.,
TITLE Spaderna, S.K., Majumder, K. and Li, L.
JOURNAL Polypeptides and nucleic acids encoding same
Patent: WO 0168851-A 26 20-SEP-2001;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.3e-73;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 GGCTATCCTTCCCTACTTTGTGGCACTGGCGACCGAGCTGGCCGCGCAGGAGGGGTGGG 180
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GenCore version 5.1.3
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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Listing first 45 summaries

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3	2620.5	89.8	157633	9	AC008687 Homo sapi
4	2402	82.3	1447	9	AF315818 Homo sapi
5	2288.5	78.4	1341	6	AX352535 Sequence
6	2210.5	75.8	1599	10	AF032099 Mus muscu
7	2203	75.5	1599	6	I26643 Sequence 9
8	1992.5	68.3	208632	2	AC073711 Mus muscu
9	1962.5	67.3	172671	2	AC128792 Rattus no
10	1584	54.3	2264	10	RATKV3AA
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25	1530	52.4	2397	9	HUMKCHN
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27	1523	52.2	191664	2	AC125751
28	1523	52.2	198849	2	AC129061
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35	1508.5	51.7	4384	4	AF286022
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ALIGNMENTS

RESULT 1

AX268121
LOCUS AX268121 1747 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 7 from Patent WO0168851.
ACCESSION AX268121
VERSION AX268121.1 GI:16516622
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Padigaru, M., Vernet, C.A., Fernandes, E., Shinkets, R.A.,
Spaderna, S.K., Majumder, K. and Li, L.
TITLE Polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0168851-A 7 20-SEP-2001;
Curagen Corporation (US)
FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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ORIGIN
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Score: 2918.00 Matches: 559
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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DB 38 ATGGAGAGACGGACAGATCCCGCGCAGAGAGGAGGAGAGAGGACCCCGGG 97
QY 21 ThrGlyLysAlaGlnSerArgArgGlyArgArgArgGlyArgGlyArgAla 40
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
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JOURNAL	DOE Joint Genome Institute and Stanford Human Genome Center.		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 157633)		
TITLE	DOE Joint Genome Institute.		
JOURNAL	Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint		
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AUTHORS	3 (bases 1 to 157633)		
TITLE	DOE Joint Genome Institute and Stanford Human Genome Center.		
JOURNAL	Submitted (27-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell		
REFERENCE	Drive, Walnut Creek, CA 94598, USA		
AUTHORS	4 (bases 1 to 157633)		
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1
TITLE Curtis, R.A.
JOURNAL 52906, 33408, and 12189, potassium channel family members and uses
thereof
PUBLISHED 2001
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Pharmaceuticals, Inc. (US)
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QY 193 GluGluValAlaPheTyGlyLeuGlyAlaAlaAlaLeuAlaArgLeuArgGluAspGlu 212
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Db 241 GAAGAGTGGCTTCTACGGCTGGCGCGCGCGCGCGCTGGCGCGCTGGCGGACGAG 300

QY 213 GlyCysProValProProGluArgProLeuProArgArgAlaPheAlaArgGlnLeuTrp 232
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QY 233 LeuLeuPheGluPheProGluSerSerGlnAlaAlaArgValLeuAlaValSerVal 252
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Db 361 CTGCTTTTCGAGTTTCCCGAGAGCTCTCAGCGCCGCGCGCTGCTCGCGTAGTCTCGGTG 420
QY 253 LeuValIleLeuValSerIleValValPheCysLeuGluThrLeuProAspPheArgAsp 272
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QY 273 AspArgAspGlyThrGlyLeuAlaAlaAlaAlaAlaAlaAlaAlaAlaPro 292
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QY 293 LeuAsnGlySerSerGlnMetProGlyAsnProArgLeuProPheAsnAspProPhe 312
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QY 313 PheValValGluThrLeuCysIleCysTrpPheSerPheGluLeuValArgLeuLeu 332
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QY 333 ValCysProSerLysAlaIlePhePheLysAsnValMetAsnLeuIleAspPheValAla 352
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QY 353 IleLeuProTyPheValAlaLeuGlyThrGluLeuAlaArgGlnArgGlyValGln 372
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Db 778 CAGGCCATGTCTACTGGCCATCTCTGAGAGTCATCCGATTTGTTGCTGTTCCGATCTTC 837
QY 393 LysLeuSerArgHisSerLysGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaSerMet 412
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QY 413 ArgGluLeuGlyLeuLeuIlePhePheLeuPheIleGlyValValLeuPheSerSerAla 432
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Db 898 CGTGAGCTGGGCTCTCTCATCTTTTCTTCATCGGTGTGGTCTCTTTTCCAGGGCC 957
QY 433 ValTyPheAlaGluValAspArgValAspSerHisPheThrSerIleProGluSerPhe 452
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Db 958 GTCTACTTTGCCGAAAGTTGACCGGGTGGACTCCCATTTCTACTAGCATCCCTGAGTCTTC 1017
QY 453 TrpTrpAlaValValThrMetThrThrValGlyTyGlyAspMetAlaProValThrVal 472
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QY 473 GlyGlyLysIleValGlySerLeuCysAlaIleAlaGlyValLeuThrIleSerLeuPro 492
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QY 493 ValProValIleValSerAsnPheSerTyPheTyHisArgGluThrGluGlyGluGlu 512
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QY 513 AlaGlyMetPheSerHisValAspMetGlnProCysGlyProLeuGluGlyLysAlaAsn 532
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QY 533 GlyGlyLeuValAspGlyGluValProGluLeuProProLeuTrpAlaProProArg 552
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Db 1258 GGGGGCTGTGGAGCGGGGAGGTACCTGAGCTACCACTCCACTCTGGGGCACCCCGAGGG 1317
QY 553 GluHisLeuValThrGluVal 559
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Db 1318 AAACACCTGCTACCCGAAGTG 1338

RESULT 6
AF032099 AF032099 1599 bp mRNA linear ROD 04-APR-1998
LOCUS

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Qy 435 PheAlaGluValAspArgValAspSerHisPheThrSerIleProGluSerPheTrpTrp 454
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Qy 455 AlaValValThrMetThrThrValGlyTyrGlyAspMetAlaProValThrValGlyGly 474
Db 1282 GCAGTGGTACCATGACACCATGGTGGCTATGGGACATGGACCGCTACCGTGGGTGGC 1341
Qy 475 LysIleValGlySerLeuCysAlaIleAlaGlyValLeuThrIleSerLeuProValPro 494
Db 1342 AAGATCGTGGGCTCTCTGTGTGCCATTCAGGTGTGCTACCACTCTCTGCTGTGGCT 1401
Qy 495 ValIleValSerAsnPheSerTyrPheTyrHisArgGluThrGluGlyGluAlaGly 514
Db 1402 GTCATTGTCTCTAACTTTAGCTACTTTTACCACCGGGAGACAGAGGGCGAAGAGCAGG 1461
Qy 515 MetPheSerHisValAspMetGlnProCysGlyProLeuGluGlyLysAlaAsnGlyGly 534
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Qy 555 LeuValThrGluVal 559
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RESULT 7
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DEFINITION Sequence 9 from patent US 5559009.
ACCESSION I26643
VERSION I26643.1 GI:1606513
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Chandy, K.G., Kalman, K., Chandy, G. and Gutman, G.A.
TITLE Voltage-gated potassium channel gene, Kv1.7, vectors and host cells comprising the same, and recombinant methods of making potassium channel proteins
JOURNAL Patent: US 5559009-A 9 24-SEP-1996;
FEATURES Location/Qualifiers
source 1..1599 /organism="unknown"
BASE COUNT 233 a 521 c 502 g 343 t
ORIGIN

Alignment Scores:
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Best Local Similarity: 83.09% Mismatches: 61
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US-09-804-014A-8 (1-559) x I26643 (1-1599)

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Db 166 ACACCCGACTGGGT-----GGCTGCGGCGTGGGGCCACACGTCCTCCGTTACCGGT 216
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Qy 156 ArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyrGln 175
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Qy 176 SerGlyGlyArgLeuArgProAlaHisValProLeuAspValPheLeuGluVal 195
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pieces
AC073711
VERSION AC073711.2 GI:9256763
KEYWORDS HTG; HTGS-PHASE2; HTGS-DRAFT.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 208632)
DOE Joint Genome Institute.
TITLE Sequencing of Mouse
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 208632)
DOE Joint Genome Institute.
DIRECT SUBMISSION
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:8810328.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1810994
Center clone name: RPCI-23_193A10

Summary Statistics
Consensus quality: 204234 bases at least Q40
Consensus quality: 207322 bases at least Q30
Consensus quality: 207805 bases at least Q20
Estimated insert size: 221930; agarose-fp estimation
Estimated insert size: 208382; sum-of-contigs estimation
Quality coverage: 8.77 in Q20 bases; agarose-fp estimation
Quality coverage: 9.34 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and

* the accession number will be preserved.
* 1 93558: contig of 93558 bp in length
* 93559 93658: gap of unknown length
* 93659 94751: contig of 1093 bp in length
* 94752 94851: gap of unknown length
* 94852 118285: contig of 23434 bp in length
* 118286 118385: gap of unknown length
* 118386 157043: contig of 38658 bp in length
* 157044 157143: gap of unknown length
* 157144 164561: contig of 7418 bp in length
* 164562 164661: gap of unknown length
* 164662 176791: contig of 12130 bp in length
* 176792 176891: gap of unknown length
* 176892 208632: contig of 31741 bp in length.
FEATURES
Location/Qualifiers
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/clone="RP23-193A10"
/clone_lib="RPCI mouse BAC library 23"
BASE COUNT 48823 a 51932 c 52697 g 54580 t 600 others
ORIGIN
Alignment Scores:
Pred. No.: 1.15e-58 Length: 208632
Score: 1992.50 Matches: 473
Percent Similarity: 40.02% Conservative: 14
Best Local Similarity: 38.87% Mismatches: 59
Query Match: 68.28% Indels: 673
DB: 2 Gaps: 8
US-09-804-014A-8 (1-559) x AC073711 (1-208632)
QY 3 ArgArgArgThrGlySerArg-----ArgGlnLysAspGlyGluLysGlyAsp 18
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Db 74941 AGGAGGATCAATAATCAAGGTCAGTACAGTACATAGACCTCGGTCATGAATCCAAA 74882
QY 19 ProGlyThrGlyLysAlaGlnSerArgArgGlyArgArgArgArgGlyArgAlaGly 38
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Db 74881 AGCCAAACAATAAATAATAGTACTACAAGGAAAGAACTCAAGAGATCCACGGAAAAAGCGC 74822
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Db 74821 CGGGTGGCAGTGTTCACAGGTGTGGGAACGACGACGGCG-----CCC 74777
QY 52 LeuArgProAlaGlyValThrValProProProSerArgProSerArgProAlaGlyLeu 71
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Db 74776 CTAGC-CCCGCGGGGTAAACACGCCGCCCTCCCGCGCCCTGGCGCG-----ACT 74727
QY 72 PheTyrAla-----ArgThrProAspThrGlyHisArgAlaGlyAla 85
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QY 86 AlaValGlyAlaThrArgArgPheAlaGlyArgGlyCysAlaArgHisGlyAlaAla 105
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QY 106 ValProAlaAlaProCysGlyCysGlyArgLeuValLeuAsnValAlaGlyLeuArg 125
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Db	73897	CGAGATCTACAGGAGACAGACGATTGCCAGGGTTGAAGCCAGTGTTGGTTACT	73838
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Db 71557 ATTTGAGGTGTGTCACCATCTCTCGCTGTGCTGTCTATCTCTACTTACTTAGCTAC 71498
QY 503 PheTyrHisArgGluThrGluGlyGluAlaGlyMetPheSerHisValAspMetGln 522
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QY 523 ProCysGlyProLeuGluGlyLysAlaAsnGlyLeuValAspGlyGluValProGlu 542
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RESULT 9
AC128792 172671 bp DNA linear HTG 24-JUL-2002
DEFINITION Rattus norvegicus clone CH230-262A9, *** SEQUENCING IN PROGRESS
***, 55 unordered pieces.
ACCESSION AC128792
VERSION AC128792.1 GI:21952595
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 172671)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
```

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Alsbrooks, S. L., Amaratunga, H. C., Are, J. R., Ayele, M., Banks, T.,
Barbata, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N. P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K. L., Byrd, N. C.,
Carton, T. F., Carter, M., Cavazos, S. R., Chacko, J. J., Chavez, D.,
Chen, G., Chen, K., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C. D., Cox, C., Coyie, M. D., Dathorne, S. R., David, R.,
Davila, M. L., Davis, C., Davy-Carroll, L., Dederich, D. A.,
Delaney, K. R., Delgado, O., Denn, A. L., Ding, Y., Dinh, H. H.,
Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J.,
Earnhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, J. C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
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Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudan, S.,
Karlssohn, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
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Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G.,
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Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Woodson, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 172671)
Worley, K. C.
Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KAJM
Center clone name: CH230-262A9
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 108496 bases at least Q40
Consensus quality: 114733 bases at least Q30
Consensus quality: 119570 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 55 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

Db 86056 ||||| GACCGCGCGCACGCTCGCGCGCTTCGCGACACGCTGCTGGGGACCCGTGCGCGC 86115
QY 147 gGlyArgPheTyrAspAlaArgArgGluTyrPhePheAspArgHisArgProSerPh 167
Db 86116 | ||||| CACCGCGCTCTACAGCGCGCGCGCGAGTATTCTTCACCGACACCGCGCCAGCTT 86175
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LOCUS
DEFINITION Rat potassium channel-kv3 gene, complete cds.
2264 bp DNA linear ROD 27-APR-1993
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ACCESSION M31744
VERSION M31744.1
KEYWORDS potassium channel-Kv3; transmembrane protein.
SOURCE Rat brain DNA and cDNA to mRNA.
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 2264)
AUTHORS Luneau,C.J.
JOURNAL Unpublished (1990)
REFERENCE 2 (sites)
AUTHORS Swanson,R., Marshall,J., Smith,J., Williams,J., Boyle,M.B.,
Bennett,C., Steun,R.B. and Kaczmarek,L.M.
TITLE Cloning and expression of cDNA and genomic clones encoding three
delayed rectifier potassium channels in rat brain
JOURNAL Neuron 4 (6), 929-939 (1990)
MEDLINE 90297965
PUBMED 2361015
COMMENT [2] sites.
[1] for [2].
Computer readable copy of sequence [2],[1] kindly submitted by
R.J.Swanson, 16-AUG-1989, for release after publication.
[1] Author Address
Merch, Sharp, and Dohme Research Labs
W42-300
West Point, PA 19486
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Best Local Similarity: 55.40% Mismatches: 124
Query Match: 54.28% Indels: 101
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QY 24 AlaGlnSerArgGlyArgArgArgArgGlyArgAlaGlyArgAlaSer----- 41
Db 199 GGAGGAGGAGG-----AGGAGCGCTCTGGACGTCGACCGCGGGCGCGCCAGCC 252
QY 42 -----ArgGlnArgAlaArgGlyArgPro 49
Db 253 CTGACAGACCTCGCGGACCGCCACACAGCGCGCGCGCGCTCGTGGGGCAGAG 312
QY 50 ValAlaLeu-----ArgProAlaGlyValThr-----ValProPro----- 62
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[illegible]

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RESULT 15

HUMPOCH

LOCUS

DEFINITION

HOMO sapiens voltage-gated potassium channel (KCNA3) mRNA, complete cds.

ACCESSION

L23499

VERSION

L23499.1 GI:385222

KEYWORDS

KCNA3 gene; potassium channel; voltage-gated potassium channel.

SOURCE

Homo sapiens.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 1836)

AUTHORS

Folander, K., Lin, S., Koo, G. and Swanson, R.

TITLE Assignment of the gene encoding Kv1.3, a voltage gated potassium channel, to human chromosome 1
 JOURNAL Unpublished (1993)
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 /gene="KCNA3"
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 /codon_start=1
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 /protein_id="AAC31761.1"
 /db_xref="GI:385223"
 /translation="MTVVPGDHLLEPEVADGGGAPPGCGGGGCDRYEPLPPSLPAA
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 SFDALTYTQSGRRIRRVNVPIDIFSEIRFYQGEAMEKFRDEGFLREERPLP
 RRDFQWLLFEYPPSSGPARGAIVSLVILITIVIFCLELPFEDRDKYPASTS
 QDSFPAQNSTSGSRAGASFSFDPFVETLCITWFSFKLLVRFPACPSKATFSRNIM
 NLIDIVAPIYFILTGLAEQNGOQASLAILRVLRVRFRIFKLSRHSGLQI
 LGQTLKASMRGLLILFELFVGLVILFSSAVFAEADDPSTGFSSTPDFAFWAVVTMTT
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 Best Local Similarity: 58.82% Mismatches: 104
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 Qy 61 Pro-ProSerArgProSerArgProAlaGlyLeuPheTyr----- 73
 Db 70 CCGCGCCACCTCTCTCAGCGCCGAGCAGCGCGCGTGCACACACGCTGTGTGAACAC 129
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 Qy 94 aglyArgArg-GlyCysAlaArgHisGlyAlaAlaValProAlaAlaProCysGly---- 112
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Search completed: February 20, 2003, 13:59:47
Job time : 4829 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

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SUMMARIES

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ALIGNMENTS

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; Patent No. 5559009
; GENERAL INFORMATION:
; APPLICANT: Chandy, Kanianthara G.
; APPLICANT: Kalman, Katalin
; APPLICANT: Chandy, Grischa
; APPLICANT: Gutman, George A.
; TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel
; TITLE OF INVENTION: Gene
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert,
; ADDRESSEE: Attn: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,405A
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,431
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-59844-1/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
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QY 241 GGCCTTCTAC 250
DB 513 GTCCTTCTAC 522

RESULT 2
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; Sequence 1, Application US/08527152
; Patent No. 5827655
; GENERAL INFORMATION:
; APPLICANT: Chandry, Kanianthara G.
; APPLICANT: Cahalan, Michael D.
; APPLICANT: Grissmer, Stephan
; APPLICANT: Goldin, Alan L.
; APPLICANT: Dethlefs, Brent A.
; APPLICANT: Gutman, George A.
; APPLICANT: Wasmuth, John J.
; TITLE OF INVENTION: Assay, Methods and Products Based On n
; TITLE OF INVENTION: K+ Channel Expression
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
; ADDRESSEE: Attn: W.H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; FILING DATE: UNKNOWN
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/170,418
; FILING DATE: 20-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/558,568
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-54444-2/WH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 150..1736
US-08-527-152-1

Query Match      54.6%; Score 136.4; DB 1; Length 1994;
Best Local Similarity 71.8%; Pred. No. 2e-21;
Matches 179; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 1 GCGGCTGGTCTCAACGTGGCGGGCTGCGCTTCGAGACGGGGCGGCGGCGGCGGCGG 60
DB 320 GCGTGTGTCATCAACATCTCCGGGCTGCGCTTCGAGACGAGCTCAAGACCTCTGCCA 379
QY 61 CTTCCCGGACACTGCTAGGGACCCAGCGGCGGCGGCGGCTTCACGACGACGCGGCG 120
DB 380 GTTCCCGGAGACACTGCTGGGCGACCCCAAGCGGCGCATGCGGTACTTTGACCCACTCCG 439
QY 121 CCGGAGTATTCTTCGACCGGCGGCGGCGGCGGCGGCTTCGAGCGGCGGCTCTACTACTACCA 180
DB 440 CAATGAGTACTTCTTCGACCGCAACCGACGAGCTTCGAGCGGCGGCTCTACTACTACCA 499
QY 181 GTCGGTGGGCGGCTGCGGCGGCGGCGGCGGCGGCTTCGAGCTCTTCCTGGAAGAGT 240
DB 500 GTCGGGGGCGGCGATTCGCGGCGGCGGTCACGTCAGTGCCTTCCTCCGAGGAGAT 559
QY 241 GGCCTTCTAC 250
DB 560 CCGCTTTTAC 569

RESULT 3
US-09-336-643A-9
; Sequence 9, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3424
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (257)...(2195)
; OTHER INFORMATION: K+hnov12
US-09-336-643A-9

Query Match      31.2%; Score 78; DB 4; Length 3424;
Best Local Similarity 63.0%; Pred. No. 5.9e-09;
Matches 155; Conservative 0; Mismatches 85; Indels 6; Gaps 2;

QY 5 CTGCTGCTCAACGTGGCGGGCTGCGCTTCGAGACGGGGCGGCGGCGGCGGCTTC 64
||||| ||||||| ||| ||||||| ||||| ||| ||||||| ||||||| ||||||| |||||||
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Db 380 CTGGTGGTGAACGCTGACGGACGGCGCTTTGAGACTTGAAGAATACGCTGACCGCTAC 439
QY 65 CCGGACACTCTGCTAGGGACACGACGGCGCCGCGCGCTTCTACGACGACGGCGCGCG 124
Db 440 CCAGACACCTTCTGGGACGCTGGAGAG---GAATCTTCTACGATGCTACTCAGCG 496
QY 125 GAGTATTTCTCGACGGGACGGCCAGCTTTCGACGGCGCTCTCTACTACTACCACTCC 184
Db 497 GAGTACTTCTCGATCGCGACCGCTGACATGTTCCGGCATGTGCTGAACCTTCTACCGAAC- 555
QY 185 GGTGGCGGCTGGGCGGCGCGGACGTCGCGCTGCGAGCTTCTCTGGAAGAGGTGGCC 244
Db 556 --GGGCGGCTGCAATGCCACGCGCAGGAGTGCATCCAGGCGCTTCGACGAAGAGTGGCT 613
QY 245 TTCTAC 250
Db 614 TTCTAC 619

RESULT 4
US-09-178-109-3
; Sequence 3, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Chang Ling, Huai-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; TITLE OF INVENTION: Polypeptides and Uses Therefor
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/09/178,109
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: human
US-09-178-109-3

Query Match 29.6%; Score 74; DB 4; Length 2064;
Best Local Similarity 61.6%; Pred. No. 4.3e-08;
Matches 154; Conservative 0; Mismatches 90; Indels 6; Gaps 2;

QY 1 GCGGCTGGTGTCAAGTGGCGGCGTGGCTTCGAGAGCGGCGCGCGCTGGCGCG 60
Db 192 GCTGATTGCTTCAAGTGGCGGAGGTTCAGACCTGGAGACCACTGGAGCG 251
QY 61 CTTCGCGGACACTCTGCTAGGGACCCAGCGCGCGCGCGCTTCTACGACGACGCGCG 120
Db 252 CTACCGGACACCTGCTGGGACGACGAGAGAGGTTCCTTCAACGAGGACAC--- 308
QY 121 CCGGAGTATTTCTCGACCGGACGGCCAGCTTCGACGGCGGCTCTACTACTACCA 180
Db 309 CAAGGAGTACTTCTTCGACCGGACCCGAGGTGTTCCGCTGCTGCTCAACTTCTACC- 367
QY 181 GTCCGGTGGGCGGCTGGCGCGCGGCGACGTCGCGCTGCGAGCTTCTCTGGAAGAGT 240
Db 368 --GCAGGGGAGCTGCATACCCGGCTACGAGTGCATCTCTGCTTACGACGAGCT 425
QY 241 GGCCTTCTAC 250
Db 426 GGCCTTCTAC 435

RESULT 5
US-09-142-791A-3
; Sequence 3, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Brill
; APPLICANT: Thierry Paul Gerard Calmels

; APPLICANT: Jean-Francois Simon Pierre Faivre
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-142-791A-3

Query Match 29.6%; Score 74; DB 4; Length 2072;
Best Local Similarity 61.6%; Pred. No. 4.3e-08;
Matches 154; Conservative 0; Mismatches 90; Indels 6; Gaps 2;

QY 1 GCGGCTGGTGTCAAGTGGCGGCGTGGCTTCGAGAGCGGCGCGCGCTGGCGCG 60
Db 120 GCTGATTGCTTCAAGTGGCGGAGGTTCAGACCTGGAGACCACTGGAGCG 179
QY 61 CTTCGCGGACACTCTGCTAGGGACCCAGCGCGCGCGCTTCTACGACGACGCGCG 120
Db 180 CTACCGGACACCTGCTGGGACGACGAGAGAGGTTCCTTCAACGAGGACAC--- 236
QY 121 CCGGAGTATTTCTTCGACCGGACCGGCCAGCTTCGACGGCGGCTCTACTACTACCA 180
Db 237 CAAGGAGTACTTCTTCGACCGGACCCGAGGTGTTCCGCTGCTGCTCAACTTCTACC- 295
QY 181 GTCCGGTGGGCGGCTGGCGCGCGGCGACGTCGCGCTGCGAGCTTCTCTGGAAGAGT 240
Db 296 --GCAGGGGAGCTGCATACCCGGCTACGAGTGCATCTCTGCTTACGACGAGCT 353
QY 241 GGCCTTCTAC 250
Db 354 GGCCTTCTAC 363

RESULT 6
US-09-142-791A-1
; Sequence 1, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Brill
; APPLICANT: Thierry Paul Gerard Calmels
; APPLICANT: Jean-Francois Simon Pierre Faivre
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1

QY 241 GGCCTTCTAC 250

; CURRENT FILING DATE: 1999-06-18
; CURRENT APPLICATION NUMBER: 00/077,350/0451

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1805 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
;
US-07-955-916-6

Query Match 23.8%; Score 59.4; DB 1; Length 1805;
Best Local Similarity 55.3%; Pred. No. 5.6e-05;
Matches 142; Conservative 0; Mismatches 105; Indels 9; Gaps 1

QY 1 GCGGCTGGTGTCAACGTGGCGGCTCGGCTTCGAGA-----CGCGGGCGGCGAC 51
DB 160 GCGCATCGTGATCAACGTGGCGGACCGGCCACACAGACGTACCGCTCGACGCTGGCGAC 219

QY 52 GCTGGGCGGCTTCCCGGACACTCTGCTAGGGGACCCAGCGCGCGCGCTTCTTACGA 111
DB 220 GCTGCCGCGACGCGCTTGCTGCTGCGAGACGCGGACGCCACAGCCACTTCGACTA 279

QY 112 CGAGCGGCGCGGAGATTTCTGACCGGACCGCGGCCAGCTTCGAGCGCGTGTCTA 171
DB 280 TGACCGCGTCCGACGAGTTCTTTCGACGCGCCACCGGCGCTCTCGCTCACATCCT 339

QY 172 CTACTACGATCCGTTGGCGGCTGCGGCGCGCGCGCGACGTCGCGCTCGACGCTTCT 231
DB 340 GAACATTACCGCACCGCAAGCTTCACTGCCCGCGCGACGTGGGCGCGCTCTTACGA 399

QY 232 GGAAGAGGTGGCTTCT 248
DB 400 GGAGAGTGGCTTCT 416

RESULT 11
US-08-403-852D-2
; Sequence 2, Application US/08403852D
; Patent No. 5891695
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanc, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,852D
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-00000
; TELEPHONE: (202) 408-4400
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: S.pristinaespiralis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1268
; US-08-403-852D-2

Query Match          16.7%; Score 41.8; DB 2; Length 1268;
Best Local Similarity 51.3%; Pred. No. 0.33;
Matches 97; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 44 GCGCGCACGCTGGCGCGCTTCCCGGACACTCTGCTAGGGAGACCCAGCGCGCGCGCGC 103
   || || || || || || || || || || || || || || || || || || || ||
Db 574 GCGCGCGCGCGCGCGCGCGCGCTCATCATCCAGCGCGCGCTCTCGCGGTGGGACGC 633

QY 104 TTCTAGACAGCGCGCGCGCGAGTATTTCTTTCAGCGGACCGCGCGCGCGCTTCGAGCGC 163
   || || || || || || || || || || || || || || || || || || || ||
Db 634 GAGTTGCGCGCGCGCGCGCGAGTATTTTACCGCGGACCAACCGGCTCTCCGAGCGC 693

QY 164 GTGCTCTACTACTACGAGTCCGCTGGCGGCTGGCGGCGCGCGCGCGCGCTCGAC 223
   || || || || || || || || || || || || || || || || || || || ||
Db 694 CAGGACTTCTACGGCGGACCTCAAGGACGCGTCCGCGGACCGCGCGCGCGAGAG 753

QY 224 GTCTTCTGT 232
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Db 754 GTCCTCGTG 762

RESULT 12
US-08-510-646B-2
; Sequence 2, Application US/08510646B
; Patent No. 6077699
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,646B
; FILING DATE: 03-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,852
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: S.pristinaespiralis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1268
; US-08-510-646B-2

Query Match          16.7%; Score 41.8; DB 3; Length 1268;
Best Local Similarity 51.3%; Pred. No. 0.33;
Matches 97; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 44 GCGCGCACGCTGGCGCGCTTCCCGGACACTCTGCTAGGGAGACCCAGCGCGCGCGCGC 103
   || || || || || || || || || || || || || || || || || || || ||
Db 574 GCGCGCGCGCGCGCGCGCGCGCTCATCATCCAGCGCGCGCTCTCGCGGTGGGACGC 633

QY 104 TTCTAGACAGCGCGCGCGCGAGTATTTCTTTCAGCGGACCGCGCGCGCGCTTCGAGCGC 163
   || || || || || || || || || || || || || || || || || || || ||
Db 634 GAGTTGCGCGCGCGCGCGAGTATTTTACCGCGGACCAACCGGCTCTCCGAGCGC 693

QY 164 GTGCTCTACTACTACGAGTCCGCTGGCGGCTGGCGGCGCGCGCGCGCTCGAC 223
   || || || || || || || || || || || || || || || || || || || ||
Db 694 CAGGACTTCTACGGCGGACCTCAAGGACGCGTCCGCGGACCGCGCGCGAGAG 753

QY 224 GTCTTCTGT 232
   || || || ||
Db 754 GTCCTCGTG 762

RESULT 13
US-09-231-818-2
; Sequence 2, Application US/09231818
; Patent No. 6171846
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
```

APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,818
FILING DATE: 10-MAY-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1268 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: S.pristinaespiralis
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1268
US-09-231-818-2

Query Match 16.7%; Score 41.8; DB 4; Length 1268;
Best Local Similarity 51.3%; Pred. No. 0.33;
Matches 97; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
QY 44 GCGCGCACGCTGGCGCGCTCCCGGACACTCTGCTAGGGACCCAGCGCGCGCGCGCG 103
Db 574 GCG 633
QY 104 TTCTAGCAGCAGCGCGCGCGCGCGAGTATTTCTTCGACCGGCACCGCGCGCGCGCG 163
Db 634 GAGTTCCG 693
QY 164 GTGCTCTACTACTACGAGTCCGGTGGCGGCTGCGGCGCGCGCGCGCGCGCGCG 223
Db 694 CAGGACTTCTAGGGCAGCTCAAGGACACGCGTCCGCGCGCGCGCGCGCGCGG 753
QY 224 GTCTTCTG 232
Db 754 GTCTCTGTG 762

RESULT 14
US-08-403-852D-1
Sequence 1, Application US/08403852D
Patent No. 5891695
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5392 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: S.pristinaespiralis
US-08-403-852D-1

Query Match 16.7%; Score 41.8; DB 2; Length 5392;
Best Local Similarity 51.3%; Pred. No. 0.32;
Matches 97; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
QY 44 GCGCGCACGCTGGCGCGCTCCCGGACACTCTGCTAGGGACCCAGCGCGCGCGCGCG 103
Db 621 GCG 680
QY 104 TTCTAGCAGCAGCGCGCGCGCGAGTATTTCTTCGACCGGCACCGCGCGCGCGCG 163
Db 681 GAGTTCCG 740
QY 164 GTGCTCTACTACTACTACGAGTCCGGTGGCGGCTGCGGCGCGCGCGCGCGCG 223

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 19, 2003, 23:59:06 ; Search time 59.8275 Seconds
(without alignments)
9410.374 Million cell updates/sec

Title: US-09-804-014A-7_COPY_382_631

Perfect score: 250

Sequence: 1 gcggctggtgctcaacgctgg.....tggaagaggtgctctctac 250

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
- 3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
- 4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
- 5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
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- 8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
- 9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
- 10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
- 11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
- 12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
- 13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
- 14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
- 15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
- 16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
- 17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
- 18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
- 19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
- 20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
- 21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
- 22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	250	100.0	1341	ABL57038	Human potassium ch
2	250	100.0	1686	AAS78540	DNA encoding novel
3	250	100.0	1747	AAS13338	Human cDNA encodin
4	250	100.0	1792	AAD37899	Human ion channel
5	213.2	85.3	1598	AAT04953	Mouse Kv1.7 voltag
6	175.4	70.2	994	ABQ19702	Oligonucleotide fo
7	175.4	70.2	994	ABQ19703	Oligonucleotide fo
8	168.4	67.4	994	ABQ19704	Oligonucleotide fo
9	168.4	67.4	994	ABQ19705	Oligonucleotide fo

10	133.4	53.4	2867	24	ABN95856	Gene #2354 used to
11	133.4	53.4	2867	24	ABL65917	Lung cancer relate
12	125.2	50.1	3147	24	AB199654	Mouse ischaemic co
13	119	47.6	1836	22	AAH21452	Human Kv1.5 DNA..
c 14	100.2	40.1	1521	24	ABQ49288	Oligonucleotide fo
15	100.2	40.1	1521	24	ABQ49289	Oligonucleotide fo
c 16	100.2	40.1	7642	24	ABL33117	Human immune syste
c 17	92.2	36.9	7488	24	ABL33113	Human immune syste
c 18	91.8	36.7	701	24	ABQ16958	Oligonucleotide fo
c 19	91.8	36.7	701	24	ABQ16959	Oligonucleotide fo
c 20	91.8	36.7	8758	24	ABL33119	Human immune syste
21	81.4	32.6	2237	23	ABL13285	Drosophila melanog
22	78	31.2	2033	22	AAH21248	Human KCND1 exon1
23	78	31.2	2578	22	AAH99538	Human protein enco
24	78	31.2	2711	22	AAH21246	Human Kv4.1 cDNA..
25	78	31.2	3424	20	AAZ11901	Human potassium ch
26	74	29.6	2064	24	ABN84401	Human Kv4.3 potass
27	74	29.6	2072	19	AAV61572	Human Kv potassium
28	74	29.6	2104	19	AAV61571	Human Kv potassium
29	74	29.6	2121	24	ABN84400	Human Kv4.3 potass
30	72.4	29.0	2104	19	AAV61573	Human Kv potassium
31	71.4	28.6	1521	24	ABQ49286	Oligonucleotide fo
c 32	71.4	28.6	1521	24	ABQ49287	Oligonucleotide fo
33	71.4	28.6	7642	24	ABL33116	Human immune syste
34	69.2	27.7	7488	24	ABL33112	Human immune syste
35	67.4	27.0	1716	23	ABL29811	Drosophila melanog
36	66.8	26.7	701	24	ABQ16960	Oligonucleotide fo
c 37	66.8	26.7	701	24	ABQ16961	Oligonucleotide fo
38	66.8	26.7	8758	24	ABL33118	Human immune syste
c 39	66.2	26.5	18028	23	ABL13284	Drosophila melanog
40	65.6	26.2	1927	20	AAZ11898	Human potassium ch
41	62.4	25.0	3174	23	AAS64788	DNA encoding novel
42	54.2	21.7	612	22	ABA76453	Human foetal liver
43	54.2	21.7	612	22	ABA40984	Probe #19450 for g
44	54.2	21.7	612	22	AAK25090	Human brain expres
45	54.2	21.7	612	22	AAK51097	Human bone marrow

ALIGNMENTS

RESULT 1
ABL57038
ID ABL57038 standard; cDNA; 1341 bp.
XX
AC ABL57038;
XX
DT 22-JUL-2002 (first entry)
XX
DE Human potassium channel 12189 partial cDNA.
XX
KW Potassium channel; ion transport; 12189; nootropic; anticonvulsant;
KW neuroprotective; antiparkinsonian; hypotensive; neuroleptic;
KW antidepressant; antimanic; tranquilizer; anorectic; antiemgraine;
KW antiarteriosclerotic; vasotropic; vulnerary; antiarrhythmic;
KW cardiant; antinflammatory; cytostatic; osteopathic; hepatotropic;
KW antidiabetic; immunosuppressive; antiarthritic; antirheumatic;
KW antipsoriatic; antithyroid; antilucer; dermatological; antianaemic;
KW antiasthmatic; antiallergic; ophthalmological; immunomodulator;
KW analgesic; virucide; human; gene therapy; gene; ss.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT CDS 1..1341
FT /tag= a
FT /product= "12189"
FT /partial
FT /note= "The CDS does not include a start codon"
XX
PN WO200194390-A2.
XX
PD 13-DEC-2001.

CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1686 BP; 236 A; 545 C; 562 G; 343 T; 0 other;

Query Match 100.0%; Score 250; DB 23; Length 1686;
Best Local Similarity 100.0%; Pred. No. 3.3e-45;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTGGTGCTCAACGTGGCGGGCTGGCTTCGAGAGCGGGCGCGACGCTGGCGG 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
417 GCGGCTGGTGCTCAACGTGGCGGGCTGGCTTCGAGAGCGGGCGCGACGCTGGCGG 476
QY 61 CTTCCCGGACACTCTGCTAGGGGACCCAGCGCGCGCGCGCTTCTACGACGCGCGG 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
477 CTTCCCGGACACTCTGCTAGGGGACCCAGCGCGCGCGCGCTTCTACGACGCGCGG 536
QY 121 CGCGAGATTTCTTCGACCGCGACCGGCCAGCTTCGAGCGCGCGCTACTACTACCA 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
537 CGCGAGATTTCTTCGACCGCGACCGGCCAGCTTCGAGCGCGCGCTACTACTACCA 596
QY 181 GTCGGGTGGCGGCTGCGCGCGCGCGCACGTCGCGCGCTTCCTCGAAGAGGT 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
597 GTCGGGTGGCGGCTGCGCGCGCGCGCACGTCGCGCGCTTCCTCGAAGAGGT 656
QY 241 GGCCTTCTAC 250
Db ||||||||
657 GGCCTTCTAC 666

RESULT 3
AAS13338
ID AAS13338 standard; cDNA; 1747 BP.
AC AAS13338;
XX
DT 18-DEC-2001 (first entry)
DE Human cDNA encoding NOV4 protein.
XX
KW Human; NOV4; ss; cytostatic; nontropic; neuroprotective; vulnary;
KW cerebroprotective; antiparkinsonian; hypotensive; antiasthmatic;
KW antidiabetic; antipsoriatic; antiinflammatory; immunosuppressive;
KW antiatherosclerotic; dermatological; cancer; neurological disorder;
KW parkinson's disease; diabetes mellitus; asthma; enamel defect;
KW immune disorder; autoimmune disease; respiratory disorder;
KW bone disorder; musculoskeletal disorders; leukaemia; lymphoma;
KW cell growth regulation disorder; lesional psoriatic skin;
KW atherosclerosis; abdominal aortic aneurysm.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..37
FT /*tag= a
FT CDS 38..1717
FT /*tag= b
FT /*product= "NOV4"
FT 3'UTR 1718..1747
FT /*tag= c
XX
PN WO200168851-A2.
XX
XX
PD 20-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-US07735.

XX
PR 10-MAR-2000; 2000US-0188277.
PR 10-MAR-2000; 2000US-0188316.
PR 14-MAR-2000; 2000US-0189139.
PR 14-MAR-2000; 2000US-0189140.
PR 17-MAR-2000; 2000US-0190231.
PR 17-MAR-2000; 2000US-0190401.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Vernet CAM, Fernandes E, Shinkets RA, Spaderna SK;
PI Majumder K, Li L;
XX
DR WPI; 2001-570869/64.
DR P-PSDB; AAU08660.
XX
PT Novel polypeptides and nucleic acids homologous to members of collagen,
PT potassium channel, tuftelin family of proteins for diagnosing, treating
PT cancer, atherosclerosis, neurological, skin and enamel defect disorders
PT
XX
PS Claim 9; Page 15-16; 128pp; English.
XX
CC The invention relates to isolated NOVX (NOVX1-11) polypeptides and
CC the polynucleotides that encode them. NOVX polypeptides, polynucleotides
CC and anti-NOVX antibodies are useful for treating or preventing a
CC pathology associated with NOVX polypeptide in humans and for treating a
CC syndrome associated with human disease e.g. disorders characterised by
CC altered cell motility, proliferation and migration e.g. cancer, e.g.
CC angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.
CC episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's
CC disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,
CC asthma, hypertension and seizure (NOV4), enamel defects, such as
CC amelogenesis imperfecta and disorders involving enamel defects,
CC including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic
CC neurological disorders, e.g. paraneoplastic limbic of brain-stem
CC encephalitis occurring during testicular cancer, diabetes, reproductive
CC health, metabolic and endocrine disorders, gastrointestinal disorders,
CC immune disorders and autoimmune diseases, respiratory disorders, bone
CC disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell
CC growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and
CC atherosclerosis, abdominal aortic aneurysm and neurological disorders
CC (NOV11). NOVX polypeptide is also useful for identifying an agent that
CC binds to it and a cell expressing NOVX polypeptide is useful for
CC identifying a therapeutic agent for use in treatment of a NOVX related
CC pathology. The antibodies and a polypeptide having 95% sequence identity
CC to NOVX polypeptide are useful for treating a pathological state in a
CC mammal. The present sequence encodes NOV4, a possible voltage gated
CC potassium channel.
XX
SQ Sequence 1747 BP; 255 A; 582 C; 575 G; 335 T; 0 other;

Query Match 100.0%; Score 250; DB 22; Length 1747;
Best Local Similarity 100.0%; Pred. No. 3.3e-45;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTGGTGCTCAACGTGGCGGGCTGGCTTCGAGAGCGGGCGCGACGCTGGCGG 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
382 GCGGCTGGTGCTCAACGTGGCGGGCTGGCTTCGAGAGCGGGCGCGACGCTGGCGG 441
QY 61 CTTCCCGGACACTCTGCTAGGGGACCCAGCGCGCGCGCGCTTCTACGACGACGCGG 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
442 CTTCCCGGACACTCTGCTAGGGGACCCAGCGCGCGCGCGCTTCTACGACGACGCGG 501
QY 121 CGCGAGATTTCTTCGACCGCGACCGGGCCAGCTTCGAGCGCGCGCTCTACTACTACCA 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
502 CGCGAGATTTCTTCGACCGCGACCGGGCCAGCTTCGAGCGCGCTCTACTACTACCA 561
QY 181 GTCGGGTGGCGGCTGCGCGCGCGCGCACGTCGCGCTCGAGCTTCTCTGGAAGAGGT 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
562 GTCGGGTGGCGGCTGCGCGCGCGCGCACGTCGCGCTCGAGCTTCTCTGGAAGAGGT 621
QY 241 GGCCTTCTAC 250

CC therefore, modulate insulin secretion. Selective antagonists
CC increase insulin release and thereby reduce hyperglycaemia
CC associated with non-insulin-dependent diabetes mellitus.
XX
SQ Sequence 1598 BP; 232 A; 521 C; 502 G; 343 T; 0 other;
0;
Query Match 85.3%; Score 213.2; DB 16; Length 1598;
Best Local Similarity 90.8%; Pred. No. 2.7e-37;
Matches 227; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 GGGGCTGGTCAAGTCGCGGCTGCGCTTCGAGACGCGGCGCACGCTGGGCG 60
DB 273 GGGCTGGTGTCAAGTCGCGGCTGCGCTTCGAGACGCGGCGCACGCTGGGCG 332
QY 61 CTTCCCGGACACTCTGCTAGGGACCCAGCGCGCGCGCGCTTACGACGACGCGG 120
DB 333 CTTCCCGGACACTCTGCTAGGGACCCGCTGCGCGCACGCGCTTACGACGCGG 392
QY 121 CCAGAGTATTTCTTCGACCGGACCGGCCAGCTTCGAGCGCGGCTCTACTACTACCA 180
DB 393 CGCGGAGTATTTCTTCGACCGACACCGGCCAGCTTCGATGCGGTGCTCTACTACTACCA 452
QY 181 GTCGGTGGCGGCTGCGCGCGCGCGCACGCTGCGGCTTCGAGTCTTCTGGAAGGT 240
DB 453 GTCGGGCGCGGCTGAGACGCGCGCGCACGCTGCGGCTTCGAGTCTTCTGGAAGGT 512
QY 241 GGCCTTCTAC 250
DB 513 GTCCTTCTAC 522
RESULT 6
ABQ19702/c
ID ABQ19702 standard; DNA; 994 BP.
XX
AC ABQ19702;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 6293.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic

CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 994 BP; 129 A; 152 C; 354 G; 359 T; 0 other;
0;
Query Match 70.2%; Score 175.4; DB 24; Length 994;
Best Local Similarity 81.5%; Pred. No. 3.7e-29;
Matches 203; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 2 CGGCTGGTGTCAAGTCGCGGCTGCGCTTCGAGACGCGGCGCGCTTACGACGCGCGC 61
DB 534 CGACTAATACTCAACGTAACCGAACTACGCTTCGAAACGGAACGCGCTAAACCGC 475
QY 62 TTCCCGGACACTCTGCTAGGGACCCAGCGCGCGCGCGCTTACGACGACGCGCGC 121
DB 474 TTCCCGAACACTCTACTAAAAACCCAGCGCGCGCGCTTCTACGACGACGCGCGC 415
QY 122 CGCGAGTATTTCTTCGACCGGACCGCGCGCGCTTCGACGCGCTGCTCTACTACTACAG 181
DB 414 CGGGAATATTTCTTCGACCGACACCGACCCAACTTCGACGCCCTCTCTACTACTACCA 355
QY 182 TCGGTGGCGGCTGCGCGCGCGCGCACGCTGCGCGCTCTCTCTCTCTCTCTCTCTCTCT 241
DB 354 TCCGATAAACGACTACGACGACGCGCGCGCGCTACCGCTTCCTCTCTCTCTCTCTCTCT 295
QY 242 GCTTCTAC 250
DB 294 ACCTTCTAC 286
RESULT 7
ABQ19703
ID ABQ19703 standard; DNA; 994 BP.
XX
AC ABQ19703;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 6294.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP10074.
PR 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX WPI; 2002-371829/40.
XX
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
XX Sequence 994 BP; 359 A; 354 G; 152 G; 129 T; 0 other;
SQ
Query Match 70.2%; Score 175.4; DB 24; Length 994;
Best Local Similarity 81.5%; Pred. No. 3.7e-29;
Matches 203; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 2 CGCGTGGTCTCAACGTGGCGGGTGGCGTTCGAGACGGCGGCGCAGCGTGGGCGCG 61
Db 461 CGACTAATATCTCAACGTAAACCACTACGCTTCGAACGCGAAGCGCGCACTAAACCGC 520
QY 62 TTCGCGGACACTCTGCTAGGGAGCCAGCGCGCGCGGCGCTTCTACGACGACGCGCGC 121
Db 521 TTCGCGGACACTCTACTAAAAACCCAGCGCGCGCGCGCTTCTACGACGACGCGCGC 580
QY 122 CGCGAGTATTTCTTCGACCGCCAGCGCGCGCGCTTCGACCGCGTCTACTACTACCAG 181
Db 581 CGCGAATATTTCTTCGACCGCACACCGACCACTTCGACCGCTACTCTACTACTACCA 640
QY 182 TCGGTTGGCGGCTGGCGGCGCGCGCGCGCGCTCGCGCTTCCTTGGGAAGAGTG 241
Db 641 TCGGATAAACGACTACGACGACGCGCGCGCGCTACCGCTCGACGCTTCTCTTAAAAAATA 700
QY 242 GCCTTCTAC 250
Db 701 ACCTTCTAC 709
RESULT 8
ABQ19704
ID ABQ19704 standard; DNA; 994 BP.
XX
XX
AC ABQ19704;
XX
XX
DT 12-JUL-2002 (first entry)
XX
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 6295.
DE
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
XX Homo sapiens.
OS

XX WO200218632-A2.
XX
XX
PD 07-MAR-2002.
XX
XX
PF 01-SEP-2001; 2001WO-EP10074.
XX
XX
PR 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI
XX WPI; 2002-371829/40.
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
XX Sequence 994 BP; 131 A; 152 C; 380 G; 331 T; 0 other;
SQ
Query Match 67.4%; Score 168.4; DB 24; Length 994;
Best Local Similarity 79.6%; Pred. No. 1.2e-27;
Matches 199; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 1 GCGGCTGGTCTCAACGTGGCGGGTGGCGTTCGAGACGGCGGCGCAGCGTGGGCGCG 60
Db 460 GCGGTTGGTCTTTAAACGTGGTGGTTCGAGACGGCGGCGCGTACGTTGGGTGCG 519
QY 61 CTTCGCGGACACTCTCTAGGGAGCCAGCGCGCGCGCGCTTCTACGACGACGCGCG 120
Db 520 TTTTTCGAGATATTTTGTAGGGATTTAGCGCGCTGCGGCGTCTTTTACGACGCGCG 579
QY 121 CCGCGAGTATTTCTTCGACCGCGACCGCGCGCGCTTCGACCGCGTCTACTACTACCA 180
Db 580 TCCGAGATATTTTTCGATCCGATCCGTTAGTTAGTTTCGACGCTCGTGTATTATTATTA 639
QY 181 GTCCGTTGGCGGCTGGCGGCGCGCGCGCGCTGCGCGCTTCCTTGGGAAGAGGT 240
Db 640 GTTCGTTGGCGGCTGGCGGCGGTCGCGGTACGTGCTGCTTCGACGCTTTTGTGGAAGAGGT 699
QY 241 GCCTTCTAC 250
Db 700 GGTTTTCTAC 709
RESULT 9
ABQ19705/c
ID ABQ19705 standard; DNA; 994 BP.


```
QY 72 CTCTGCTAGGGACCCAGCGCGCGCGCTTCTACGACGACGGCGCGCGCGAGTATT 131
Db 659 CACTCTGGGGACCCGCGCGCTGCTGCTACTTTCGACCCCGCTGAGGAGGAGTACT 718
QY 132 TCTTCGACGGGACCGCGCGCGCTTCTACGACGCGTCTCTACTACTACCGTGGG 191
Db 719 TCTTCGACCGCAACCGCGCGCGCTTCTACTACTACTACTACTACTACTACTACT 778
QY 192 GGCTGGCGGCGCGCGCGCGCTGCGCGCTGCGCGCTTCTTCGAGAGGTTGGCTTCTAC 250
Db 779 GCCTGGGAGCGCGGTCAACGCTCCCTGCGAGGTGTCGCGGAGAGATACGCTTCTAC 837

RESULT 11
ABL65917
ID ABL65917 standard; DNA: 2867 BP.
XX
AC ABL65917;
XX
DT 15-MAY-2002 (first entry)
XX
DE Lung cancer related gene sequence SEQ ID NO:4254.
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
XX 13-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US10838.
XX
XX 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 22-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 25-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
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PR 01-NOV-2000; 2000US-245084P.
XX
XX (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX WPI; 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX
XX Claim 1; SEQ ID 4254; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.
XX
XX Sequence 2867 BP; 565 A; 839 C; 845 G; 618 T; 0 other;
SQ
Query Match 53.4%; Score 133.4; DB 24; Length 2867;
Best Local Similarity 72.4%; Pred. No. 3.8e-20;
Matches 173; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 12 TCAACGTGGCGGGCTGCGCTTCGAGACGCGGGCGGCGACGCTGGCGCGTTCGCCGACA 71
Db 599 TCAACATCTCCGGCTTTCGAGACGAGCTGGGACCCAGCGCACTTCCCAACA 658
QY 72 CTCTGCTAGGGACCCAGCGCGCGCGCTTCTACGACGACGGCGCGCGGAGTATT 131
Db 659 CACTCTGGGGACCCGCGCGCTGCGCTACTTTCGACCCCGCTGAGGAGGAGTACT 718
QY 132 TCTTCGACCGGACCGCGCGCGCTTTCGACGCGCTTCTACTACTACTACTACTACTACT 191
Db 719 TCTTCGACCGCAACCGCGCGCGCTTTCGAGGTATCTCTACTACTACTACTACTACTACT 778
QY 192 GGCTGGCGGCGCGCGCGCGCTGCGCGCTGCGCGCTTCTTCGAGAGGTTGGCTTCTAC 250
Db 779 GCCTGGGAGCGCGGTCAACGCTCCCTGCGAGGTGTCGCGGAGAGATACGCTTCTAC 837

RESULT 12
ABI99654
ID ABI99654 standard; cDNA; 3147 BP.
XX
XX ABI99654;
AC
XX
XX 07-MAR-2002 (first entry)
XX
XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:683.
DE
XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX
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DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 35879.
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
XX WO200218632-A2.
XX
XX 07-MAR-2002.
XX
XX 01-SEP-2001; 2001WO-EP10074.
XX
XX 01-SEP-2000; 2000DE-1043826.
PR
XX 05-SEP-2000; 2000DE-1044543.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
DR
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
XX the disclosure of the invention.
XX
SQ Sequence 1521 BP; 220 A; 179 C; 533 G; 589 T; 0 other;
Query Match 40.1%; Score 100.2; DB 24; Length 1521;
Best Local Similarity 62.7%; Pred. No. 5.3e-13;
Matches 156; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 2 CGGCTGGTGTCAACGTGGCGGCGTTCGAGACGCGGGCGCGACGCTGGGCGCG 61
DB 700 CGGCTAATCATCAACATCTCCGAACTACGCTTCGAACGCACTAAACCCCTTTACCAA 641
QY 62 TTCCCGGACACTCTGTAGGGGACCGAGCGCGCGCGCGGCGCTTCACGACGCGCGCG 121
DB 640 TTCCCGGAAACGCTACTAAACGACCCCAACGACGACGATAAATACCTTCGACCGCTCCG 581
QY 122 CGGAGTATTTCTTCGACGGGACCGCGGCGCTTCGACCGCTGCTCTACTACTACCAG 181
DB 580 AAGCAATATCTTCTGACCGCAACACGACCACTTCGAGCCACTCTCTACTATCA 521
QY 182 TCCGGTGGGCGGCTGGCGGCGCGGCGACGCTGCGCTGACGCTCTTCCTGGAAGAGTG 241
DB 520 TCCGAAACCGCATCCGCGGACCGGATCAAGGTACCCATCGACATTTTCTCCGAAATATC 461

QY 242 GCCTTCTAC 250
DB 460 CGCTTCTAC 452
RESULT 15
ABQ49289
ID ABQ49289 standard; DNA; 1521 BP.
XX
XX ABQ49289;
XX
XX 12-JUL-2002 (first entry)
XX
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 35880.
DE
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
XX Homo sapiens.
XX
XX WO200218632-A2.
XX
XX 07-MAR-2002.
XX
XX 01-SEP-2001; 2001WO-EP10074.
XX
XX 01-SEP-2000; 2000DE-1043826.
PR
XX 05-SEP-2000; 2000DE-1044543.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
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PT for diagnosis and prognosis, comprises selective hybridization of
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XX
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CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
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XX
SQ Sequence 1521 BP; 589 A; 533 C; 179 G; 220 T; 0 other;
Query Match 40.1%; Score 100.2; DB 24; Length 1521;
Best Local Similarity 62.7%; Pred. No. 5.3e-13;
Matches 156; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 2 CGGCTGGTGTCAACGTGGCGGCGTTCGAGACGCGGGCGCGACGCTGGGCGCG 61
DB 822 CGGCTAATCATCAACATCTCCGAACTACGCTTCGAACGCACTAAACCCCTTTACCAA 881

